

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 37110/030019
J014 Rec'd PCT/PTO 26 DEC 2001

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

10/030019

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/BE00/00077

DEC 26 2001

July 3, 2000

July 1, 1999

TITLE OF INVENTION

CELL DEATH RELATED DRUG TARGET IN YEAST AND FUNGI

APPLICANT(S) FOR DO/EO/US

Contreras, Roland Henri

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☐ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371 (c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☒ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: Copy of the International Preliminary Examination Report; Copy of the International Search Report; Express Mail Certificate; Sequence Disk; Sequence Listing; Version to Show Changes Made; Preliminary Amendment; Letter to Correct Name of Inventor from Isabelle Karin Luc Malcorps to Isabelle Karin Pieter Lenaerts, and 4 figures (Fig 1 1-93; Fig 2 94-157, Fig 3 158-159, Fig 4 160-161)

10/030018

PCT/BE00/00077

531 Rec'd PCT 1000000-19 JAB-1521 26 DEC 2001

17. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) (5)):

Neither international preliminary examination fee (37 CFR 1.482)
nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO
and International Search Report not prepared by the EPO or JPO.....\$1040.00

International preliminary examination fee (37 CFR 1.482) not paid to
USPTO but International Search Report prepared by the EPO or JPO.....\$890.00

International preliminary examination fee (37 CFR 1.482) not paid to
USPTO but international search fee (37 CFR 1.455(a)(2)) paid to USPTO..... \$740.00

International preliminary examination fee (37 CFR 1.482) paid to
USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4)..... \$750.00

International preliminary examination fee (37 CFR 1.482) paid to
USPTO and all claims satisfied provisions of PCT Article 33(1)-(4)..... \$100.00

ENTER APPROPRIATE BASIC FEE AMOUNT =

\$ 1,040.00

Surcharge of \$130.00 for furnishing the oath or declaration later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(e)).

\$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	
Total claims	54 - 20 =	34	x \$18.00	\$ 612.00
Independent claims	45 - 3 =	42	x \$84.00	\$ 3528.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$280.00	\$

TOTAL OF ABOVE CALCULATIONS =

\$4140.00

Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement
must also be filed (Note 37 CFR 1.9, 1.27, 1.28).

+

SUBTOTAL =

\$

Processing fee of \$130.00 for furnishing the English translation later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

TOTAL NATIONAL FEE =

\$

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property

\$40.00

TOTAL FEES ENCLOSED =

\$5220.00

Amount to be
refunded:

\$

charged:

\$5220.00

a. ☐ A check in the amount of \$_____ to cover the above fees is enclosed.

b. ☒ Please charge my Deposit Account No. 10-0750/JAB-1521/MHM in the amount of \$5220.00 to cover the above fees.
A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any
overpayment to Deposit Account No. 10-0750/JAB-1521/MHM. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137 (a)
or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Philip S. Johnson, Esq.
Johnson & Johnson
One Johnson & Johnson Plaza
New Brunswick, NJ 08933-7003
USA

Signature

Myra H. McCormack
Reg. No. 36,602
Attorney for Applicants

10/030019
531 Rec'd
26 DEC 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Masure, et al.

Serial No. : UNKNOWN

Art Unit: UNKNOWN

Filed : HEREWITH

Examiner: UNKNOWN

For : Cell Death Related Drug Targets In Yeast
and Fungi

I hereby certify that this correspondence is being deposited with the
United States Postal Service as first class mail in an envelope addressed
to: Commissioner for Patents, Washington, D.C. 20231 on

December 26, 2001

(Date)

Myra H. McCormack

Name of applicant, assignee, or Registered Representative

Myra H. McCormack
(Signature)

December 26, 2001

(Date of Signature)

Hon. Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Dear Sir:

Prior to the examination of the above-referenced
application, kindly amend the application as follows:

IN THE CLAIMS

Kindly cancel claim 48

Kindly amend the following claims:

1. (Amended) An isolated nucleic acid molecule
encoding a polypeptide wherein the nucleic acid
sequence of the nucleic acid molecule is selected
from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOS 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90%

similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97%

identical to any of the amino acid sequences shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOS 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91,

93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
 113, 115, 117, 119, 121, 123, 125, 127, 129,
 131, 133, 135, 137, 139, 141, 143, 145, 147,
 149, 151, 153, 155, 157, 159, 161, 163, 165,
 167, 169, 171, 173, 175, 177, 179, 181, 183,
 185, 187, 189, 191, 193, 195, 197, 199, 201,
 203, 205, 207, 209, 211, 213, 215, 217, 219,
 221, 223, 225, 227, 229, 231, 233, 235, 237,
 239, 241, 243, 245, 247, 249, 251, 253, 255,
 257, 259, 261, 263, 265, 267, 269, 271, 273,
 275, 277, 279, 281, 283, 285, 287, 289, 291,
 293, 295, 297, 299, 301, 303, 305, 307, 309,
 311, 313, 315, 317, 319, 321, 323, 325, 327,
 329, 331, 333, 335, 337, 339, 341, 343, 345,
 347, 349, 351, 353, 355, 357, 359, 361, 363,
 365, 367, 369, 371, 373, 375, 377, 379, 381,
 383, 385, 387, 389, 391, 393, 395, 397, 399,
 401, 403, 405, 407, 409, 411, 413, 415, 417,
 419, 421, 423, 425, 427, 429, 431, 433, 435,
 437, 439, 441, 443, 445, 447, 449, 451, 453,
 455, 457, 459, 461, 463, 465, 467, 469, 471,
 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139,

for the preparation of a medicament for treating diseases associated with yeast or fungi.

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,

76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,
 98, 100, 102, 104, 106, 108, 110, 112, 114,
 116, 118, 120, 122, 124, 126, 128, 130, 132,
 134, 136, 138, 140, 142, 144, 146, 148, 150,
 152, 154, 156, 158, 160, 162, 164, 166, 168,
 170, 172, 174, 176, 178, 180, 182, 184, 186,
 188, 190, 192, 194, 196, 198, 200, 202, 204,
 206, 208, 210, 212, 214, 216, 218, 220, 222,
 224, 226, 228, 230, 232, 234, 236, 238, 240,
 242, 244, 246, 248, 250, 252, 254, 256, 258,
 260, 262, 264, 266, 268, 270, 272, 274, 276,
 278, 280, 282, 284, 286, 288, 290, 292, 294,
 296, 298, 300, 302, 304, 306, 308, 310, 312,
 314, 316, 318, 320, 322, 324, 326, 328, 330,
 332, 334, 336, 338, 340, 342, 344, 346, 348,
 350, 352, 354, 356, 358, 360, 362, 364, 366,
 368, 370, 372, 374, 376, 378, 380, 382, 384,
 386, 388, 390, 392, 394, 396, 398, 400, 402,
 404, 406, 408, 410, 412, 414, 416, 418, 420,
 422, 424, 426, 428, 430, 432, 434, 436, 438,
 440, 442, 444, 446, 448, 450, 452, 454, 456,
 458, 460, 462, 464, 466, 468, 470, 472, 474,
 476, 478, 480, 482, or 484, or encoding a
 functional equivalent, derivative or
 bioprecursor of said protein;

- (b) a protein having an amino acid sequence
 which is more than 70% similar, preferably
 more than 80% similar, more preferably more
 than 90% similar and most preferably more than
 97% similar to any of the amino acid sequences
 shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14,
 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,
 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58,
 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80,

82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
 104, 106, 108, 110, 112, 114, 116, 118, 120,
 122, 124, 126, 128, 130, 132, 134, 136, 138,
 140, 142, 144, 146, 148, 150, 152, 154, 156,
 158, 160, 162, 164, 166, 168, 170, 172, 174,
 176, 178, 180, 182, 184, 186, 188, 190, 192,
 194, 196, 198, 200, 202, 204, 206, 208, 210,
 212, 214, 216, 218, 220, 222, 224, 226, 228,
 230, 232, 234, 236, 238, 240, 242, 244, 246,
 248, 250, 252, 254, 256, 258, 260, 262, 264,
 266, 268, 270, 272, 274, 276, 278, 280, 282,
 284, 286, 288, 290, 292, 294, 296, 298, 300,
 302, 304, 306, 308, 310, 312, 314, 316, 318,
 320, 322, 324, 326, 328, 330, 332, 334, 336,
 338, 340, 342, 344, 346, 348, 350, 352, 354,
 356, 358, 360, 362, 364, 366, 368, 370, 372,
 374, 376, 378, 380, 382, 384, 386, 388, 390,
 392, 394, 396, 398, 400, 402, 404, 406, 408,
 410, 412, 414, 416, 418, 420, 422, 424, 426,
 428, 430, 432, 434, 436, 438, 440, 442, 444,
 446, 448, 450, 452, 454, 456, 458, 460, 462,
 464, 466, 468, 470, 472, 474, 476, 478, 480,
 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116,

118, 120, 122, 124, 126, 128, 130, 132, 134,
136, 138, 140, 142, 144, 146, 148, 150, 152,
154, 156, 158, 160, 162, 164, 166, 168, 170,
172, 174, 176, 178, 180, 182, 184, 186, 188,
190, 192, 194, 196, 198, 200, 202, 204, 206,
208, 210, 212, 214, 216, 218, 220, 222, 224,
226, 228, 230, 232, 234, 236, 238, 240, 242,
244, 246, 248, 250, 252, 254, 256, 258, 260,
262, 264, 266, 268, 270, 272, 274, 276, 278,
280, 282, 284, 286, 288, 290, 292, 294, 296,
298, 300, 302, 304, 306, 308, 310, 312, 314,
316, 318, 320, 322, 324, 326, 328, 330, 332,
334, 336, 338, 340, 342, 344, 346, 348, 350,
352, 354, 356, 358, 360, 362, 364, 366, 368,
370, 372, 374, 376, 378, 380, 382, 384, 386,
388, 390, 392, 394, 396, 398, 400, 402, 404,
406, 408, 410, 412, 414, 416, 418, 420, 422,
424, 426, 428, 430, 432, 434, 436, 438, 440,
442, 444, 446, 448, 450, 452, 454, 456, 458,
460, 462, 464, 466, 468, 470, 472, 474, 476,
478, 480, 482, or 484; or a functional
fragment thereof

for the preparation of a medicament for treating diseases associated with yeast or fungi.

10. (Amended) A yeast or fungus comprising the nucleic acid of claim 1 wherein the yeast or fungus is selected from the group consisting of *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

11. (Amended) A compound identifiable according to the method of claim 6.

12. (Amended) A medicament comprising the compound according to claim 11.

13. (Amended) A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a medicament according to claim 12 with a suitable pharmaceutically acceptable carrier.

14. (Amended) A method for treating a yeast or fungal infection in a subject comprising the step of administering a compound according to claim 11.

15. (Amended) A method for modifying the endogenic flora of humans and other mammals comprising the step of administering a compound according to claim 11.

16. (Amended) The method of claim 14 wherein the yeast or fungal infection is an infection caused by the yeast or fungi selected from the group consisting of *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

17. (Amended) A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320,

322, 324, 326, 328, 330, 332, 338, 342, 344, 346,
 348, 352, 354, 356, 358, 360, 362, 364, 366, 368,
 370, 372, 374, 376, 380, 382, 384, 386, 388, 390,
 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
 418, 422, 424, 426, 428, 430, 432, 434, 436, 438,
 440, 442, 444, 446, 448, 450, 452, 454, 476, 478,
 480, 482 or 484;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOS 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOS 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; or a functional fragment or complement thereof.

18. (Amended) A nucleic acid according to claim 16 wherein the nucleic acid is derived from *Candida albicans*.

20. (Amended) A nucleic acid sequence according to claim 17 which is mRNA.

21. (Amended) A nucleic acid sequence according to claim 17 which is DNA.

22. (Amended) A nucleic acid sequence according to claim 17 which is cDNA.

23. (Amended) An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to claim 17.

24. (Amended) An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

(a) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; or a functional fragment thereof.

25.(Amended) An expression vector comprising a nucleic acid sequence according to claim 17.

27. (Amended) An expression vector according to claim 25 which comprises a sequence encoding a reporter molecule.
28. (Amended) A host cell transformed, transfected or infected with the vector of claim 25.
29. (Amended) A nucleic acid molecule according to claim 17 for use as a medicament.
33. (Amended) A pharmaceutical composition comprising an antibody according to claim 31.
34. (Amended) A method for treating a yeast or fungal infection comprising the step of administering an antibody according to claim 31, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2.
35. (Amended) The method of claim 34 wherein the fungus is *Candida albicans*.
36. (Amended) A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid probe selectively hybridises with the nucleic acid molecule.
37. (Amended) A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid primer selectively amplifies any of said nucleic acid molecules.

38. (Amended) A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of claim 1 or a human homologue thereof or at least one of the polypeptides of claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

39. (Amended) A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of claim 1 or a human homologue thereof and/or at least one of the polypeptides of claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

41. (Amended) A medicament comprising the compound according to claim 40.

42. (Amended) A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 with a suitable pharmaceutically acceptable carrier.

43. (Amended) A method for for treating proliferative disorders or for preventing apoptosis in comprising administering the compound of claim 40 to a subject in need thereof.

44. (Amended) A method for treating proliferative disorders or for the prevention of apoptosis comprising administering a nucleic acid molecule of claim 1 to a subject in need thereof.

45. (Amended) A method for treating proliferative disorders or for the prevention of apoptosis comprising administering a polypeptide of claim 2 to a subject in need thereof.

46. (Amended) A pharmaceutical composition comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

47. (Amended) A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.

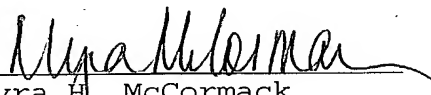
51. (Amended) An expression vector according to claim 49 which comprises a sequence encoding a reporter molecule.

52. (Amended) A host cell transformed, transfected or infected with the vector of claim 49.

REMARKS

Claim 48 has been canceled. Claims 1, 2, 10-18, 20-25, 27-29, 33-39, 41-47, 51 and 52 have been amended to better align them with U.S. Patent practice. The specification has been amended to incorporate the priority information for this Application and to include headings. These changes have been made to the substitute specification that is provided herewith. No new matter was added in incorporating the priority claims and headings. A substitute sequence listing has been provided along with a Computer Readable Form of the Sequence Listing. The undersigned hereby states that the Paper Copy and the Computer Readable Form are identical. No new matter has been added by these amendments. A version to show changes made to the claims accompanies this amendment. Favorable consideration of the remarks provided below is respectfully requested. Should the Examiner have any questions he or she is invited to contact the undersigned at the telephone number provided below.

Respectfully submitted,


Myra H. McCormack
Attorney for Applicants
Reg. No. 36,602

Johnson & Johnson
One Johnson & Johnson Plaza
New Brunswick, NJ 08933-7003
(732) 524-6932
Dated: December 26, 2001

VERSION TO SHOW CHANGES MADE

1. (Amended) An isolated nucleic acid molecule encoding a polypeptide wherein the [Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which] nucleic acid sequence of the nucleic acid molecule is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354,

356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435,

437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; [and]

- (f) or the functional fragment or complement thereof [a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),

- (g) the complement of any of the nucleic acid sequences as specified in a) to f),]

for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. (Amended) An isolated [Use of a] polypeptide which is involved in a pathway [eventually] leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232,

234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,

192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; or a functional fragment thereof [and,

(d) a functional fragment of any of said proteins as defined in a) to c)],
for the preparation of a medicament for treating diseases associated with yeast or fungi.

10. (Amended) A [method according to any of claims 6 to 9 wherein said] yeast or fungus comprising the nucleic acid of claim 1 wherein the yeast or fungus is selected from the group consisting of [is chosen from] *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

11. (Amended) A compound identifiable according to the method of [any of] claim[s] 6 [to 9].

12. (Amended) A medicament comprising the compound according to claim 11 [for use as a medicament].

13. (Amended) A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a [compound] medicament according to claim 12 with a suitable pharmaceutically acceptable carrier.

14. (Amended) A method for treating a yeast or fungal infection in a subject comprising the step of administering [Use of] a compound according to claim 11 [or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi].

15. (Amended) A method for [Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for]

modifying the endogenic flora of humans and other mammals comprising the step of administering a compound according to claim 11.

16. (Amended) The method of claim 14 wherein the yeast or fungal infection is an infection caused by the yeast or fungi selected from the group consisting of [Use of a compound according to claim 12 where the yeast or fungus is chosen from] *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

17. (Amended) A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358,

- 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; or a functional fragment or complement thereof [and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e)].

18. (Amended) A nucleic acid according to claim 16 [characterized in that it is] wherein the nucleic acid is derived from *Candida albicans*.

20. (Amended) A nucleic acid sequence according to [any of] claim 17 [to 19] which is mRNA

21. (Amended) A nucleic acid sequence according to [any of] claim[s] 17 [to 19] which is DNA.

22. (Amended) A nucleic acid sequence according to [any of] claim[s] 17 [to 19] which is cDNA.

- 23.(Amended) An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to [any of] claim[s] 17 [to 22].
24. (Amended) An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
 - (a) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; or a functional fragment thereof [and,]
 - (b) [a functional fragment of any of said proteins as defined in a) to c)]
25. (Amended) An expression vector comprising a nucleic acid sequence according to [any of] claim[s] 17 [to 23] .

27. (Amended) An expression vector according to claim 25 [or 26] which comprises a sequence encoding a reporter molecule.
28. (Amended) A host cell transformed, transfected or infected with the vector of [any of] claim[s] 25 [to 27].
29. (Amended) A nucleic acid molecule according to [any of] claim[s] 17 [to 23] for use as a medicament.
33. (Amended) A pharmaceutical composition comprising an antibody according to claim 31 [or 32].
34. (Amended) A method for treating a yeast or fungal infection comprising the step of administering [Use of] an antibody according to claim 31 [or 32], or an antibody capable of binding to at least one of the polypeptides as defined in claim 2[, for the preparation of a medicament for treating diseases associated with yeast and fungi].
35. (Amended) The [Use of an] method of claim 34 [antibody according to claim 34] wherein the fungus is *Candida albicans*.
36. (Amended) A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid probe [and which] selectively hybridises with the [any of said] nucleic acid molecule[s].
37. (Amended) A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid primer [and which] selectively amplifies any of said nucleic acid molecules.
38. (Amended) A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids [as defined in] of claim 1 or a human homologue thereof or at least one of the polypeptides of [as defined in] claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

39. (Amended) A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of [as defined in] claim 1 or a human homologue thereof and/or at least one of the polypeptides of [as defined in] claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

41. (Amended) A medicament comprising the [A] compound according to claim 40 [for use as a medicament].

42. (Amended) A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 [or 41] with a suitable pharmaceutically acceptable carrier.

43. (Amended) A method for [Use of a compound according to claim 40 or 41 for the preparation of a medicament] for treating proliferative disorders or for preventing apoptosis in [certain disorders] comprising administering the compound of claim 40 to a subject in need thereof.

44. (Amended) A method for [Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for] treating proliferative disorders or for the prevention of apoptosis [in certain diseases] comprising administering a nucleic acid molecule of claim 1 to a subject in need thereof.

45. (Amended) A method for [Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for] treating proliferative disorders or for the prevention of apoptosis [in certain diseases] comprising administering a polypeptide of claim 2 to a subject in need thereof.

46. (Amended) A pharmaceutical composition [for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases] comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

52. (Amended) A host cell transformed, transfected or infected with the vector of [any of] claim[s] 49 [to 51].

10/030019

161/PRTS

531 Rec'd PCT

26 DEC 2001
JAB-T521**CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI****Field of the Invention**

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Background of the Invention

This invention claims priority from International Application Publication No. WO 01/02550 entitled "Cell Death Related Drug Targets in Yeast and Fungi", filed July 3, 2000 which claims priority from EPO Patent Application No. 99870141.1, filed July 1 1999, the contents of which are hereby incorporated by reference.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients.

Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism.

These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

5 Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that
10 such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

 It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997).
15 However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

 Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in
20 yeast cells and other unicellular eukaryotes.

 It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

25 It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

 It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

30 It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

35 It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast

Detailed Description of the Invention

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 10 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 15 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 25 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 30 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 35 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356,

- 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- 5 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 10 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 15 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 20 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID 25 NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 30 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 35 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411,

413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and

(g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.

- Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

- As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to

determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are
5 codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention
10 from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173,
15 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as
20 represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439,
25 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

30 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic
35 reactions caused by said organisms, such as the so-called "professional diseases" in,

for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352,

- 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 10 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- 25 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,
- 30

Polynucleotides according to the invention may be inserted into vectors in an
35 antisense orientation in order to provide for the production of antisense RNA. Antisense
RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such

5 nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in

10 diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid

15 support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the

25 yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the

30 invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected

35 using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,

- 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270,

272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302,
 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334,
 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366,
 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398,
 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,
 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462,
 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or
 fungi.

The term "functional fragment" of a protein means a truncated version of the
 original protein or polypeptide referred to. The truncated protein sequence can vary
 widely in length; the minimum size being a sequence of sufficient size to provide a
 sequence with at least a comparable function and/or activity of the original sequence
 referred to, while the maximum size is not critical. In some applications, the maximum
 size usually is not substantially greater than that required to provide the desired activity
 and/or function(s) of the original sequence. A functional fragment can also relate to a
 subunit with similar function as said protein. Typically, the truncated amino acid
 sequence will range from about 5 to about 60 amino acids in length. More typically,
 however, the sequence will be a maximum of about 50 amino acids in length,
 preferably a maximum of about 60 amino acids. It is usually desirable to select
 sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or
 unique for the proteins according to the invention. Epitopes may be determined using,
 for example, peptide scanning techniques as described in Geysen *et al.* (1996).
 Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from
Saccharomyces cerevisiae, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16,
 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,
 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140,
 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174,
 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,
 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,

278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474 . Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector

5

10

20

25

30

35

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

5 When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

10 One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

15 Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

 This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises
20 providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating
25 domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the
30 presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

 An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a
35 protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These

binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an

immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting, band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention

therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
5 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

10 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

15 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

20 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*,
25 *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

30 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the
35 nucleic acids or polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of

5 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenous flora of humans and other mammals.

10

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 454, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484; and,
- (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic

The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof
5 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically
10 acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with
20 any of the above described vectors.

According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

25 The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the
30 invention.

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are
35 hereby incorporated by reference.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

Plasmid constructions

5 The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII* GAL1 promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
10 the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final
15 expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCMTM/LMBP culture collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

20 The Yeast GeneFiltersTM were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFiltersTM are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right
25 corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and
30 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs
35 designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly

provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results

Induction of Bax-expression in yeast cells

S. cerevisiae cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YIpUTyLMuBax and the yeast cells containing YIpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YIpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YIpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNeasyTM Reagent (Qiagen Corporation, Crawfordsville, TN, USA) according to the RNeasy protocol. 1.5 $\times 10^9$ cells were concentrated in a microcentrifuge tube and 1ml RNeasyTM Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 μ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was

precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

5 ***First strand cDNA synthesis in the presence of α -³³P dCTP***

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α -³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C
 10 for 10 min. After cooling down on ice for 1 min, the following components were added:
 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
 1 µl 0,1 M DTT
 1 µl RNase Block (40 units/µl) (Stratagene)
 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
 15 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
 10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)
 and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column
 20 (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 · 10⁸ cpm/µg for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the
 25 detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

30 The Yeast GeneFilters™ were successively hybridised with the α -³³P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

35 The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250

mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 µl polydA (0,5 or 1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating.

- 5 Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from
10 Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

15 **Example 2. Quantification of Hybridisation Signals**

- Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster
20 corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

25

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity
30 range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

- 35 Subsequently, the results of the two experiments (hybridization with cDNA from YIpUTyL containing INVSc1 cells and hybridization with cDNA from YIpUTyLMuBax

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

15

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a

wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

REFERENCES

- Altschul, S.F. Gish, W., Miller, W., Myers, E.W. and Lipman, D.J. (1990). Basic local alignment search tool. *J. Mol. Biol.* **215**, 403-410.
- 5 Bairoch, A. and Apweiler, R. (1998). The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. *Nucleic Acids Res.* **26**, 38-42.
- Bishop, M.J., ed. (1994). Guide to Huge Computers, Academic Press, San Diego.
- Carillo, H. and Lipton, D. (1988). *SIAM J. Applied Math.* **48**, 1073.
- 10 Casadaban, M.J., and Cohen, S.N. (1980). Analysis of gene control signals by DNA fusion and cloning in *Escherichia coli*. *J. Mol. Biol.* **138**, 179-207.
- Chien, C. T., Bartel, P.L., Sternglanz, R., and Fields, S. (1991). The 2-hybrid system - a method to identify and clone genes for proteins that interact with a protein of interest. *Proc. Natl. Acad Sci USA* **88**, 9578-9582.
- 15 Devereux, J., Haeberli, P. and Smithies, O. (1984). A comprehensive set of sequence analysis programs for the VAX. *Nucleic Acids Research* **12**, 387-395.
- Gatignol, A., Dassin, M. and Tiraby, G. (1990). Cloning of *Saccharomyces cerevisiae* promoters using a probe vector based on phleomycin resistance. *Gene* **91**, 35-41.
- 20 Geysen, H.M., Rodda, S.J. and Mason, T.J. (1986). A priori delineation of a peptide which mimics a discontinuous antigenic determinant. *Mol. Immunol.* **23**, 709-715.
- Hinnebush, A.G. and Liebman, S.W., in : The Molecular Biology of the Yeast *Saccharomyces* (1991). Broach, J.R., Pringle, J.R. and Jones, E.W., eds., CSH Laboratory Press, NY.
- 25 Jürgenmeiser, J.M., Krajewski, S., Armstrong, R., Wilson, G.M., Oltersdorf, T., Fritz, L.C., Red, J.C., and Otilie, S. (1997). Bax- and Bak-induced cell death in the fission yeast *Schizosaccharomyces pombe*. *Mol. Biol. Cell* **8**, 325-329.
- Kohler, F. and Milstein, C. (1975). Continuous cultures of fused cells secreting antibody of predefined specificity. *Nature* **256**, 495-497.
- 30 Ligr, M., Madeo, F., Froehlich, E., Hilt, W., Froehlich, K.-U. and Wolf, D.H. (1998). Mammalian Bax triggers apoptotic changes in yeast. *FEBS Lett.* **438**, 61-65.
- Lockhart, D.J. Dong, H. Byrne, M.C., Follettie, M., Gallo, M.V., Chee, M.S., Mitterman, M., Wang, C., Kobayashi, M., Horton, H and Brown, E.L. (1996). Expression monitoring by hybridisation to high density oligonucleotide arrays. *Nature Biotechnology* **14**, 1675-1680.
- 35

Raff, M.C. (1992). Social controls on cell survival and cell death. *Nature* **356**, 397-400.

RiboGene Inc., Patent application (1995) PCT WO 95./11969.

5 Sambrook J., Fritsch E.F. and Maniatis, T. (1989). *Molecular Cloning: A Laboratory Manual*, 2nd Ed., CSH Laboratory Press, NY.

Sandbaken, M.G., Lupisella, J.A., DiDomenico, B., and Chakraborty, K. (1990). Protein synthesis in yeast Structural and functional analysis of the gene encoding elongation factor III. *J. Biol. Chem.* **265**, 15838-15844.

10 Sherman, F., Fink, G.R., and Hicks, J.B. (1979). *Methods in yeast genetics*, CSH Laboratory Press, NY.

Schiestl, R.H., and Gietz, D.R. (1989). High efficiency transformation of intact yeast cells using single stranded nucleic acids as a carrier. *Curr. Genet.* **16**, 339-346.

Stoesser, G., Moseley, M.A., /Sleep, J., McGowran, M., Garcia-Pastor, M. and Sterk, P. (1998). *Nucleic Acids Res.* **26**, 8-15.

15 Thomas, B.J. and Rothstein, R.J. (1989). Elevated recombination rates in transcriptionally active DNA. *Cell* **56**, 619-630.

Walsh, T.J. (1992). Invasive Fungal Infections: Problems and Challenges for Developing New Antifungal Compounds, in : "Emerging Targets in Antibacterial and Antifungal Chemotherapy" ,J. A. Sutcliffe and N.H. Georgopapadakou, eds, 20 Chapman and Hall, NY, pp 349-373.

Zhu, J. (1986). One step selection of a multicopy integrant based on yeast genomic transformation. In "Heterologous gene expression in *Saccharomyces cerevisiae* using a dominant selection and amplification system". Ghent University, doctoral dissertation, p 45.

CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,
332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360,
362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390,
392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420,
5 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480,
482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence
which is more than 70% identical, preferably more than 80% identical, more
10 preferably more than 90% identical and most preferably more than 97%
identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6,
8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46,
48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86,
88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118,
15 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148,
150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,
20 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,
25 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,
450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of
SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
30 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75,
77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141,
143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171,
173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201,
35 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231,
233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,
293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321,
323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351,
353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381,
5 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411,
413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441,
443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471,
473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more
10 than 80% identical, more preferably more than 90% identical and most
preferably more than 97% identical to any of the nucleic acid sequences
shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29,
31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69,
71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107,
15 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137,
139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167,
169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197,
199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227,
229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257,
20 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287,
289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317,
319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347,
349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,
379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407,
25 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437,
439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467,
469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the
nucleic acid sequences as specified in a) to e),
- 30 (g) the complement of any of the nucleic acid sequences as specified in a) to f),
for the preparation of a medicament for treating diseases associated with yeast or
fungi.

2. Use of a polypeptide which is involved in a pathway eventually leading
35 to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

5 11. A compound identifiable according to the method of any of claims 6 to 9.

12. A compound according to claim 11 for use as a medicament.

10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.

14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.

15

15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.

17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

(b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,
 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,
 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,
 5 478, 480, 482 or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
 preferably more than 80% identical, more preferably more than 90% identical
 and most preferably more than 97% identical to any of the amino acid
 sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,
 10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
 454, 476, 478, 480, 482 or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to
 any of claims 17 to 23 .

20 26. An expression vector according to claim 25 which comprises an
 inducible promoter.

27. An expression vector according to claim 25 or 26 which comprises a
 sequence encoding a reporter molecule.

25 28. A host cell transformed, transfected or infected with the vector of any of
 claims 25 to 27.

29. A nucleic acid molecule according to any of claims 17 to 23 for use as a
 30 medicament.

30. A polypeptide according to claim 24 for use as a medicament.

31. An antibody capable of specifically binding to a polypeptide according to
 35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10

35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

15

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.

20

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

25

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30

39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35

40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20
25

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
30

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
35

20

ABSTRACT

The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACCTGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTTGTTCAGTCGTAATAAATCGTTTCTGGGAAGTGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTGTAGG
GACGTTTCGATACCAAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCTT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVSSTQACLPGVPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTCTCTACATTCGCTTTTTATTCAAGATTATTTGGTTTTT
CTAACCGCCGCGCCGCGCAGGTACCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGCGCGCTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACCTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTTAACGTG
ATAGACGCATTTTGTATTATACAAATTAAAAGAAATCAAAATATAATATGTGAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTTCGCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTATCGGTTTCATTCACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTTCAGAAAG
TCAAGAAGTATGAAAATGGGTTTATTAACAACCCTATAGTGATTTCTCCAACCTACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTGTCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTACTCGTTCAGGATGTCATGACCAAAAACCCTGTTACCGGCGCACAA
GTATCACATTATCAGAAGGTAACGAAATCTTAAGAAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACCTTAGTTTCTATGCTTTCCCGAAGTATTTAATGAAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTATGGGGTGCCTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCATATTGGATTCTCTCAAGGTAACCTCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAAACTTTCCAGATTGGAATCATTTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCAATATTATACCAAGCTTTGGCTCTTGGTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCTPEDQADMVRRVKNYENG
FINNPVIVISPTTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQGNSIFQLNMIKWIKETFPD
LEIIAGNVVTKEQAANLIAAGADGLRIGMGTGSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFSGSWFFCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAAGTCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTTCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCCTTTGTCGTCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTTAGCGTATGATTTCTTTTAAGAATCTGGTCTTTCTTCTTCTATTT
TGATTGGGTATATTTCTATTTCGTGTTTCATTACTGGTCTGGGTTAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTCATTGTGGTATTTTATCTTATCGATTT
ATACTTTTTTTTATTCAAAGAAAATTAACACAGATAATCTCTTATGAGCCTAGCTACTTGT
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTTGTA
TTTTCAATAATGTCTGTTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLVWVNWVLVWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTTAACTTTCAGGTTAATGATGGTGTTCTTACTATATTCTCGAG
TCGTACAGAAGTTAGTTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCCTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACCGGAACTGGTG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCCGT
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCCTTCCTT
ATGCCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGTAGAACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAAAATGAGTGGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAACAGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGGCTCTCC
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTTCACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTTCTTCAACAGCAATACTATTAAACAGTAATAACG
GTAACGGTAACAATGTTCATCTAATAACAATAGCGCCAGCTCAACACCAAAAAATTTCTT
CACAGGGACAATTTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTTATCAAATCAATTTCCGTTAATCCCT
TACTGAGAAATTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

10/030019

3/161

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATAACC
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGGCAGCTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQQSIETRDAIDKENGVOETETGENSAKNA
EQNVSSSTNLNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDIIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTVITSLNGKEISGRKLKVEYKMLPQAERERIEREKREKR
GQLEEQRSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFDREKYYYELAYPMGISASHKRIINVLCSYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLOAHAAAAANSISNQAV
NNSSNSNTINSNNGNNGNVIINNNSASSTPKLISSQGQFSMQPTLTSPKMNHHSSQYNSA
DQPQPPQPTQQNVQSAQQQQSFLRQQATLTSSRIIPSGYSANHYQINSVNPPLLRNSQI
SPPNQIPIINSQTLQQAQPPAQSQTTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQQLP
QHTNGSVHSNFSYQSYHDESMLSANHLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCCCTATTTAAGATTCACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTCAATTTCTTATTATATCTCATCTCTCGTACGAAGGGCCGCTCATTTGGA
TCATTTTCTCTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATGAAATLGRNATG
TAATAAACTCTCTGAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC
CTCATCTCTGCTCCAGATGCGAAAAAATTGGTCTCCACTGTGAAATCAATCCTCAATTC
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTTCATCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCCTTCCTCAGGTTCTCCAACCTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATATGAAGCATCTTCTCATGACGTTGCG
GCGCATCTTCTTTAGCGCAAGATTTCGAAAGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAATGGCTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACCGACTATGCCATTATTGCCTTCGCCGATGCAAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACGATA
TTTTCGTGACTAGGTATCTGCCGATTTTTCCTATTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCAAGCTTTGTGTAATATTGTGCATTT
GGCCTTTGCCTAACCAAAAAGTCCTAGATGATTGTTCTTACCGTTTGTAGGATTAGCAA
AGTCACATGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGCCACCAACTTCACAGACAGACTATT
TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAACAATGATAAAAGGAACAAGAAAGACGAGCCGCACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTGTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTTGT
CTCATATCATTTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAGTATCGTG

4/161

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTTCTTTATGTTAAATTAACGTGTCTGTTGTTTG
CATTCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAAATGTCACTCTATTGAATAATCTTTTAGAAACACACCAATTAATTGAAC
TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCCTGACAAATATTTTGATTGAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTTCCA
GAACTGCAAGTATGTTAGAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTTACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAAGCCGCTAAGAAAAGAAAATTTTCCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAAACTGTAAACAAAAACAACACCAAGTGGAAACCACTGTTACCA
CTTTAGTTCTTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTCTTATAATGGAGATTAACGGGATACCTCTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAATTTCAAAGTTTATTTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCCTCTAATTCAATTTATC
CAGTGGCTTCTGTCCTCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTTCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTTACGCTACACCTTTGTTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDQDQDFSSAHMKRQPEQQQLQHQFPSKKQRISHHDDSHQINHRPVTSC¹THC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIIPNPDSSPSSGSPTSSAAQRDSKVSQV
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLLND
ALPNNSKESLPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT
SHVATNNNADRTKTPVVATTTMPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSQLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSIDNNND
KRKKDEPHVESIKYKLPGSFRLLSLANFQAKLSHIIIGSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNLFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKI
VTLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNQ
LTAWATSVENDISRTASMLEKLNFLVIMHPEVFEEDGIIISRMRSHLTGSIFYDLVWCVH
EARRREMDPEYNKQALEKAARKRFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE
TVTKTTPSGTFTVTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNNDYNNRLLDASNDISIPNSIYPVASVPASNPNPQSTKVDYYSNGPSVI
PDL¹⁰⁵⁷SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNV¹⁰⁵⁷TMNYNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPV¹⁰⁵⁷L

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCATTTTCAAATTAAAAGTGTTCA
AATTATGAAAACAAC⁵⁰¹TCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAAGTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGCGCGCAAAAATATTTGGTATAATTATGGAAATACAAAAAGGGGAACCAT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGCTGCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGFVYVTSYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACCTTAGCGTGCTCGCA
ACACAAAAATTAAGTAATATGCGAGTTTTAGATGTCTTTCGGATCTATGCACGTTCTTGA
GTGGTATTTTATAACAACGGTCTTTTTTACCCTTATTCCTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAAAACAGGTATCCAAAAAAGCAAACA
AACAAACTAAACAAATTAACATGTCAATTAACAGTCCATTTTTTGATTCTTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAAAATAACTATGCTGGCGCTCTTTATGATCCCAAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTGCGAGTTC
CAGTTGATATTTTGGACCATGACAACAACACTACGAGTTGAAAGTCGTGGTTCCTGGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAAAATTTTGGTTTCTG
GTGAAATTCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGTCAGACA
ACATTTAAAGCAGACTACGCAAAATGGTGTGTTTGGACATTAACAGTTCCAAAAATGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDWFDNDLSLFPSPGFGRSVAVPVDILDHDNNYELKVVPVPGVSKKDDID
IEYHQKNQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGCGGTA
ACTAAAGTGACCTGGCTCTATAGTGTGTCCCTCTCGCGAGGACCATTGTTGCTTGCATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCTTGTAAATTACCAAAATCTTC
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAACCTACTATAAATAACCGATTAG
AATCGAGTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAACCGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACCTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC
CAAGTGATTCAAGATTCTCTCTTTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATGCACAAA
ACATGGGAAATCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCTTCTACGAAGA
ATGACGGTGGCAAATACCAAAATGCCTCTGTCTCAGCTGTTTTTACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC
AAAATTCCAAAGCCAAAAAATATTTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA
TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATCTTGGCGCCTCATCAGAGGGAAGGGTGAAGTTCATGTATGATTGCTTAAATGGGCT
TGGCAAGACCAACTATTGAAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

6/161

AAAATGACTCAGATATTAGTGGATGCCCTTTTGGCTGATGATATGGGTTTAGGTAAAACAC
TAATGAGTATAACTTTTGATTGGACATTAATTAGGCAAACCTCTTTTGCATCAAAAAGTTT
CATGTTCCGAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCTGATATGGATAAAAATGGCTGTCAGAA
ATTTTTTAAAGTGCAACGAACTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAAGTACCTTCCCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCACTTCTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAAC
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGCTAGTGTCTAACTACACTCAAACAT
TGGATATAAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTGTTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTCGTTTCGC
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAAGCCGTGCTTCATATATAGACTTGTCAACAACATGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATTCACAG
ATTCGTTTACCCTGAATGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCCGCGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNLSSNENTRYFTIMYRKPTTKKH
KTSWGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLFAKGSNEVQLDYELKE
NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNIVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIMVNKNAAEVDVIVDPLLKFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCPTLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDGHRCLKNG
ASKILNTLKSLLDIRRKLTLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIRKGTEKEVVVVSNYTQTLTDIIENLMNMAGMSHCRLDGSIKQK
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCTIDEKILQRLMKNSLSQKFLGDSEMRNKESNDDLFNKEDLKDLSV
HTDTKSNTHDLICSDGLGEEIEYPETNQQTVELRKRSTTTWTSSALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDELDFDEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAAACAGCACGAAGCATATTATTGCGCATAAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTCTCTTAGGGACGAAAA
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTCAAACAAAAAGAT
TCCACCACTACATCAGTGTAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTTTGCAGCTATTATTGACTTCATTAAAGAAATAT
CCCTTTTTTCCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAG

7/161

CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
TGAATATACATTTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTCATTTTTGCAGAATCTGGACTTCATGT
AATCCATACATACCATATCATGATACTGAATTGTCCGATGATTGTCATAAACTGATTTCTA
TCAGCAAAATCAAAAATAC'TGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCCACATACTCGCTGTTTCGCCATCCTATGGACATTGTCAITTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTTCTACCA
TTGAGTTTCTTCAAGATAAAACAGAAAGCCCAAAAAAAGCTAGTTTCGGTTATCATGTTGA
AGAAATGTTGTTTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATAITACTATCATTCCAGC
TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGTCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAACTTTGTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTGTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACCTTTGTTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA
ATGGACCAAAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTGTTTATGT
TTTTCTACAATTTGGCCACTAGCTCCATTTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACCTCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTTGACCTATATGTACC
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCCTCGTGGGATAAATATTTGACTATATGCTGTTTTTATTG
AGCATGTTAGTTGCTATTTTCTTCTCTTTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTTGCAAATGGCATTTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTTCCCTCCCTGAATTTAATTGCAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT
TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATTTCTTTGGTGAAGGTGCC'TACCGTTGGCTCATATGGTGTTCGGG
GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAAGTAAGCTTTTGGCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTTGCTGTTACTGGTGGCGAAAATAACGAAAAATACCC
AGGCCAAAGACGATGCTGCCACTAAGACTCACTCATTAAGATGCAAAATATTAAAGCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCCTAAGACAACCGAATCCTCTTCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTLSDDLHLKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYKFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNVNAKKSKEA
KNFVIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQYQTDWPWGATFDLDANFKLLLQFGYLVMFSTIWLPLAPFICLIIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMFSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

10/030019

8/161

PKHVNVQNPPEVFEKIPSPFNSNNEKELVQRKGSANEKHLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTTEKRN
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTATQPHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSAAKEPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTTAAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCACTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAACATCTTTGAATTGTGCAAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAATAAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAATGCAGGTACCATTCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGACCATACTACTCTTCCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCCACTGTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTTGTCATTCTTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTGGAAATGGAACCACTTTTGCCAACCTCGGACG
ATGTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTCAAAAACCAACCAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTTCAATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGACAGACTGTGAGTGAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAAC
CATGTCCGTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACCTGACCTCAA
CTGACGCTAGTACTTTTATTCTCGTGGTGATGATTTGAAGTGAACGCTAAAGTTACAGTG
ATGCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACCTTGT
TCAATGCCTCAGTCAAATTATTAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTTACCCACGATACCGATATCCTAAACTTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAACTGCCGAATACGTTCCATTATGCGGCAACACTTTCCACAGATCCTGGT
ACGTTCCCTCAAGGTGCTCGTGTCTACACCGAAAAAATCCAATGTTCTAACGACACCTACG
TCAGATACGTCATTAAACGATGCTGTTTGTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACCTCTACTGAATTGACCTTCTACTGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGLADVDKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPTYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVDCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDTDILNFLTLAGIIDDKNLTA
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKR VAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTTCTTACTTTTTTTTCTACAGTTTGCACCATTAAACCTCTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTGCTGTTTTTTTTCAGTGTCTCGG
GCATACAGGCCGCTTATCTTCATGCCGCCCCATCATCCTAGGAACTCTTTCGGGTATGGG
CCAAGGGCAGGCCGAAAATCCTATGTGCGTGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

9/161

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTTCTAA
TGAATCAGCACGCGCTAACC GGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACATATAATAAAAAATTCTCAAGAACAACGTTGTTTAAACGAGATAATTCCTCTAA
TATACACGTACCGACACTTAGGAAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTTCGTTGGAATTTGTCGATATTTGGCTTCGGACAACCTTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAGACCTTC
GAAATTGATGATGAACACCGTATTTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGTATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAAGTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCCTTGGCTTTGGTCAATGTCAGAAG
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAACAACATCAGAAAGTTCTTCGGTTTTGTCCAAGGAAGATGACGTTTCGTGATTTT
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCTCTCAAAGATTGCAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHRQALKVRNAQAQREAAEYAQLLAKRLSERKA EKA EIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGT'TTGTGC
AGTGATATTACCAACTTGC GCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAACGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA
TTTCTATTTCGTATTTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA
ACGTCAC'TTGGCTTGATATACTCGACGCTTATTTCTGCAAATTCAGGTCTCAAATCTGAA
CGCGCTGGAGCCCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCATCAAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAACTCTTGTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCAGCGACATG
GCACTAACCCTATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAGGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC
TCATTACTCTTTGTTCTTTATTTATTCGTTGGACCTTGTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLV IWRHIVKKMLHIRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRVSRRRRK KREAERRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCTATGCGTATGACAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAAATCCACCAGAGATTTTGCTCAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAGTCATTGGACAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTCTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGT'TTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCGCCAAGACTG

10/161

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTTCAGTACCAATAT
ACAACGGAGAAGTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCCTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGTATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAATAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGCTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFakteSEFETRETHGELNLSNVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSFLPPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAGAAAT
GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTTGAACGCGACGCTA
CATGAAGTACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGAGCTTCTTACAAGGTAAAATTTACCGCGGTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCGATGATAAGGTCTCCAATCTGGCAGATTGTA
AAAAATTGATAGAAATGGATTCCAGACTAGATTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTACGTCTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTGCGACTTTAAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACCGGATTCGTCAATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAACTCCAGGAGGAAATTTAGACGCACTGGAATTGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA
ATGTTGTGCAACCGTGAACAAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGATGTAGATGTGTGCGC
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAAACTACGTGAAATCACAAAGCTTGCCTTGCACTTGAAGTCTAGTGCTC
AAAAATACCAGTTTTCACGAAGTGTCTTTGCATCCAAGAGAAACGCTGACTACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCGAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAACATGACAGGTCACTAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRRLDTSINLPT

11/161

NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDKRLKPLGMGKKRKRDRSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSDAE
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDGVE
GSTPKDKPELGEVKLDSLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTTIDLSD
TTYGATTLDDVDVSHILHQPQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAACGGAATAATATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAATGGGAAAGTG
GTCGTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTCGCGTGTCTTCTCCT
CTAACTGTGCACGAGGCACCCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTTTCGCGCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTTGGGCATCTCTGA
GTTGGATTTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLFWASLSWISKSVRVGLIFSNPSGAGLDDLVMF
RGMSFCEVSFASLDGCRGVYIDDES LRKFFFFFQYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCCCTTCAGCCGCTTTTTGTTGCTGTGTATTTCAGTATATCCATCATCA
TTTTACCTACAAGGAACCTTTTATAGCCACCCTAAGTAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTTCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAAGACCCGCGAAATTTTCAATTTCGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGATGAGTATGGACTAGAACAGAAA
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTTCGCGTTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCATGGATATGA
CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACCTC
CGAAGGTGTACCAATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTTCG
ACTTGTTCCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAAATTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTCG
TTGTCGAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTTCGTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCTCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

12/161

MTTTVPKIFAFHEFSDVAEAVADHVHQAQD GALAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSSGSGSSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF
ADERLVFPSSNESNYGCAKRKILDLDIDTAKYGT PKVYHIDESLIDDPQECVDNYEKLIR
GFAGRDSVKLPMFDLFLGCPDGHIASLFPNFQDNLREKLAWVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTAAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGCACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTTCGCTCTTAAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTCTGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATCTCTAAAT
GAACTTTTAAGCAAATTAATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAAATTTTAAGCA
TTACAACGCATATTATTGTTGTTAGTGTTCGTTTCGTTAGCGCAAAATGCGAACTCTTGACGG
TAGAGATAAAAGAGGAACTTCTAAAGCATTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTCTCGGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTCATATAGCAAGGGCATGAAGGAACTGCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAACGTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNRILSITLLLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQOPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIIFSKSTCSYSKGMKELLENEYQFIPNYII IELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGNEEIKKLHTQGKLLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAAATAGCATTGAAG
AGGATAAGAATTTACGCTATTTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAAATTTGACATT
GAAGCAATGTGATTCCTCGATAAGTAAGCTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTTCATAAAAAACTTTTGAAAATGGATGAGTGCTCG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG
GTAATGCAACCTCAAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAAGAAAAAATAAAGCGAATCAATCAAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGAGTATGAAATTTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATTGGTTGATGTCTTTATAT
CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGAAG
ATGATAACATAATGGTTATTGATAAACCAGCGGTATACCTGTTTACCCAACCTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT
GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTTGTTGAAAAACCTCTAAACTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

10/030019

13/161

CTGTTTTTAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRNLFVPMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEKHRQLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRNTITKMLQNNLGFVVPNCNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIIVEKPLKLIIEPRLALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLKGKGQADFDIVITKLDEIGKRKPAKSWFHSNGGYEVLRLQEKCSICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TAT'TCCGACTAGAAAAAAATTAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAAACAGGAAATGTATGGGTCACATATTAATAGCTTGT'TTTACTCCATAAAAGAGT
CTGATATTTCAGAAAAAACACCCATACATGTTGAAAAATAATGCAT'TGTGAAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCTTAGGTTGTTCGCTCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCCTCTGT'TTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTATT'TAGCAGTGT'TTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCCTCCCAAGTGTCCTCAAGTATGTTAAATAATTT
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA
GAACAACGGATCACCATTTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT
GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCT'TTTCGGGTCTT
ATTTAT'TCATTCGCTCCCTTTCGAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGGTACCTCACTTGT'TTACCCTTTTACACAGTTCATAATATTTTGTAGGATTTTGAA
TTTCTGTTTTTACTAACATGTGACACGAAATGTTTTCATTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAAGGCCGGTAAGGGTTTGATTA
AGGTCAACGGTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCACTGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAGTACGTTGACGACAATCCAAGAAGCAATTGAAGAAGGCCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCACAAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAYHQKYVDEQSKNELKKAFTSYDRTLLIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA
AGCTTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAATGTGA
TGTGTGTTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCTTC

14/161

CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTTAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTTCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIKSEIPSKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPDEFLLTDAMPIAKRLAKAMKLDTYNVLQNNGKIAHQEVDHVHFHLI
PKRDEKSGLIVGWAQETDFDKLGLKHLKELLAKLEGS

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTATTTTCACGACGGTTACCACACCCGTACACCCTTATCTCATTTC
ACCAGTACCTTTCTTTATTAGATTCACTCTTATTTTATTTTAGGATTTTATAGGTCAATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTCGACGCTGCGATGCTATCCATTACCCGTCAT
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTATATATATATGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAGAAGAGAAGACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRRKRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTTGTTTCTAGATTGTTTTATTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACCTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGGCCCTGCTTTGAACCCGTACATTTTATTTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTCCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACATTT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACCTTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTAACAAGGGTAAGAAGTACCAACCAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGCTTTCCACAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGGKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCAATTGCG
CAGATACCCCCAAGGATCAATGTGCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGAATTTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAAATGCAGCCAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC
ACAAAAAGTGTACTTCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCCGACACAACCTCAAAGTGAGTTGGAATCATGTTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCCTAACGTTAATAAATACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGGAAACATGTCTTGGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTTCAAAGACGTACTG
CATGTTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAAATACATACTGCGAACCTCAA
ACAAATATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG
CTAACAAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAAATTATAG
CGGATCATTTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTTCCAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAACCAATCATTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTTCGCACCGATGGGA
ACGATAACAAAGGTGCTGATAATTAGTTTGTATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAACGAGTTCAAAAGTG
ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLPDTPKQDCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHEILGQKKAISSNNCNTKSSISINAAKNTKDLDEIVRILEVSIPTEEAGSVPEIY
SLLKRTTDILILHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTTQS
ELESWFTQYGVPRVPGFWTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN
CPSCGFSNFQRRRTACFRCSFPAPSNSQIHTANSNNNVNSSRNLLNNRVNSGSSSNISNTA
ANHPYGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPIIIIADHFSGN
NNIAPNYRYNNNNNNNNNNNNNNNNMTNNRYNNNNNINGNGNGNGNNSNNNNNNNNNNHH
NGSINSNSNTNNNNNNNNNNNNNSNNCNSNIGMGCGSNMPFRAGDWKCSTCTYHNFQAKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRDTGNDNDKGRD

ISLMEFMSPPLSMATKSMKEGDGNGSSFNFKSDKANVNF SNVGDNSAFGNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAAC TAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCTTGAGCGTTTCGAAAATTAGAC
TGTACTTTTCTGATGCGCTCCCGTACACCTTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTCACGCGCTCTCGATCAATGAACCTTTAAAAGTAAC TG
ACCCCTAACTTTTTTCCAGGCAAGGCTGGCCTCATTACCC TACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAAACAAGACGAAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTTCTCAAAAGATACTTTTAAACCTAAAAC
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAAC TTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC
ATTTAATTTTTTATACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCACTAACGGGC
GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTTCGCAAGCAAAAGAAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTGTCTGAATTTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTTATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT
TGGAATATTATTTTCAATTTTTTATCCTATTAAATAGGCCGGTGTTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC
TTTCCCACAAAGAAAGTACGCTATTAAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGGKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCTTTTAAAGGGATATATAACAGATTCTAAAAC TGACAGAAATATTTGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAGTTCTACTCTGATACATTTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTA AAAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCTATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTTGGGTGCGGCGATATGTAGCTTGTT
AATTTACACATCATGTACTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAAATTTCCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAAAC TGTTTTAACCCTCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAAC TTTTAAATGATGGAACTCCTACAGACAATATAGTTCCCCCTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAACTCCCAACCAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAAGATTCTCACCTTCTCCTATTT

10/030019

17/161

CCTCCTCTACATTTTTCGTTCCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCGAATCTCTTTACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAAATTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCATTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCCCTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACCTAAAGGATATTCTAATTTCTGATT
TTTTGATTTCATAAGATTCCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCCTC
CTTATTCACCACTCTTGCCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAATCAAACTATACATTTTACATTCACCCCTGGGGCACA
GAAGAATTCCGTCCGGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAACCAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATCTTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATGATGA
TTTCCAAAGATGGTCAGAGATATATAAATGCTGGTGTCTTATTGTAAGACGCAATTTG
TAATAGACAGAAGTGGATAACGATGTTGATGTTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCATTGCCAACCTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAGAATATAAATT
CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCCCTGCCTATTCTTCCCATTATAAAGAACCTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTCTAGGTTAATCAATCCTTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTTCAGGAGAATGTTCTAGGCAGAGTACTGTCGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAATTGTTGTTTATAACAGTC
TAAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTGTGTTTCGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGATTCCCTCGACACAATTTTCACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAAATATTCATGAACATTTGGGTAATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTTGTGTTTAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTGACCGGATAATGAAC
TTGATAATAGTTTCAGGATCACTGTGCGGATGCTGAATCTACAACCTACTATTTCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTAGAAAACCTGTCGCTTCTTCAGTACAGCCAGCTC
TGATTCCCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCAATCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIELEKPSLSPLSRGKKWTEKLARFOR
SSAKKKRFSPSPISSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPKVAPFGYPPIQRTSIKKSFLNASCTLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRLFPFCTKCKKBDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNYTFLHSPLGHRRIIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLRSYFIQILLNNFQEELQDWRIDGDYGLLRVLVDKLMISKDGQR
YIQWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC
ADLSLDLYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECRQSTVDSIQSVLTTISSIL
SLKREKPDNLAILIQIDFTKLKEEDSLIVVNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSMDMDKGIDGITRRSSF

18/161

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGTATGCTAATGCTAGAAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTTCTCTGGGGCATGGCTTGGCGTGTGGCAAACC
CTGATTACAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTCAATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACTTTCTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCTATGCCTTCTAAAAATA
AGGAATTAAGAAAGCTTTTGTACTTCTACTGGGAAATTTGTTCCCAAAGTAGCTGAAGATG
GAAATTTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAGTTTAAACGAAATTTGAGAGAGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTACAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTTATAGTAGCTGAAACTGATCCAATATGTAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAACACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTTGATGGAAC
TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCCGATTAGCCCTAACTGTGT
TGTCTGCCAATCCAAATGTCTTGGTTCCCTGCGGTAAACAAATTGATTGACTTGCCCGTCA
AGGTTTCTGATAATAACATTAAGTTAATTTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGCCACATCCAGAAATG
CTGAAGATGTTGTTGAGCTTTTGAAGAAAGAGCTGCAAAACAACCGTAATAAACCAGATC
AAGACAAGGCAATGTCAGTACAGACAATTGTTAATAAAAACTATTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTGTCGCGCCAGTGGTATCATTGCCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTGATG
TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTGCGC
GGTTTGTTTTAAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAC
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAAAAGTGTATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAA
AAATTGATGAAGATTTCTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCCCTGGACACCA
CCAAATCCTCATTCAGAGACAAATTGAAATTCGAAAGAAGAACAAGCATAAGAGAGCAT
TAAAAGACAGTTGCAAAAACATCGAACCAATTGATACGCCGATTTCTTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTTGAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG
TGATTCCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTGTGCTGACACAG
GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG
AACATTTCCGTACCATTGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC
AATACCAACATTTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACATAATGGGTATTC
TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTCCAAAA
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

10/030019

19/161

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPPEL
LMHIIRFVMPSPKSKNELKKLLFYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTLRFLTKLREAELLEQMVPVSLACLEVRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTAVNVFVEMAASVVSLLDFIGDLNSVAASG
IIAFIKEYIEKYQPLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNQEHTENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTI I KLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDSCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDAIH
ATSSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNPVPHGFHKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRMTWNAFEWENKISVKSQPLTHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCNLYAKSSFGEALANLCIEKDSKTNDVIGYVRIRSKGQGLALSGLDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTTT
ACTGCATGTGGATAAAAGTTTTCGAATCGTTTGCAGGCAAATGTAACTATTACTTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCTGTCA'TACTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGGCCCTGCTTCTTTTCTTTTGATTTCTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTAAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC
TACAGAACCAATAT'AAACACAATCTTTCTCTCAAACGTAAACACCGAGTTTTTTTCCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCCTCCGTTGATTTCGTCCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGACACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGCTGACTATAGATCGATGCATCAAAGTCCATATACATC
CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAACAATCAGCTTCTTACAACAGAC
CTCAAAATGCTCATGTTAGTAT'TCAACCTTCCGTGGTATTCCCCCCTAAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAA'TCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCT'CCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCCCTGATAAAGACACCCAAC
TCATAAGTAGTTCAGGCAAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTTGACGATTTTACTAGCAGAAAATAAATACTTCAAATCATTAACGATTATTA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAATGAAAACCTAAAACTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAG
ACAAGAACAACGAGATGAAATAGAGCAACTAAAAAATAAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDYMNQSSSMATYNASEKNLNEHPSPQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGSPDYRSMHQSPHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNNDNDNVTKPVPDKDTQLISSSGKTLRNTRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFDDLLAENNNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNMLKNENSI I KNEHNMSRNENENLKENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

20/161

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCATATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTTCAGTACACATATAAATAAAACCCTCAATTTGCCTCT
CCAACCGTTATACTATTCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC
TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTGTTTTGTGATCTTTTGTGTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTTGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACATAATAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAAATGGAAGGAAGGAAAGGTCTCTGGTGGGTTT
ACCACGGTGGTGATGATTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTTCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT
CTATGGTTTAAAGAATGTTTAAATGCCCTTCTGTACAGGTTGTGGTACCACAACCTTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACAGAAATAATTGCTCCCGTAACGTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGGTCCGTTCCG
CTCCAAACTTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAACTTCCTTTACACGTGACAGTTGTCTAGGTTCCCTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTTCACCAAAAAGGCTCGTCAGTTATAATGGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGCTATTGTCGTAGGTTGTTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCAGACCTGAATATAATGGGCAACC
CTAGATATTTCAGTCATTTTCATTTCTTCAAAGACCTTGAACATACACGAACCTATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATTCATAAACCATCCCCAGACGGAAGTACGCTCTAT
ATGGTGTGCGCCGGGAGCGTTAAAACCTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFQAQFMILTINELKIAIHGYLRNTPWYNMLKDYLL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFQPLPSNGIPQDDVIEELNKLNDLI PHTQWKEGKVS GAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVRKMESEVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLSFSFIVSFMEKAGYKN
LPLLD FRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESCQEIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRLSAHVVEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTGT
TCTTGCAGCTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCTTCAAAGGTATA
TATATTTAGAAGAGAGGAAATTATTTTTCTCATGTCCTTTTAAATCCCTTTGGGTGGCG
AAAAAAGAATGTAAAAAATTTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACCTCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAAGCATTGCTTTTAA
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCTTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTCCTTTTCCACTACGAACCTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGTATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
GTAACATTGTTTTCAAGGTGTTGCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACTTTCACGTACGGTAACTTGCCATTGGTGGATACGT
TAAAGCAATTAAATGAGCAGTTTCAAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCATTTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTTGTTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTT
CTGTAATGTATCAAAAATTAATAGAAATCAGGAATTTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAAATAATATTTTCAAAACCTGTTGGAAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTTCTATACTACCTGGTTGGACAAACAAAA
TCGATCCTTTTGGAGAGCTTGTGTTTGGAGACGTTTTCGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACCTTTTATTTCCAAGATTATATCCGTAAATATATCGTTTATAAACCTT
GTTTCACGTTTTCATTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAAGACATCCCAAGAGCTGGTGATAAATATTCATCGAACAGAGAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCTTTTGAACCTCTTCCCTACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAACTCCTTCAGTGAAATAGAAGATCAGATAAAATTTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC
TGATTTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGAATTCT
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA
GGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCTCAATGGTA
TTGAGCAACTACAAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTCGACAAGCTAACTGAATTCGAAAAGTACATTGTTGATACCAATAACA
TGAATTTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTGTCTTTATAGCGCCTTAGCGGGTATTTTTCAGTTTCTATTCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACCTTTAGACGTATCTCTCCTGGACGTTT
ATAGAGTCGCCGAAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTCACCAAAATGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGVEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKNPDPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSANFMNAMTG
PDYTFNPFSTNPNQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSYGKRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDITYDTFLLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFG

22/161

QLLYSILPGWTKIDPFESLLFEDVLRFRGDLETGKDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLNDIIPFELFPYLPPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE
TDFHKNSDKLKVLRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTLELQKYIVDTNMMNFFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVYPYTHKDGSAQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIQQVDAPKSPKGEVTVFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1612 bp, CDS: 500-1612 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCCT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCCATACAC
ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA
TAATAATCGAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTGTTTGGGTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTCACACACAAGAATCTTTTTCAGAGTTCTCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACAGCAAG
TGAAGGATACAAATGAGGTTGAGTCTGCTATTTTGGCGTCTTGTGGTTCGTGGCAAAATTTGG
CGGCTAACGCTGCTTTGTGCTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAACTTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGCTTTGTGTTGGAATTATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCTTCCCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTGGGTTACAGTGTCTATACAACCTTTTGAATAACGAAATATCATCCAAAGGTC
TCAGACTAGACATTCAGATGTTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAAT
TCCACATTTCTTTTCTTGTCATGTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT
GGTGTAAGCCCTCATTTTGACATCACCTTTGGTGGTTACCGTTGCCTTAACTTTTACTA
TCCCGTTAGCCATGTTTCGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTTATTTTCATTTTTGTTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISFALYLTP
DLWRIIQSRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFTKKLLGLFV
SLFGIILIVMQSSKQQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLFWPILIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIVSFVFLVNRHGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2: 983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAAACCTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTTCTTGGCGAGACGCGCGCTCAGGGGAACGCGATTCCGAAAG
ATGCCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGAGAGCAAATGTCGCC
CCAGCCAGGTCGGACACATCTGTCACTTCCAGCCACTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

AMENDED SHEET

23-11-2000

23/161

TTTTACGGTATGTTTATTTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTCACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTTTAC'TAACGTTTATCAATAAGTTCCGGTTTC
CCGTCTAAATTTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGGTTCGTTCGTTACTCCAACCTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTTATGCAAAACCCAACTCACTACAAAATCCCAGCTTGGTTCTTGAACCGTC
AAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGGTTTGCCTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQQSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFVGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAAAGTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCCGGTGTGATTTGTGTAAACTAAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCCCTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTTCTCCATTCTATCTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAAC'TTTGTATATATCTTTTGT'TTTTTTGACCTTTTTCTTCTCTATG
TTTTTCAGCCATACAAAAATATGGGATTTT'TAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAACA
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCAGTTAACAA
ATGATAACTTTACAGAACACAATGATCACTATAAACGCCTAAAGCAAAACAAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAAATATCGACAAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACATTAGGTAACGATATGCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHKKVVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKSHDQLLQESNQSMNQA
QQSLSNRIQLDQTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNNAMKAQYKINIDKLQDMQDEMLDLIEQG
DELQEVLMNNNSGELDDISDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEENLDTEDKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAATAATTCCTTTTCTCTCTACCTTTGCTAATATTA AAAACCATAGTTGT
AAAGGGTACTTTAATGCTATATTCCTGTTAAGTTTCCTATTTTACCTTGTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCCTTTTTTTGGGTGAAGAGAAGTAGTATTTTGT'TTTTTCATGGGAGTGGAAGTCCTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG
CAGCTAGCGTTTTTGT'TTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAGCAGCAATATA

24/161

CACATTTAATGGTTTGCCC'TTAGTGACTATTAGGGCGT'TTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAAT'TTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACT'TTCAGGTGCATAA
GATGGGAAATTTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAAGAGAGGGCCCGGGGAGCACCACATT
CACGACCAATCGTGTGATCTGCAAAAAAGGCACATGGAAAATGTAATTTATCAGTTCTC
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAAC'TTCCAGGGAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAAATATCATTAGAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTCGTTGTTTCGTGGTTCGTTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCGGTTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAAAATCAAGCCATTCATCAAAGTCGTCAACTACAACCACCTATTGGCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPKSVTKKHGAK
KVAKRTKIKPFIKVVVYNHLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAAT'TAGAGCTTAAGTGGTACAAACT
AGGGCTAATAAAGAGGTAACGGTTCGGTCTCTACTAAGGTTTCGTATTGTGTGGCACCAGAT
GTTAAGCACTTTTAAGCGGAATAAAGTTCGATGGAATTTTATGTTTAGTTAGGTTTACC
TTGAATTTTTTTAAAAAAGAGTCAGACAGGCTCGCTCTTTCCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCCAAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCCTCTATTTTCTTCGATTATTGGTGATTTTTC
CCGCTCTAGCCAAATCCGAGCGTTCATCGATTTT'TTGGGGAAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAAGTCT
TTTGCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCCAGATGACG
ATGATGATATTTCTTTTGGGAAT'TAGGCACCAGGCCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCAT'TACAAACACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTAA
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAAAATAAATTTTGAACATTGAAAGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCACCGTCAACAACA'TATCAACAA
ACACAAACACTATAACGCCAGATTCGTCTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA
ACCCAAATAGGATTA'TTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTTCGTATGTTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTGGGATGTAAAAAGAGCTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGT'TTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTCTCGTTGCATTGATGTATCAGATTGTACAATTTTCGTCTTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTAAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAGA
TTTTCCAATATGAATGATAGACTATTGTATAATTTTCGTATTCCCTTTGATCTCCTAGAAG
GTATATTAAAGGTACTGCAGTCGCATCCTTAAGCAAATTTATATGGAATTTT'TGATGAAA
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGCGGACGTATATAATGAAA
ATGTGGATACTACAACCTCTCATATGTGCAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTTGGGAGGATTGATATCAAAGCTGATTTTATACTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCCATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTAA
ATATTTTTTGAATTTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATTC'TTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

25/161

TGGGACAAGACTCCCCGAACCTTGGACCTCAGATGCCATCTTATTGAACATACTTTAAACCA
TAATATATAGGCTATGGAAGACCATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTTCTTGAGTCAAAATCATTTCGATCTAACCA
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDDLLELGTRPPRFTQIPPSSAALQTQIPTTLEVT'T'TTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTTLSTNTNTITPDSSSSVAIEAKPQSPQSKKRK
ISDNLKKNMVLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCCKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGLRLVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMVNVIFS
AVEVVNIITSIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLKLLKDEVLNIFENLLMIYGDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHPKQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKQFQM
ARTILESFSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAAATGCATTCCCT
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAACTGGGTATTCAAGGTAAAGAAAT
CATTTGTTTTTGCGCCAAGTTTCGTCTGACAAAGAAATTTTTTATTTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTTCGTTACTACGCGCAATCTGCGTTATTTCTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCTTTTGATGTTAAATTA
AAGCGACTGAATGAAGTGCACACATTTTTTATTTCTTCTTGATTTTTCTTTCTTTTGT
TTTGCTTTCTCTTCTGTGCGACAACGCTCTCAACTGTACTCACCATTAGTATTTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTCGCAGCACA
ATACAATAATAACATTTCAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGCGGCAGTTAAGGTAATATCAAAAGCAG
TATTAATACCGGTAAATGTACGCGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTTATTATTGGTGTGTCGTACTGTCTATGCGTTGGGTATTGTCC
ATCGTGATCTAAACCGGAAATCTTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCATGCGGTGTGATCCTATTTCGCCCTTCTTACTGGTCGGTTACCTTTTGACGAGG
AAGATGGAAATATAAGAACTATTTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT
CTGATGATGAAATTTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTTCTTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAAGC
AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGT'TTCCCCATCTAAAAAG
TATCGACAACCTCCACAACGCAGAAGAAATAGAGAAATCTTTAATTAGTGTAACTCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCTTTCAAAAACCTTCTCTTCAAGAAGAAATTATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAGAAGTCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTGGGAATACATTGAGA

26/161

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGTGAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACCTCAAGAAGCAAATTTGAAA
TTGATATAAGTGTCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAAATCGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTTCCGTCGCCGCAACTTTTCTTTACAAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGGAACCAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAAGAAATTTTGTAGAACTATCAGAAGAT
CAAAATTTCTTGGGTTTCATCATTTTAATATCGATAAAGAGTTGAAATTTGTCTAAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTGAGGAGCGAGTGGTGTGAGATTCTTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTTGGTTGATATTTTGAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTTCCAACACCAAGAAGTGCGGATGATT
CAGAATTTCTTTTGTAACTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTCAAGC
ATGAGAGATTGTCGATGTCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGTCAGATCGTTTTTAATGGATCGAACGAAGCGAAACAACTGATAACTTACATCTTC
CGATCCTTCTCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAAATGAGGAAAAGGAAGAGAAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAAATTAGGGAAAAAATGCTGGCTCGCAGGCAAGGATCATTCAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGTTTCAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGCGCTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINNSIPAIKDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEAAVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFRQIIIGVSYCHALGIVHRDLKPENLILDHKYNIKIADFGMAAL
ETEGKLLSETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLQKYPsirDSKS
IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANAECTLYALL
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLSVTSSRKKPISE
NKFTASSASSSNLTTPGSSKRLSKNFSSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYEKYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRISAPMENEKKNINHLEVDIDNIL
RRRNFSLQTRPVSRDLPGIMFSSPTEEVSPEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVSQLKDSTATTAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTRSADDSEFLFETVNEEAETGNSSNDERLYDVGDSTIKDKSALKLNLFADRFN
GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTKEEENE
EKEKKPEQHKQEEDEKREKVVDDMEPPLNKSQKIREKNAGSQAKDHSKDHLKEHKQD
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLT
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSFSKAVKKLVNEVENVLNKEGV
LK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGTACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAACTATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTGCAGTATGTTATTGATCCATCG
AATCAAAATTTTTCACCGCCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAA

27/161

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTTAAAGGTTTAAAAAGTAGTGTTCAGCAGT
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCAAAAATATAACCAAGATAAAGAAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTTCGGGGTCAATTAAATTA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
ACAATTCACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAATAATT
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTTGAATTTCTATTTTAGTGAAGAGAACTTGAAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAAGCCAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTTACAACATAAAGAAACAAACCATTTGGAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAGTAATTTTGATGAAAATGATGACGAAACGAAA
AATACAACATTGAGAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLNDNPKNNTSSAEDKKKQTSLLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTNWKTPITPSVIIISGSKD'NSKSGKNSKNSKTNKKMKRKGKYNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNNNSRNSYKQLS
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKPKK
ANDGFI PMSLIGKFYRMVNL SLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCCCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTCACAGCACCACCGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACCTTTCCTGGTTAGTCTTTTGGTTTGTTCATAGCAAAATTAAATATATA
TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTTCAAAGGCACGCGTGTCTTTTTTTGTTAAGACAATAGATATTTTAGC
ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCTGTTTGGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCGGGATCAG
ATTACTCGTTCTAACAGAGAAGAAATTTAAATCATTTCATCGAATCTCATCCGTTAGTCC
TCGTGAGTTTTTTGTCTCCATGGTGTGTTCATCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCTCTATTTTAAAGGAGCATAACGTCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCTGATTTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTTCAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC
AACCATACTTGGAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTTATCCCTTC
TAGATTGAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATCTGT
TTGATGGAATGTAGACTCTTTGGTTCGAAATTCGGTTGCTCTAACTCAGTGGTTAAAAAG

29/161

CTGGTGTCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGTCGTCAACCAG
CCAACACAAAAATTGGTGTCTAAGAGAATCCACTCTGTTCAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAATA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAAGCTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCGGTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFLGRQPANTKIGAKRIHSVTRGNGKRYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCATATATGGGAGGCAACTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGTTGGGCCCCGTCCAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATTT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACCGGAACACGTCAATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCCAGACATATAGCATACATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCCGCTGCTATGTGAAAATGGCTGGCGTAGCATTGTACAGGACA
GGCTCTTCTTACCCGCGCAGTTCCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA
TGGATACGCTACCAGGGCAGCCGCCATTAAAGGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCCTTT
GGCATGTTCCCGGCCAGCGCAGGCGGACGCTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAC TAGTGATAAAGAGAAGAGGATTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQTSVDVELLHHTMLARAAALAHAD
TIAWMWYQHVMPRRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCATTGACGTAGAAAT
TGAAAGAAGGAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAAC TAGATCTACAGCCCTTGAAAATCGTTTGGTCAACTTTGAGGT
TCCGGTCTGCTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAACGTATAA
ATAGGACGGTGAATTGCGTTCTACTTCTCAATTGCGTTTGATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTTCGATAATCTCAAACAAACAACCTCAAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTTCGGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTCGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

28/161

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT
CTACAATGTTCCACACCACGTTAGATTCTTAAATATGAGAGAACAGTTCCCATTATTTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCCTAGACAGAGATATGATCGTTTCAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGGCGCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTATTCAGGGGCAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTTTRFISAIVSFCLFASFTLAENSARATPGSDLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNPVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLPNTTEPILFDGNVDSL VGNSVALTQWLKVVLIPYF
TDIEPDLFPKYISSNLPPLAYFFYTSEELEDYDFTQLGKENRGQINFIALNSTMPHH
VRFLNMQRFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPOPLDRDMIQVLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT
GAATTTATCAAGGAATCAGGTACACATCAGATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAAGCATATATAATGCACATTTTTTAACATCTGATTACTCGCATCGTTTTCTGGAA
GAAAATAGCTAATATTCTGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAAATTTTACCTTTTCGTCACCTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTGATTTGGAATTCGGTATTATCAAGAGAAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTCAATTATACAGGATCTT
TATTAGAATCGGGAAGTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAGAAAGCTGCAAATTCAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
CGCTCATTCTCCTCAAGTGCTGATTTGGTGTTTGATGTCTGAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 135 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDKVKVHYTGSLLESSTV
FDSSYSRGSPIAFELGVGRVIKQWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPP
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTTCCAATGCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTTAACATTTGAGGTTAATATATGAGAAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTCGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAATAATAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

30/161

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCTTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT
TACCTTGTTTACGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTTTTGAGTTGT
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTGTTTGTGGGTGTATTAATGCTTGCCTATACCTTTCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTTCTTCTCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTCTTACTACGTTTCT
ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTTGCTATTTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCTTGTCCCAAGAG
CCAAGGGCCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTTCCATTTTTCGGCTGGGCCGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGATTTGCGCGTCCCCCTTTTTTTTCTTCAATCTCTGACTCCCCCTACCTTCTCCCCT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPLSLRFRVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHCHYRQLAPTHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVSQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCTTCCGTACGTACACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTACCATTTATCTTGTGCGGTGTTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAAATCAAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTGTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCCTCGGA
AGAGTTAACTTACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCCTTTTGTCTATTTTGTGTTTATATAAT
GGCGTTGATAAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTATCGATTAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCCAGGACGCTAGTTCTTCGTCTGTTGCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG
GTTTAAGAGGGCAATCTGGCCTTGCAGGCGAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTCCCTTGAAGTCTTTAAAGGGGTCCCTCCTCACCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTTCAACCCGACGAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCCG
ACAAAGTGGATTATTTCTATTTTCACTACCCAACAAGCCGTAGCTATTGGTTTCAGCCACCC
CTATAAATATTTCCATTGTACCTCTTTTCGAAAGGTTTGAATTTGGGCTCAATCAAAGTCG
TATTATTTTGAGAAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCATTCCAAGACAAGTGGG

31/161

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTTCGCCATAAGCTCAAATTTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG
TGGCACTTTCAATAAAACCATTGTTCATCCTCGAATTTGTATTTCGCTTTTTTAGCACCCTA
ACCAGAAAGACGAAACTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTTCACTCGCACGGCTGTGGAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTTCGACTGTTCGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTTCAGCCCATGAAGTGTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCTCCTTCCCTACCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACCTTCGACAACATTGTTCAT
CTTCTATACCAACTAGCTTTTCATTCCTCTAGTTTATGAGTAGCACTGCTTCCCCATTT
CCATAATTAAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT
TAACCTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPNEAPSVLLSGCIVLSINPEMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFNKYAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKSSSPSSCTLDKGNYPFPFSAILPGSLPESVES
LPNCFVITYSMESVIERSKNYSDLICRKNIRVLRITISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVVLFFENYQYCDFFPPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNVCVDQCDVRSNIKV
RHKLKFFIILINPDGHKSELRASLPILQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEYYLFSRSASVTGLELLADMRSGGSVPTISDLMTPPNYEMHVDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRILRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSSVPGVHSNVSPVLLSRSPAPSVSAHEVLVPVPSGLNYP
ETQNLNKVPSYGMKYDIIGEDLPPSYPCAIONVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCATAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAACGTTCTTAGGATTGTGGTGGTAAAACTTGTAATAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAAGAGACTATATTCT
CAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCCTG
GATTTACCTTGGCATTCCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTGGGTGCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCAGATCACTATCTTTTCCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACCTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAAATCCGTTATAAATATGGTTATGATATGCCAT
CGGTATATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCACAACAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

32/161

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATTCT
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGYKATATGPKQQEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLAEN
IEERLVIAIEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTC
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAAAATGAATTCGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGCGAACGCCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTT'TTTTCAAATATGTTTGAAAAACG
TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCT'TTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTTTGTCCTGGTGACTCCAAAATCTTCAGATTCCAAAAC
CCAAATCTGCCTCTTTGTTCAAGCAAAGAAAGAACCCAAAGAAGATCGCTTGACTGTCT
TATTCAGAAAGCATCACAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAAT'TGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLQKQKPNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKTQVKAQRPITGASLDLIKERRSLKPEVRKANREEKLEKKAEEK
AARKAEKAKSAGTQSSKFSKQQAAGAFQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTTATTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCACT
GGATTACATTTCGCACAATAGAATAAATGACTAATTTTCAAGAATTTGTTTCAACCTGCCG
GCATTCAGTTATTATAAGTTATTGTTTGATGGTAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTACTGAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTTGACATGCAAGTTTAAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAAGGA
CTGTTTCATACCTTCAGATCCAATATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTTAGCACAGGAAGTGAACAATATATGCGAGCAAAATCCCTCACCAACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTTGAATATTACAAATCAGTAACGTTTGTGAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCFSIFSIVLASVLAQELTTICEQIPSTLESTPYSLS'TTILANGKAMQGVFEYYK
SVTFVSNCGSHPSTTSKGSPINTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTTGTTCTGTACCCCCGCATTCACACCGCTCTGCCTATTCATTTTATC
GTTTTCGTCTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATCCCTCTAACAATTATTACAAGTGTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATTTCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCCACCTTAACCTTACGGACCTTCTTTTGAAACGA

33/161

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTCATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG
TCCGCATAAGAGCATTTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACCTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCAGGCAAGCACAGCAGCATCATCAAGATCATGCCG
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATAACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAAGTGAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAAGATAGAAGAAATTGCCAAGCAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDDKEFVPTEKLLRETKVGVENVKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLDRQVLKALYDVLAKESHPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVI SKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRFTCGKCKEKKVSYYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTTCTTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTGTATTGTCTTTT
TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTCAGCCAACCTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCATAAATGGA
GCAGTTTCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTCTTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA
TGTTGACCACCGGCATACCCTTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDDNWNINWSTLTQDLTVTGCQSVNNWSSFLRSR
FQVLVSLVFWDDQCPQFVQVDWLPMSLLLEVSHNTLTEITWMVFIHVNVSVMMLTTGHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATATAGCACTAGTCCCAGGAAACCCTTTC
GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAATTTATTTTTCTAATGCCTGTTATTTTTCTTATTTTTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTCTCTCGCAGTTTTTTCGCTTGTTTAA
TGCGTATTTTTCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

34/161

TTTGGCTTTCTCCGTTGATTTTTTTTCCTTCTTAGTGATTTTTTTTGCATTAAATCCCAGAAC
AATCATCCAATAATCAAGAATGCCTTCCAGATTCTACTAAGACTAGAAAAGCACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGACTCAACATATTTCTTTGTGTTTTGATTGCGAAGCTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTGCATACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTTACGGCTATAAAAGGTAAGTTTCATTTAGAT
TATGGAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA
TTTAAAAATTGTATTTTCATTACAATATTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACAGAAAGCACCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAAATACCATCCAGGTTATTTTCGGTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAAGTTGGACAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGTTAGAATTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTCTGCTCCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
Y FHKQQAHFWKPVNLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN
VPVIVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCCTTGGTCTTAGCACCACTTTTTTCCGCTATTTGTATTTGT
TGAATAATTTAGTATCTATTTCCATTTTCATTATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTTGGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTCCACCAGATAGTTTCGATGGCATTTTATTTT
TAGTCTTTTGAAGAGATAATATCATAAATATATAGTTCTCCATGATGTTTCGGGTCAGT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT
CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAGTAGAGTGGCACCGGAAATTC
CTGGGCTCATTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATAT
TGAATTTCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTCAGCATT
CTGATGTGGAAGAGAAGCTGCTTGCGCATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCCAAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAACTAACCCTAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCACAAAGTTCTAGACTAGCCCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCTAATCGTTGTACTA
CTTTTCCGTTCAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTTCATTGTTATTTAAAATGGAAGCCAGAACAAAGAAA
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA
ATGGTAAATCATACATCGGTGGTCCAGAAAGTTTGGAGAGTATCAACGATTCAGTTTCAT
TGGAGGACCTCGAGGAAATTTGTTGGTGATTTAAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTCCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

35/161

LAHDYYVCEKTDGLRVLMLFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGLVLIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTVPVKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRYWYNYDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTA AAAAGAGCATTGGGCAGAGAGTATTTGTCTGCGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTGCTTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTATTATTTTAAATTTTTGAACATTTTTCATCCTTTCTC
ATTTTGTTCATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTT
CAACATCCTCCCATCATCCCAATATTGGCATACACACACATGCAGCACAGCGGAAGTGC
GAGGTGAGAGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATAATAGTATATTTT
ACACTCAATTCATTTTGTATTAATAGTGTGTA AAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG
AAGGTGCTACTGTCAGCATCAAGTCCAGAACTCGTCAAGGTTGTTGCTCCAAGAGGTACTT
TGACCAAGAAGCTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTCCCAAGGTTACAAGTACAAGATGAGATACGCTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAACTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATTTGCTTGTGTCAGGTAACCTCTGTCGAAGACG
TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTCTCAACAGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFKVNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKMKRYVYAHFPINVNIVEKDGAKEFIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCCTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGCTTCTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGGAATACCTTTTGTAAAGGCGCTTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCCCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAAGTAAA
GAAGGAAAAATTAGGCGATATTAAAAACAATCTAAAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCAG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGCGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTTGCTACCACCTTCATTTTCTGGCGATTAC
TCTTCTATCGTATCACTAGAGAAAGATGAGACTAAAAAAGTTATATTTCGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCACCCGTTTGCAGATGAGTCAAATCTTTAACACTAAATTTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTGCA
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCACGATT
CAAATTCATTTGGTTGCATCACTCTATATGAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

37/161

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTTCCT
GTGTAGCCTAATGTTTAAATGCCTAATTTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA
TTTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTTTAATATTCTTTTTGTTTT
CACCGCCTTCTTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGA
GAGGCATTCAATTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCATGCGGTGATTGGAAGA
TCGAGAAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCCGTATCAGAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMDLKIIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRKRCKGTGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTTTGGCATTCTTATACATTTTCTTTCCTTCTGAAATTAAGTGTACACCCA
TACCCTATATACACCCATACCCCTATTTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAGAGCTCTGCTCTTGTGGCTGGTTTCACTGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCACTCTGCGGATTTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAAATAAACAAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACCTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAACAAAAAAGTATC
AACCCCTATTTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAAAAATAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCGGTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGAAAAATTGGGTATCGAATCCAAGCAACCTAAGTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCAGTCTTTCGT
TCCAAACGATGGTTGTTTGAACCTTTGTGACGAAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGCTTTGTGGAAGAAAAAGAAGGAAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTTCAGCCGTATTTTTCTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTCTAGAAAGTCCGGAAAAATTGC
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTCTTGTTCGGCGATATTCGAACCA
GGTCCGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAAGATTTTATAGAAGCCTTC
AGTTCTTGCCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTTCTATTGCTCTATATATATTTTCTT

38/161

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTAACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCCACATTTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAA
GCGATGCAAAATGTTCAGAACCTTTGAGGTATGCACCTTGCTGAAACACCAATGGTTATA
CATTAAAGCTTGCTTAAGCGGATTCATATGAACFTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTCTCTCTAGACCAAGTGTGTTGAAGATGTTTTTGTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACFTTTTAAAGATTTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCAGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAACGCG
AGAAAGCGAAAGAACCCTAACCAAGAAGACCAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA
AGCAAAAAACCAAGAGGTCCCAGCAAAAAAATTGCAAAATTCCAAATCATTCGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC
TAAAAAAACACGCTTACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE
PLRYALAETPNGYTL SLSKRIPYELFSKYVNEKLGLKENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLD FRAIGKKIAKDLFDQYEIELNHRGDELSILSKKDKIFKEFSLD
QVFEDV FVIGCGVENID DGSREKYALLKIGLVKHEEEI SEGGINEPKMPIIESKIDESH
DVMNSES LKEEEAEKAKEPLTKEDQIKK WIEEERLMQEESESRKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQQKQLQNSKSLPISEIEASNKNMNSNSGSAESDNESINSD
SDTTLD FSVSGNTLKKHASPLLEDVEDEEVD RYNESSLRSRSPKGN SIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCACTCACAAACGGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATTTCTTTTCGTAATTTTGTTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGATACCCTT
TAAAAGGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAAATG
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTTCAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCGTCACATAGCTTAGACAACATCAACG
GCGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA
ATCATGTAAGGGAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAADVPTAYMRRGYTPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMMDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHST
NGEGDCDF

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAATCCACAACATTTTTTACAAATTTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTCTGTAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTCTCTCTGAAATTTAA

39/161

TGCTTTCATCCTGTATGGTAGCGGTAGACATGCTGGT'TTGTAGCCTTTTTATTCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAAATCCAGAGTTTGTATTGTTCTTCTT
ATACACCGCCTAGTGCTACTTTGTCAGAGGATTATAGGGCAAACCTATCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCAT'TCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATA'TTCAACAATATTTCATTTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGT'TTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAAT'TTCATGTCACCGCATTGGGCGGAACGTTTCGACCACA
TTCACGATGGACATAAAATAT'TGTTGAGCGTCTCTACATTTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACAGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPLFRECQSQLDIVIVPEFKTSFQLDSALGKM
YSITRDVLLGYGMINSGINIIFNNIHFVESNLQWKVLLPQESTFETWKLELGGQYHSI
EHYALHDNIMEEIEGPKDANKFHVLTALGGTFDHIHDKILLSVSTFITSQRILICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPETECILVVSR
ETVSGAETVNKTRIEKMSPLAVHVNVNLGGREEDGWSEKLSSTEIRLLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGT'TTGATCGTTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCCTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATPATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTTCGGGTAACGGTTCCCTTTTTAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAA
AAAACCTGAAAGGATAGATCAATGTC'TTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCCTTTTGAAAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTTCGTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTAAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCCTAAGAAAACCTTTAGTGTTATTTGGTGGGTTGTAA
TTGCATTACAGCGATTCAATTGTTCAAAACAAGACAACATTCCGTATGCTTCCTGAATTAA
ACAGCAAAAACGCAAGGCGAAGGGTTACCTGTTTGTGCTGGTAGAATTTTAAATTGTTT
TAAGTGTATATCGCTTTTACCTTTCAGTAAATCATGGT'TTACTGTTGTTTGGACCATTATCG
GCACAATATGTTTCGCCATTTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTTACAATATCACGCTAAACAACCTACTGGTTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTACCAGAACTTAAGCATCATTTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASTRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNATGVLCACVISQALVYGLFTGSSFVLRNFSVIGLLLIASFSDSI
VQNKTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNTLNNYWFYNNTKRDFLKYEFYQNLISIGLLLVNTNTGAGE

40/161

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTTTGGGCAATTTTTTTTATATCTTGAAATGATAGTTGCCTTGACTTTTCAACCGTT
CATTTTCATTAAGAACTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA
AATAATCGAATATAAACGATGGAATTTTTTATAAAATTAAACACATATATATATATATT
AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTTCGAAATTTTTATTTCAAGAGCTGGT
AGAGAAAATTTTCATAAGGTTTTTCCCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCCTGCTACCAAAACCCCATTCGTCCGTTCGTCCGGTCCAACCGGTTGGTA
AGTTCTTTTTTGCAACATGCTCAAAGAAGTTTGAGAAACCACACCTGGTCTGAATTTGAAA
GAATTGAAGCTGAAAAGAAGCTCAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT
TGTTATTCGACACTGAATTGGCCGATGAAGATTACTGACTCATGATGCTAGAGACTGGA
AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTCAAGATTATTCAAAAGGCCTTTGAAA
CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTGCCGATGTTT
CTCCTCCAAAGAAGGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTTCGAAG
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCCTTCTCTAGGTAACAAAGATTCTTCCA
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCCTTTG
AGTTCTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTTGAAAAGAGCTGTCAGTGAAGATCCCCGTATCAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAGAAGAAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA
ACAAGAGAGCCATCCGTAAGCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCACCCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAAT
CTGCAAAGACTATTGTGCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTTACTTCGTGT
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDENVDPELLEFDTELADEDLTHDARDWKTADLYAAMGLSKLFRATESQIIKAH
RKQVVVYHPDKQSAAGGSLDQDGFVKIIQKAFETLTDSNKRAQYDSCDFVADVPPPKGT
DYDFYEAWGPVFEEAEARFSKKTPIPSLGNKDDSSKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAKAKAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTTCACTGAATATTTTTTACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTTACATTTTTTGCTGTTG
CACCTACACTGTTTTTTTTTTTTTTTACCTTATGAGTCCTGTATTTCTTGAAAGAGCCGAT
AACAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCCCTCTCA
AACTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAAGTGTCTGAGACAAAAGTC
TTTCCAGCAGAGTCCGCCTACGCTCTTGCTGCAGAGATTGCGCCGAAGGCAGGTTTCTCTG
AAATTCTTTTCACTAGTAAAGTGTTCGTTCACTGTAACACATACTGCCGTAGTTTGGCT
AAAATTAAAGATATATTAGATTTTGTAGAATTTCTTAGATAGTCTCAACGTGTTAAACAA
AAGCATAACCAAAGAAAAAAATGGCTAAGTTCTTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTGGACATCAACAAAAAACCGTGCAACTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACTAACGATT

41/161

ATTCATATTCATTGAGCTATACGAGGCAGTGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAAAAAATTCGTGGGCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAACTTTAAGAAGGGTTACATTTACTAACTATTTCTTTTCCTTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTTACGCCGGTAAGAAGGTGTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCATTGGTTCACGCTTTGGTTGCCGGTATTG
AAAGATACCCATTTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACCAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTGTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA
ACCAATGGTTCCTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPLKVTKKHGAK
KVAKRTKIKPFIKVVNYNHLLPTRYTLTLDVEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTTCAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGGCCACC
ATAAACTTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAAACTCCACCAGGACGTGGTGGGAAATGCAG
CAATTCCCCCTCTGCTTCCCGCTGACCTTTCTTGGGCCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAATATTGAGGAATGAATTCGGATGAAATTCTAGTAGAAGAAAAAAG
CCTAAAATAAAAAAGAAAGAAAGGAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG
ACGTGCAAAGAAAGCAATTAATTTTATAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGTACTGCTGGGTAATGAT
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTCTCTCTCTCTAATTTTCTG
ATGTATCCTACCCAACCCTACAGTTTTCAAATTACTAACATCAATTTTGTGAAACGA
CTTTCGTTTTCTGTTTCTATTTATTTTCATTACAGGTTTATAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGGATGTCAAATGCCAGGTTGTTTGAACATCACCAGTGTCTTCTCATGCT
CAAACCTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVFSHAQTAVTCESS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTTCCATAGCATTTCTCTGTCACAACTTCAAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAAATAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCCGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCGTCCGTGCCGCAAC
GCTGACGGTTTAGTTGTTTCGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTCC
ACCAAGAGAGGTAAAATTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTAAACGTAAATTGAAGGAGATTAAG
CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

42/161

TTAAACTTCATTTACTTTTGTAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAAGTCTGGTTAGAAAATATATTGAG
GATATCATTTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCCATTACAGAAA
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCCAAGA
CCAGAAAGACCTACTGTAAAGGGTAAGACCTGTCTGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGTAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFEKGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAAGTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACCTTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCCCTATTAGGTATACGACCT
CGCGCTTTCGAAGTAGAGGAGCCCTTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTCACCCACGAC
GTATCAAGTTACTTCCCTTGGTGCAATGTCCCACTATAAAAAAATTTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTTCGTACAA
GGTTACTTCCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCACACCCACACCCACACCCACACCCACACACACCCA
CACACACACACCCACACACACCCACACCCACACCCACACCCACACCCACACACACCCACACC
CACACACACACCCACACCCACACCCACACCCACACCCACACCCACACCCACACCCACCTATCTA
ACCTGTCTCTTAACCTACCCCTACATTACCCCTACCTCCCCACTCGTTACCCCTGCCCACT
CAACCATACCTCCCAACCCATCCATCTCTCTACTTACTACTACTACCATCCACCCGCCA
TCATAACCGTTACCCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCCTGCTATTAC
CCTACCATCCACCATGTCTACTACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPLTPSSMQYSDIYIHTPHPHPHPHPTHTHTPHPTPTPTPHPHPHPTPHPHPTPTPT
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYHPPPIITVTLQ
LPISNSTITLLLPYHPPCPHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGAGAGAGAGAGAGAGAGAGAGAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTTCTTGTAAGGAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTCCGGGTAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAGGATATTATTATATGTGACAGAGAAGAATTG
CTGTAGAGATTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTTCTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTTCGCTCACAGACTACAA
GCGTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCGGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTATCATCATCAT
CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTTC
GAGCGATGTTGAAAGAACCAAAAAGGAAAACCTGTTGATGATTTTCATAGAAGAAGAGGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC
CAGAAAATGTGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

43/161

GAAGCGATGATCCACGGCACCCAACTCACCAATAAAACTTGGTCGTCGCAAACCTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGT
CTTCACCTGTGAAAGAGACAAACAACCTTTCAAATATGAATCTTCCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGTCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAACGTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTCCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCGGATTTCGCCGTAATCAAACCTTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTGCTGGCCATCTTGGAACTGTTAAACTGCTAT
TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCATTTGATTGAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCACCTCTCTA
TGGAACCTCATTTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAACACTACAAAAGCTGGCCGAAGATGAGAAAGAAAAA
GGATCGAAGAAGACAGGAGAAGCAAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
ACAAAAGATTTTTCGCGCTATATTATTTGTAGACGAAAAAACGATAAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTAAAT
TCATTTTCTCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAAATAAAAGAT
ATGTTGTAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGATATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATGGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPFSSRDQLRAMLKPKRKTVDDFIIEEGLGAVEEE
DLSDEVLEKNTTEPENVEKDIEYSDSDKDITDDVGSDDPTAPNSPIKLGRRLVLRGDLDA
TTSSMFNNESDSELSDIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRNSDNSKSSHIAVSKRPKQKGIYRDSGGRTQLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDSEFDDEEDQKILREIKKRLSIAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHLPPYVGTIVENGKIDLRSFESVKCGHEDITSIFLAFGFPVNQTSRDNKTSAALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRALYYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPSLMEPHSPK
KAKSVEISKIHEETAAREARLKEEEYRKKRLEKKRKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRVRDLYPLGLKIINFNDKLDYKRFLPL
YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPShLTPLWNMLKFIFLYGG
SYDDKKNMNMENKRYVVNFDGVDLDTKIGYELLEYKFVSLPMAWIKWDNVVIEHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQRLKIPREL PVKFQHRMSISSVLQOTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTTCTGACGTTTGTCTTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT
GATCAAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTGACATCGGCGTTTAGGCTTGTCTGTCTGTACACATACGCTGCTTCAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTCAATAACGATTTTGCGT
GAAGGTTTAATTTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTAAGT'TTTTAGGTCAAAAACAAAT'TCTACCTTCTTCAATGAAAAAC
TGCCATTGTCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
CCTCTGGTAGTAAGGCGGTGGTCGGCGAATTACAAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCAGATGTAATATTTGTGTGCT
TTCATGGTGATCAGGTTTGGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG
AATTGAGTGAATTTTCAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCTCAATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAACCGTTACCTCTTTTGATGTACACAAATTCGCAGT
TAGCAGTTTCTACTAAAAGATAGAAGTTTTCAAAAGTTTTCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTCTACCGTCAAGATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTCGGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG
ACGGCAGCGCCTCATTTCAAGAACTTTTGATATTACACCTCCATTTCGGGCAAATAGTAA
GGTTCCTATATATGTACAAAGTTACCTTGTCTGGTTAATTGAACCTGATGCAAACTGAA
AATGTGCTAGCATCATCATGTTCAAGTGAAGTAAAGTATATGGGACTCGAAACAAGTTAT'TG
AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTTCAGGCCTATTCTAGAACCTTGT
CCGGTGTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAGCGGCCATTATAGCATAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAAATGAATCAAGTAAGGCTTTATCAGAGAAATC
CTTTCACATCAGCAAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCCGGCAAACCCGCGTTCGGAGCTATTG
CCAAAGAACCCTCAACATCAGAATATGCCTTTGGCAAGCCATCTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAAGCCT
CTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
CTGCATCAAGTAACGAAACTAATCTGGATCCATATTTGGAAAGGCTGCATTTGGTTCAT
CATCTTTTGCACCCGCCAACAAATGAACCTTTTCGGATCAAACCTTACTATTTCAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCTTTGATTTTGGGAGTCTTCCCTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTACCTTTCTCTTACAGTTAGGAAACAAATCACCATTCAGTTCCTTCAAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTGAGG
AGGAAGCGCAAAAATCCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTCAGCATTTGCAACAAATATTACCAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG

45/161

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
 TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
 CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG
 ATACCACAGCAAACGAAGAAATTCAAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
 AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA
 TGAATGAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG
 ATGGAATAGCATTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
 AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
 GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACCTCAACAGTGACCGGGATGAAAAGTA
 TATCTGAGTCTTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
 AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAAACTTCATTAG
 AAGACAATTTATGCTGAATCTGGCATAACAGACAGACCTTTTCAGAAAGTTCCAAGGAAAAATG
 AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAAACTGTTAAGAAGGAAG
 CAGTCGACAATGGTCTGCAAACCTGAGCGCTGTTGAAACATGTAATTTTTCTGTTCAAACAT
 TTGAAGGTGACGAAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAATATT
 ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCACAAAATTCTACGTTAAGGTGTA
 TTGAGAGTACATTTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAAACATCCGGA
 ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
 CTATCAATAATCTGTATACTTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTCAGA
 ATAATATCAAGTGTGAACAAATGCAAATAACAAATGCTAACATTCAGACCTGAAGGAAA
 AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
 AAGAGGAGTATCTGTTTTTAATGCATTTTGTATGATGCTTCGAGTGGATACGTTAAAGATC
 TCAGCAGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTTCGATTCGTCG
 CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAAAATTGTTCACTGTAAAGAATA
 AGAGATTGGACGATAATCCATTAGTGGCAAAACTAGCTAAAGAATCTCTTGCACGTGACG
 GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
 AAGGTAAAAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
 TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
 AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
 VGELQLLRDHITS DSTPLTFKWEKEIPDVI FVCFHGDQVLVSTRNALYSLDLEELSEFRT
 VTSFEKPVFQLKVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD
 RSFQSF AWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
 VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPPYMYKVTL SGLIEPDANVNVLASSC
 SSEVSIWDSKQVIEPSQDSERAVLP ISEETDKDTPNPIGVAVDVVTSGTILEPCSGVDTIE
 RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSP TSEKIPIAQEQEEK
 KKNNESSKALSENPF TSANTS GFTFLKTQPA AANSLSQSSSTFGAP SFGSSAFKIDLPS
 VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAP SFGSGKSS
 VESPASGS AFGKPSFGTPSFGSGNSSVEPPASGS AFGKPSFGTPSFGSGNSSAEPPASGS
 AFGKPSFGTS AFGTASSNETNSGSI FGKAAFGSSSFAPANNELF GSNFTISKPTVDSPE
 VDSTSPFPSSGDQSEDESKSDVDSSSTPFGTKPNTSTKPKTN AFDGSSSFSGSGFSKALE
 SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
 NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEEAQKSP IGLTETIKKSANIDMAGLK
 NPVFGNHVKA KSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
 EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSES AFDTTANEE
 IPKSQDVNNHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
 DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK
 LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTD AI
 PVKHNSTQTVKKEAVDNGLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTS AKVS
 NIPFVSQNSTLR LIESTFQTVEAEFTVL MENIRNMDTFFTDQSSIPLVKRTVRSINNL YT
 WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYLF L
 MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVDVSAKINHTEELLNLKLFVKNKRLDDNP
 LVAKLAKESLARDGLLKEIKLLREQVSR LQLEEKGKKASSFDASSSITKDMKGFKVVEVG
 LAMNTKKQIGDFFKNL NMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2: 943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCATAATATCCACTGTTTCATTAAACGAATATTGGTCTT

46/161

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTCATTTT
TTGTGCTCCGTGTGATATTTTCGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCCTGGACATAGGCGGAGCATATTCTCTCTATGGGATGGGTTTTGTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAAGGTAGTTGAATCTCTATTTGTGTGTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAGAGCTTAAAGGGACAATTTATTTTAGAACTGAATTTTTACCCAGTGGAA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACCTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTGTGGAATAATGATTAGATTTTGGAGCGGGTGATGCGACTTAACAGTCTCATTGCCT
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAATTTTTGTCTTTCTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC
TTACTAACTTGTCAATTTTTTATAAAATTTATTTTTTAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGTACCAA
CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKLTGKTTITLEVESDITIDNVKSKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDSVCRKCYARLPPRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTACAATAGCACCGATGGAGCAAAAATAACAGAAATTTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTAAAGAGAGTCCAGCAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATATAAATATGAAACAT
CTACATATTTTAAATGTCACTAATGTCAATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTFTTTCACGCGG
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCGCATTA
AGCACTTGGTTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG
AACGAAAGAGGCGAGGCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCTTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTCAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACCACATACCTTTA
TGGAGAAATTTCAAAACGCAAGAAGAAGCAAGATAAACAATTTGCCAAGTTTGAAAGCA
TGATGAATGCAAGAGTACATACGTTTCACTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAACGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTGTCTAAAA
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACCTGGGCCACCGTAGGCCCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTTCA
CCATAACGGACTTTTACGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTGTGGCATT
AACATAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTAATGGTGGGT
ACGCCTTGGGCGCGCCTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAATATAATCAAAGGTACTCGTAAGCGCCTGTGAGAAGAGGAGGAAAGAC
TAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCCTGCCAAAGCATTTTTCGACGAGA
AATTTTCAAGATCCAGATATGCTGGCAAACCTTAGACAATAAAGAAGGAAAAATAAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAAGTGGCAAAATTTATGAGAAGGAGGGAATCCA

10/030019

47/161

KCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTCGATCCCACCTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AAACTGTTATAAACGATCTCTTGCATTACAAGAAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCGGAT
CCAAGGAAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSNATQOGTKFEFSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQEPYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYNLRGLDVIAILNPEVLPWRPSGRGNFIKSFNLRIHDFKCILEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
KVDSQPSLYKAKGENGFNIIKGRKRLSEEEERLKKSSHNFNSNSAKAFFDEKFQNPDM
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGDPDTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDDLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGAAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTTCGTCAATTTTGAACAATGGTAAGACAA
ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACCTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTTCAAGACACTATATG
TGCACCCGTTTGATAACGAGACAAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCGGGTGCTTGTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCCGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLYVHPFDNETIWEHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVAVETAGCDVLNKSLLKGSPTLEKLTSVATSLASPYIASFA
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIIACGGSCMTYEDLVKASSTLNV

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCCTCATATGTTTAAATATGCTGCATAGTGT
GAGTCCTCTAGTTTTTACCAGCAGCCACCAGCCGCTTCTCGAGCAAAGTGATAGATCCCATT
AGGACTCATCATTATCTAATTTTGCTATGTTAGCTGCAACTTCTATTTTAAATAGAACC
TTCTGGAAATTTACCCGGCGCGGCACCCGAGGAACCTGGACAGCGTGTGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAAT
CTAAAGATTAACGTGTTACTGTTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCTGTACGCCCTTTTTCGTGGTAATATTACCTTTACAGAAATCTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACCTACGGAACGTGTTATCG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCGGATGATG

48/161

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAAGAGATTGATCGGTTTGAATATAACGACAGATCTGTTTCAGAAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAAATAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTCA
AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACATAAGGTTACCCATGCTGTCTGTTACTGTTCCCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTTGA
ACGTTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCC'TACGGTTTTGGATAAAT
CTGATAAGGAACATCAAATTATTGTTTTATGATTTGGGTGGTGGTACTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGACTATAAGATCGTTCGTCAATTGATAAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGATAAACGTCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCC'TTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC
TATTCAAGAAGACCTTGAAGCCTGTCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGG'TCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTTGGTATTGAAAACCACTGGTGGTGTCTATGA
CTCCATTAA'TTAAGAGAAATACTGCTATTTCCTACAAAGAAATCCCAAATTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAA'TTGAAGTCACATTTGCACCTGACGCTAATGGTATTTCTGAAGGTGTCTGCCA
CAGATAAGGGAAGTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTATTA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAAC'TACGCTCACTCTTTGAAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAAATGGTTAGATGATAACTTTGAAACCGCCATTTGCTGAAG
ACTTTGATGAAAAGTTCGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSNNVLVRGADDVENYGTVIGIDLGTT
YSCVAVMKNGKTEILANEQGNRTTPSYVAFTDDERLIGDAAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKSKEHQI
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKTLK
PVEKVLQDSGLEKKDVIDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGA
QAGVLSGEEGVEDIVLLDVNALTLGIETTTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPOIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRILTQEEIDRMVEEAKEFASEDASIKAKVESRNKLENYAHSLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTTAGTTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAACAGTAA
CACGTTAATCTTTAGAAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTTCGACACGCTGTCCAGTTCCCTCGGGTGCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAATAAGTAAAGTTGCAGCTAACATAGCAAAATAGTA
TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAATCATAGGACTACACTATGCAGCATATTTAAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAAGTGGAGTAGCAC
ATGCTGAGTTTATGGGGATCGATCAGATCAAGGCGATGTTGGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTGTGGCAACGAGAGATTTGGAG

49/161

GCAACGGTACTGTCTTGTCTAGTAAATCATGATACGTGTACATTTAGTGCCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCATATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTTGAGACTTTTGGTGATGATTACAGGACTTGT'TTTGCGAATAAAGTTGACTTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCACCAAGATAATATAATCCAAGAAGTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFVFCGNERFNGGTVLS
VNHDCTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCTTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCTTCTTGTAGCGTGTTTCAGCAACTGGCCTACCAGCGGGACGCCCTTTGGGT
AAAGTTACCAGTGTGCGATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTAAAAGCAATGTACAAATACATACACAAAATATCACTGTAAAAAAATTCGGAAGAA
ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCATTTATAGTCAGAAATG
AAAAATTGTCCGAGAAATTAATATAATATATATGGAAGAAAAGGGGACATTGAGTTTAAAG
AATTTGATTAAAATGTCCTCTCAATATCCTCTGTAAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCATCTGT'TTTGAAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAAACAAAATTTGATCCACTTCCTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTTGGTTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTT'TGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAGTACCATAACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATT'TAAGTAATCAGGAAAATACGC
AAAACCCACTTTTACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCTACGTTTCAAGAATT'TAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAATTCAACGAGGTTTTCAGGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTTCAGTACCTAACTCTAAGAAAGAAATTTAGCTAATAAAAATGTTCCCTACAGAG
ATTTTATAAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC
AAGACCCGGAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTGATTGATGATGAATTCCTGGATTGGT
ATAGAAATATTTACC'TAATAGATTACCATCTAACTCCTAACAAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTTACCTATTAGCCAAAGTGT'TTCTGGAGTTTGATAATTTCAATG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTGCCAGGATTTTTCCTCAAACTATTCAAGGAAAATGTCGTGTCAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTTATTCACTCTGGAAGAGGAGCAGTTACCAA
TAGATTCACTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGAGTGAATATTACTGGAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAC'TGTTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAAATA
CAATCACCTAAGAAATTTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGCTACAGGTAGAACCCTTTGGGATACTGCAACAATGATTCAATATTTATTTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGT'TTCATTACTGAATTCGCAAA

50/161

AATCGACCTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTACAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGCTGAACCCAACAGATTTGTGCGAGTTGTGCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSENDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEEDKRFQDPSDS
DLNDDGDSTGTGAATPHRHGYYPYFTDHYYYTKSGLKGKGNIKVPYTGEYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLSNKEILANKNPYRDFYNSRKVDRDLSLSGCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSINFQEFDLDI
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPVTAHYMYIYKSLAKVNFRLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDATMIQYLFYLFQIPILAAPLSSVLLNSQKSTFLKN
KNVLEHDYLDQETAKINPSRDITVGEQRSYETNPFMKFMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG
GIDNWYDTAKDTSIKHNVPMIIRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTGCTTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTTTGGTCTTTTCGTATATTGC
GGGTTCGCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGGAAGAA
TTCTCTAAAACATATTCTATACTTCAAAGTTTTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATATAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACTTAAAC
AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTTCGGGTGTCTTAACGCATTCCGATG
GCCCATATGGTGAGAACCTTGCCCTTGTTTACACAGACACGGGAGCGGTGGACGCCCTGGT
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCTCCTGGAACTACCTGGGTGAGT
TTGCAGAGGAAGTGAACCACTTATAAGCACTGTTTCTCTGCTCCTCATCCTCGTCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAAATCGACGA
CCATAAACCCCTGCCAAGACCGCTACCCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCTCTCTAGTGATGCTACTTCATCCACTACCACCA
CCTCATCGGTTGCTACATCGTCCAGTACCCTTCTTCCGACCCTACCTCGAGCACTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTCTCCAGCGGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTTACTACTTCCACCGCAAGCTCCAGAAGGTAACTTCCAATTCAAGTTA
ATTCTGTTAAGTTTGCAAAACAACCTGTGTTTCTGCTCAAACAACCTTCTGTAAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG
CAACGAGACTTGGGTCACTTCCAGAAGTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATAACCACAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA

10/030019

51/161

TCACCTTCGGAAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTACTCCAACAGTGCCTTCTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACTTTAGAAAATTTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGCGAG
CTACCGCAGTAACCATAGATCCCACATTGGACCCCTACCGACAACCTCAGCTAGTCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCCTAGCTTCGCCATCTCCACTGCCACCACCACTG
AAAGCAATCTGATCACAAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAACTTCGACATCTTGTA
GCACCTTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG
ACACTGCCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAAACCCGGAG
AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTCCTCGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAACTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGLVAVKAQTTFPNFESDVLNEHNKFRALHVDAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTDTGAVDAWYGEISKYNSNPGFSESTGHFTQVWWK
STAIEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSTESVGS
STVSSASSSSVTTSYATSSSTVVSSDATSSTTTTSSVATSSSTTSSDPTSSSTAASSSDP
ASSSAAASSSASTENAASSSSAISSSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNI SNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPSFAISTATTTESNLITN
TITASCTSDSNFPTSAASTDETAFTRTISTSCSTLNGASTQTSELTTSPMKNTVVPAS
SFPSTTTTCLENDDTAFSSIIYEVNAATIINPGETSSLASDFATSEKPNPTSVKSTNE
GTSSTTTTYQQTVATLYAKPSS'TSLGARTTSGNSRSTTSQQDGSAMHQPTSSIIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCTCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCCTTTCTCAACATCCCTATT'TAGTGACACCTTTTCCCAAAACTTCT
GTGAAGTTTGTCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTCGGTATTCTCTTTTGTAGGGTTTCG
TTTGCCTTCAAGTGTTTTGTCTTATTTAGCCTTTTCCTTTACCTTAATTTTTTCTTTT
CTCTGAAGAAAAATGAATGAGTTTAAAGATATAGCAATTAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC
AATAATACATACTTACAAACATGTACAGATAGCACAAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAACTATTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AA'TAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTTGACCATATCCAATTTGTGTCTGGCGTTTCTTA
AGCTCACTGTCATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTTT
TTCAC'TGTTACTTTTTTAATTGCTATATCTTTAAACTCATTCA'TTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCAC'TAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACCTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC
TCTTAGCATACCTATTAAAAC'TGGAGTGGTCCCTATCCAGTCTTTCCATCAAAACTC
ACTCTTTGCCACTAACTTCA'TTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTTGGTCTTTTCCCCATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCA'TCCGAGCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTC'TTGAAAAAACTGTATTAACCACAAAGT
CCTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAAAGATACTGCGAACTTAATTCCCC
CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGCFFIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRITIKTPLNGNIIVDNAKSLLAYLLKLEWSSLSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTD'TLLVFSPMNEFEGRRLRNA
QNELYIPIIKGMEEFLRNFSSASNIRLQILDADIHGLRGNQQSDIVKNAAKKYSLSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTA'TTTATATAAACAAGATATA
ATTT'TTAAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGGAATAATGGCA
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCTTCCAG
GACGTACGCGCAAACATATTATGGAGATATTCAAGGAAGAAGAAGAAGCTTTTTTCGG
CGATAGAAGGTATAATATATGCC'TGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTCAAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAAACAATTC'TTTCAGAAAGTATTTCTCTCATGTTTGACC
GCAC'TGATCTATCTTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GCTTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCT'TTTCGGGGTTGCATACAACCTTGTAATTTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCGAAAATTTA
ACATATCTAATATATTAATTGAAATTTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCTGGGTAATGCAGTGGA
AATCTTGTCTTCAAATTAATGAGAGAAGGGCAGCAATGACAGTTCATTTATCAAAACAC
ACCTACAA'TTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATAT'TCCAACAGATGATTTTACGCTAGCT'TCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT
CTGTTATTCGTGAAGACTT'TATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTTTAACAACCAAGTCACCTCATTATTTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA
GTCGGTGGTCAAATTACTCATGGCAAAAAATTTACCCGCATCAATTACAGGTCTCTATTA
TCCAACTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTCAGTTTCATCAGCAA
TGGATCTCAAGCATTCATTACAGAAATGTTCTCTACAATAATGCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAAATCAGACCTAATCAGTAATATTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDVPVPRHLHKSCTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQILSESI SLMFDRTVSIFRKCTIEGGFPHLIARLYLRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNILIEIFHLLDGLAFKVNPDLSISISTASAETIFRSISEGNHGV
LELGRSLMFPLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANNFNEDNNGLLGLIVDRNIPDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVITDENTIIISLENTQVSRWSNYSWKISPHQLQVSIILQRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTAEVSHSNNQDATASPLSSVSSAMDLKHSLOKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCCTTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTTTTTATTCTC
CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA
CGCGACGCGAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTTGTA
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGGCGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCTATTAAGTAATA
CAGCTTTTGTACAGAGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTTCTCGTATTAAAAGGTGGTCTCCGTTCC
ATGAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC
CAGAAACACCAAGTGAAAAAATCACCTTAGTGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCTTTAAATTTTGTTGAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG
ATCGTCAACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAACAGTTTACAACAATTCAAAGATGATTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATCAAGTCATCATTTCAACTAGAAAGAACCC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGTCACTCTCTCTGCCATCGTGACAAACACAACAAGTGACAGAGACGCATTCCATATCTT
CCACCGATTCTTCGCCGTTAAATTCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

54/161

AGTTTTCCACGGTCTACCAGGTTACGTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAATTAACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCCTGGAAGTTTCAAATTCATACTATATTATGACAGAATTGTGCCGAAATGGTA
ATTTGGATGGATTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAATAATCATCGTGGAAATTAAGCCTGGCTTTACGATTTCATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTACCGTTGGAGGATAAAAGTTTTGAAAATG
AAGGTGACAGAGAATATATTCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTCCCTGGGTCTGATGATTGTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTTCATAACAATAGTAATATCAACAACCTAATATGAATAATGGCAACGATAATAATA
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTCCTCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPSNNKL
TRSTGTNLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNISPISLKQWNQRFKNDARTENTSSSSSYSAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPETPVKKSPLVEGRDHKHVHLSSSKNASSLSVSPNLFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELNTSLQQFKDDLYGTDENFPPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLLISSNKL SANPD SHLFEKFTNVHSIGKQFSTVYQVTF AQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGLDGLFQ
EQVIAKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPDNGNAWH
KLRSGLDSDAGRLSSTDHSESLFSDITKVDNTDLDFDERDNI SGNSNNAGTSTVHNNSN
INNPNMNNGNNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTATATGATAAATGGAACAAAAAACCTTGTTTTATTATACA
TACTTTTTTCCCAACAGTGTCTTATGGCCGCAATTTGTATAAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTGTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAAAGGGAACATATCGTGCACATACGA
AGTGTAACAATTGTA AAAAATGTTAGTAACAATGTTCAAACCTCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGVSQSDPLWQWSVLLLLSLSHFLLD SERL
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

55/161

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTTTTCATTTTTTTAGC
TTGATTTTTCAAAAACTTATGGGCGT'TTTAGGCT'CCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAAACAGTACGCC'TTGGCGGGGACGCCGAAGCGACTCCTTCT'GTTCCAA
GCTCAATGGTCTT'GCGTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCCGCTTTTGG
GCTGTGAGAACCGAGAATTATCTTTCGCTTGATAGATACTTTAAAACTTCTACTTAAT
ATACTTTCTACAAT'TTTTGGTACATTATATATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACCTGATCAATAGCAAATTATAAACCACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAAAATATAGGGAAAGGATTAGGAGTGTAAAC
CATACTAAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGT'TTATGTCAGGT
GGTATTGCCTTGGATCCGTGAA'TGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA
GTC'TTTCAGAAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGT'TACAACGCTAAGAGAAGAAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)
MAAQKSFRIKQKMAKAKKQNRPLQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)
TCTCGACAGCCCAAAGCCGAATTGCGTTAGTTAGCCCACGCGGAGCGTAAACGCAAGG
ACCATTTAGCTTGGAACAGAAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTTGC
CTCGGCCTGCCGCGTGGTGGTGGTAGTTT'GAGCCGGAGCCTAAAACGCCCATAAAGT'TTTT
TGAAAATCAAGCTAAAAAATGAAAAAAAAAAAAAGTTAAAT'TGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATCTTAAATTTGTAAGGTTTTTTAATGGCCTTTCAGTTCTAGTATTTTTTATAAAACAA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTT'TAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTT'TAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTT'TGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAA'TTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT
TGCCAGCCAGACAATTCGGTTACGTCTATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)
MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFEYIDDHRSKG
IVVQLNGLRNKCGVISPRFNVKIGDIEKW'TANLLPARQFGYVILTTSAGIMDHEEARRH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)
CTTCTTCGGGGTTCCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGT'CATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTTCCTAT
GTGTCATTACTCT'AGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATAT'TTCGTTATTC'TTATAAGCTAAAAGATTAAAAAT'TTTTCCACTTTCCTT
GAAATTTGGTCGGTTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAAAAATAAAGGGAGGAAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTTCGAAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCA'TGG
TTTATAATGAAGATCCCGATTTACCCGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGTAGTAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAACATAATGGTCAAG
ATGGAAGAAATGTCTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA
AGGAAACGCAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACCTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TAAAAATTTGGTTTGTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATTTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTTCATAGAAATTAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACCTATTTTGCTT
ATAATAAACTCGAACCCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCCCTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTGTAGCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGATACACAGAAAAACCATCATTTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTGCGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGGTTGATACAGTGTGGGATAAAACTATAAAAAATTTTTCCCATGAACCTCTC
CACCACCTTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT
ATGTTGGTAAAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTGAATGCTCAATTTTTTAACCTTGCAGG
AATTGATCAAACCTGCTGATGACGTATTTTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCCCTGAAC
CTGTAGGAAATCGAACCGATTTTGTCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGCTATTAAGGTGACTTGACA
AGGATAAATCCTTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAAATAAGAAA
CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAACATA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTTGACTTCCACTCCGTTTGGCGATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTTGGACGATTTGTCTCCAATTATTTTCCAAC
CAGAAATACTAGGATTAACCGATTCTGTGTTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAACAAATAACAACCTTTGGAATACACCGATATTTCTGCTAATTCACCTTCAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA
AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACCTGAAACTGCGC
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCCCGTCATAAAGATG
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTCAATCGAGTACGTCTGAAATATCTGAGGGAT
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVLDLMNVLDDKDEIKQESVPVSDREIEDT
ESDASAVSSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

57/161

LSEIYGMTSGSYPVVTNLVINQTTGELETEYNKWFFRLHYLITEKQDGRKRRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFPEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLLFLDLSHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKLADDTWEMHLKRNC SVITDLFVGMKSTLYCPECQ
NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLLEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFVGPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQOFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDDDEGTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQWLWNTPDILLIHLKRFESQRSF
SDKIDATVNF PITDLDL SRYVVKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK
WYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEI IQKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMI ECNEDVQAPEYSNRSLEVGHIETQDCNDEDDNDGDGE
RTNSGRRKRLRLLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3146 bp, CDS: 501-3149 (SEQ ID NO 167)
TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCTTGTGCTGATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCC
TAAAGCGGGGCGCTCACAAATATCGCCGCAGCTACAGCCGTTTTTTTTTTTTTTGTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTTCATCGATATAAA
GAACACTGTTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTCACTTCTTGAAGTACAATGCTGTCCCAG
AATGGCAAAAACATTATATGGACTACAGCGACTGAAAAATCTTATTACACGCTACAAA
CAGATGAACCTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTGCCTGCCAAACCTTCTCCTTTTCAAGAAGATGAAGGAAAAGATATTTTACA
AAAGAAGGTGCTTCTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAAATCTGCAATTAG
ACACTTATGATACGTTTGTGGTGATTAAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCACTGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACCTGATCGAATCGGAGCAGTTTTC
AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTTCCAAAATTTCCAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTATTTTACCAAGAAAG
CATACAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGAGTGTGTCGCCTTTTTGTGGGCTA
GTGAGGCCATCCCATACACATTACAGCATTCCTTGTACCACTACTTGTAGTCCTTTTCA
AAGTCTTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCAACAATAACATCGCCAAAGTCTTGCCTCGTGGTGTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCCATCAATGTGGA
TTTCCAATGTGCGCAGCACCTGTTCTAACAATATCGTTGTTATCTCCCTATTGGATGCCA
TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTAGGTGTAGCGTTGGCTGCAATA
TCGGTGGTATGTCTTACCAATCTCTTCACTCAAAACATCATTTCATGTCGTAATTGA
AACCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA
CTGTGGCCACTATTTTGTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT
CAGGTCAAATTGCAATCATTCCCATCGTTTTGTTTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTTTTTGCCATTCTATGTATTTTCCGTATCCTGATGTTGGTTGTGG
GTACTTTCGTCTCGCATACAGTATCCGCTATTATCATCATTCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTTTTCCGTTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCCGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAAGGGCGATCGCTATTTAAGTGTCAATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTTCTATGTGTCACTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYDSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA
SSVSSTANENLQLDITYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLQCLKSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ
AETIELLSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWRPLRPINLKFTSINNVALPKLFFTKKAYKLIYFI
ILVTGLLLGIKTFNDAAQHRCMALVECVAFWLWASEAIPHLHTAFLVPLLVLVFKVLKITS
GAIMSAAASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIITVTIVATILLWCVESQIEGAFGSSGQIAIPIVLFFFGTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVVSHT
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVT AISKVDKGRD
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTTCGTTAAGTTCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTGTTTTATCTCTTTACTTA
CTTGTCTGCTTCCATTTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCTTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC
GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCCTTTCGATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG
CATCCTGAAATATTTACCCGCACTACGCAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTATCGTAAGCAAAAAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAAGCTCTTGAGATGAAGGAGATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGTGGTGCAGATGATCATATAACAACAATAATAACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAAATGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTCAT
CTCTCGTGAACGGCAATGCAACAGTGGCGGTGGTACGAGCA'TTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTGAAGATGT
TGAGTAAAGATATATCTAATAACCAAAGTGGAATGGATGTGGAATAATTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTTGTAAAGTTCCATTTTTTTCAGAGACATGTACCACCCGTTATGTGCTTTT
CATTAGGGTCTCTAGGATTTTTTAACAAATTTAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTATGAAATCATAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGACACATTT
ATCGTAGACACCCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAAATGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

59/161

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAACCTAAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAGTGCAGAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVDKWVNEEDGRNDHHNNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE
SSSRSSSLNKNLNGNANS GGTSINGTRGSSKSSNTHFYASTAYGVRMLSKDISN
TKVELDVNLMIIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHVVFFDLVVTLGGDGTVLVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGPSFPLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMSKSRAPAWAAFDGKDRIELQKGDFFITICASP
YAFPTVEASPDDEFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLV
IRDKYSLEADATKENNNGSDDESDESVCNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2: 877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTTCAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTGCTGAACTTTTTTTTT
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATATATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAATGTATGTTACGGCGAATACAGAATACTATGTTTC
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAAATGAAAATGTTCGCATATGTGCTG
AAGGGTTTGTGTTGTTCCATCTTATTTTGCATAACATAGTTATATTTACTTGGTTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACCTTATTTCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACCTG
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRITLSDYN
IQKESTLHLVLRRLRGIIIEPSLKALASKYNCDSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAACATAACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAAGTC
AAGCCATGTCTTTACTTCGTTTAAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTCAAACGTTATCTTATGAACGCCCAAATAGGGAAAAAATCCTGGC
AAATTTTTTATTGCTGTCATCCAAGGCTATGCTAGAAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAATAAATATTC
TCCTGGTAAGCTTCTAATCAGCCACAGTTTGTCTGCCAAAACCTTAAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

60/161

TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATAACATGATGCAAAACCATT
TAACCCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTCCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTTCTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCCA
TGGCGTTGTTTCGGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLTLPQPVADYYYHMDLASTADLQSDIAQSFPFTQFQTFITAFPWYT
SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVSNVFPSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCTTTTTCTTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCCGAATTGAGTGCCTAGGCCGAAGTTCAGGGCA
CGGTACCCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTGGTAGG
GAACATCACCTTCTCTAGTTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAAATAGGTCTCGAAAAGAAATATGTCCCCGA
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTTCAAGAGGAATTTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACCTCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTTATTTGGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTGTAGGTCCACCAAGA
ACCATACGTTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAATTATGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATGCTTTGACTGATTTGGACTCCCCATCTGA
ATTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG
GTACTTGTGGCTAGAGAAGTTTGTAGACTAAGAGGTGCTTTGGTTCGACAGAAGTCAACC
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPIVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTPQWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT
EWAEEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTT
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAAGAAATGACATTTGCTGCTTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGCTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTGATGCCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAG
CGATGGTGCCTTCCGTTCCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTTGACTGGTGGTTCATTGAAGCTGCTGTTGTGTTGGATTATTTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT
TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTCTCTTTCTTTATTTGTTATTAGCACACGTCAGTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCGCCATAAGTTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAAATATCCTTATTTTCCGAGTATAAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCAATTGGTGATATCATTTGTTGTTTTCACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCACATCATACAGGTTGAAAAATGTTGCTTT
TTTTATATTTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTTCGGAC
TATTTTTTGTATGATGAATTTTCATGGATTTGATATAATAAACAACTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTCGAAAGAAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMSGWLQEFGKTAIYENEQYGETL
YGMHAPRGDGEATAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIIVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVVDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHGLPSDQLTNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGN SGHDITTFGRIPeamFRSINNLEKFHQSF FFYLLLAPRQFVSIS SYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVL
ILTNPFISITLFGFLFFDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAAGCGGTATGACGTTT
TTAGCAATGTAATTATATTA AAAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTGCTGCCAGATC
ACTAGTCACTTGGTCGCATTCAATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAGGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTTGTACAAACGCCAAGCCCGATAGGTGAGACAATTCCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT

10/030019

62/161

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCCTCCGTTCCGCAACCGTGCTCTCTGTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKKLISKHHLPEYYFSDLFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCEFLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMVGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTTCCTTGAGATATCTTTCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTATATTTTAGTACAACTTTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACCTCATCAAAATGAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTCTGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GAACCTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTTACTACAAGGTGCGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTGTGGTGTGGTGT'TTCTTGCTTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGTCTACAAGGTAAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGGKKRKKKVYTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTACCT
CTATGGTATCCAGGATACTTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTTCTCAGGTTCCGAAATTCATGAATTTGCACTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGAGTT
TATAAAAAGTAATTAAACAATGAATTCAAATTTGCAAGTGAGACTATTCATTACTGCAACTT
CATTTTCTTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCCCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAATTACCAGTTTGTTCCTTTTCCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMILTQGTFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTAGGTGCCCTGCA
ACACTAGTCATGGTAACCTTCGCAGTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTT'TTTTATCAAT
GTGATTTTCGCGTTTACGCCCATTTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTT'TTAGCAAACCTTATCAGGGGAAAAAGTATAT'TCCATTAAAT
GACACATGCCACCATAGATAAATGGATAAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAATGCATATATCACGTTTCTGATGCTTCTGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTT'TTGAACAAGAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCGGTGATACCATTGGT'TCTGAAACTT'TTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTT'GAGCACTGGTTCATGATATCATGCGACTAAGTAACAGAAGAAGGT
TCAGAGTTTTTAGAATTTTTCAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAAGTACGATATGAATTCCGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATATAAAACACTACTAAACAAGCCGTCTAACA
AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATAT'TGCCTCACTCT
ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGTTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTTCAATTTTGACTCCTGAT'TTCCGGAAAGAAGACGTC
TGATGAAAAAAT'TGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG
AAGGTCAAAT'TGTTTTGCAAT'TCTATCGATAGTAGAACACACTTTGGTTCCACAGTCA
GGAACGCATCACGTGCTTCTAATTTGTTGGTTAT'TGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTACAGTAATATTAATGTTATACTTGAACACTTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAGTAAGGAACAAAAGAACAACAACTCAAATAG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCCCTCTGGCAAAAAACATGGAAGACTTTCGATATCTAG
CCATTATTCGTTTTGCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTT'GCACTTCATTTCGCCCTTGTTGCTGAACGACTTGATAAATAGTC
CACTGAATTGTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTATTTTTCAGGGAATTTTCTTGCTTAACCTT'TGCACTAACAGATTTTATGAGC
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAATTGGATGCCCTACAT'TGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTTTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAATAAATAAACGCCAAATAGCATTATCGGAAAT'TTCTCCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACACGCGCAAAAGAGCCGGGAAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAAATGTCCGGAGAACAAAAAATTTGTCTCCGCTCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPKSVEGFEXSIRYLNIAISLYLPAVGD
TYFQRAKIYELITGKFSLYFFELVRGALVRIPSKCALNNLKDILTPDFPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVLPQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSDLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRHRKFCTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDENDDYVYDSPDMINNIIGCPTLTKVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTITGPLSSDFLSYPDIDADEDITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTGTTATTATGGTACATATTTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCATTATCC
ATTATCTATGGTGGCATGTGTCATTTAATGGAATATACTTTTTCCCTGATAAGTTTGCT

64/161

AAAAACGGTTCGGATCATACAGGCATGTAAACATTTCATTATCCTTTTTTGACATTGGATA
ATGGCGTGAACGCGAAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAAGTGT
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTCGCAGAGAAAAATCTATAGCGA
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAAGTATGATTTTCATGTTTAGTGGGTTCCTGTTGCCAGAAATGGGGCTAACT
GCGAAGTTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT
CGCATGGGTGGGGAAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAATGCAGCACGAAACCCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA
CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG
ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAAACAAAGACAACCGCGGAACAACAA
CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTTTACGAGA
CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCCAAACAATCACTAGACGCAGCAGAAAAAGCTATACCAAAAGGGGTCA
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAATCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGAGGCGGCAGAACCGCCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACCTTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCCTTGTGTTGGACTGGGGCCG
TTGAACGTTTTCTCAGCTTCAGGTCTCGTAGTCTTAGAGAGAAATTTCTTCGATGTTTACC
CTTGGGCCCGATGGGAAACCACCAAGCAGTTTACCGCGGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCCAAGCCGATGACTGAGA
GTGAAGTCAATTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAATCT
GCGAAGTCACTGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAGCAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEKNLSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPPFARNGANCEVTMTS
VAGHLEIGIDFSDSHGWGKCAIQELFDAPLNEIMNNQKKIASNIKREARNADYLMIWTD
CDREGEYIGWEIWQEAQRGNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHAVG
TRIEIDLRAVTFTRLLTETLRNKLNRQATMTKDGAKHRGGNKNDSQVVSYGTCQFPTLG
FVVDRFERIRNFVPEEFWYIQLVVENKDNNGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKSPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFPHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACCCSEDAKGQSM TLVLVDWAVERFSAS
GLVVLERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTSESELILLM
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FORREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAATAACAGCTCTTTCCTAATAATAACATATACACTAGAT
ATATAATACCAATAAATTAATAAAGAAAAACAAAAATAACGTAGCTTTGTACAG
TCGTAAAAAAGAACAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTTGTTGTTATTCCGTAATCGTGGTGTCTCACTTTTGAATTTCACTTGTTTACC
ATAACGGAACATAATTAATAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCCTCACAAGGAGCCTGTCTGTTGGTTATATTGGAAGC

65/161

TATAGATATAATCGAATCCAATGACTGGTCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTCTAGTCCTCACATCACTAAATGGAAC'TTT'GAGAGCAAACATGTGGTGATACCAT
TTAAACCAGATGGTTTGAATTTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTAAAGTTGCGACCCGC
TCACGGGTAAGGTATATATACGAGACTTAAATCCAGTAATGGTACGTTTATTAAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAAC'TAT'TGTAC
AACCTTTATTAGAATCACCGATTTTGAATAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAAT'TTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAAACTTTTAGTGGAATAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAGAAGGAACTGTCTGGGGAATAACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAAGGGAAATAGAAGACTTGA
AAACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAATCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGCATGAATCCTTAAGGGTACTGCACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAAC'TAT'TCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYPYILVLTSLNGTFESKHVVIPIFKPDGLKLGRPVANSNSSSSSLRGGK
RVDSTHFSQVRSNDNGNFDNRVLSRNHALLSCDPLTGKVIYIRDLKSSNGTFINGQRIGSND
VEIKVGDVIDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEELVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTTHLEYTNKLLVEKNDDQQLVKLQNLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFFKKSFEVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTTCAGAATCTAATCAATGATA
GTGTAATGCTTTTGCTGCCTATCGTGATTGATCATTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACTTTT'TTATTTAAAAATAAAAAATCACAGTTAATTTTTCATGATCTTGCAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTGGCTTTGCTTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTCGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTGTGATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGTGTTTTTCA
AAATGTGCATCAAAATTAATTTCTATTTTGTCTTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAATAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
AGCTTCGTGATTCTGGAAGCCTTAAAGACCAGAATTGAACAATTAATAATCGGCACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTCAITGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

66/161

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAATAATTTATTGATGCTGAAATTTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTTAGTCATTCCGTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAGTGGGCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTACATTTGACTTTAACTTTGGAATCCCCATTTTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATAACGGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTAT
TAGTTGGTAGTTTGTATCGGCTTTCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC
TGATTTTGAATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCATTTCTACAGGAAAAGTATGGCCATTAATTTTTAGAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCAAGGAGGATGGGTTT
TGTCACTTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTTATATGATTTGAGA
AGAATCATTTTCCCGTTGTCAAAATATATCGCATTTGAGTTCAATTTCGCGAGTACGAAAAG
ACAATTTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAAASYLDTPDEHDFRKPCTAKVVTTLQTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSSLFGWLTVLVKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDGNDSSSLIHLVKRIVEGSGDGDNHSAPERTNV
YLWMYVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLHFCRKKILKNLELKYSECPRELRTQPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANQAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTGVYSTTVFVIGLSSFLVIVPSYLATLLNLKTLKFWPSVQQLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQIGIMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGLQLPQPILILIIITLIYSVMSTKILTSGLAYFIIIG
FYVYKYLIFATDHLPHSTGKVVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCAAAATTACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTTGTGCAATTTGAAAG
ACTCTTTCACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTG
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTCGCACCAAAACCAGCTTATTCACAAGCTTATATTT
CTAATTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT
CCGAATACAATGTCTAGAGAACATGAATGGAGCTGATAGTATTATCTTAACAACAAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

67/161

CTTTCATTAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCAATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACACAAATGACGACTCCATATCTCCGGAGG
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAACTCAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTTCATCCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTTCAGGACCATGTCC
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAAATTGGTGCCTTGAAGATTAATAAGAGAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQQLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNVAEYDNDLFDEFNM
NGSNFNADTHYKDNVSHENTPALTNVMTDGSSEYNVLENMNGADSII SNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDISPEEFASIYC
KDLDMTSATLQTOIANIIKEQLKDLENIAATEIMSDLHVIINLTCLNLDQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHVPNDAAFG
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLKRETDRLSRRGRRLDDL
ETMTRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCTCTCCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTG
AGTCTATATGGAGACACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATTTGAAGGGGTTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATTGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACATA
TCAGCTCCATTTCATGTTCTCTAGGACATTGTATTCGGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATATCTTTATAGTGTGTATCAGCATTTG
TTGAAATTAGAACCGTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCCGCATAG
TTGCCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGGCAGATTGTGTGCTGCTATGTGCCTTTCTTCTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTTGTCGTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDIIIFVCQ
SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTTCGCTACTGGTGTCTTTTAGCTCATTTCCGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCAGTGGAAAATTATGGAGAGTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTATTTACAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAATCACCGACATCAAACAATTTTGGGAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAAACAAAAAATTGAACAAGG
CCGGTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTGGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNR

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AATAATCCTTTCTCTTCTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTT
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCCTGGATGCGTAACGACGACAGCTTGCTAGAAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAACCTATTTAGGTGATGTCTCATAAAGTGAACCACTGGAAAATGACGCAAAATATC
AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAGAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCCGCCCATCCCT
CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTTCGTGGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCGAATTAACCTTGACCCCATCCAAGCTTG
TCATTACTAAATTACATTTTGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTTGTCTGCTGCTGGTTCGTTTGTCTTTTCGTTTTTAAAATTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAAC
TGGATATTGTTACAAGAGTTCTAGTCTTTTGATACCATTTTACGCAATTACAACCGCATT
ATTTACCTTTTTCATCTTCAGTTTACGGTTTCAGTTTATTCTGTTACGAAAGAATGATGGT
GATTCAAAGGCGAAGTGCCTAGGATTGTAACCTCCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTTGAGACCTTCTTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACATTTTTTCAATATTT
TCACATGTGTTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATGCCATTGTTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCTCAAATCTCACTCTTAAAATTTCAATGGCAAAATTTCTCCGCACAACCTT
AGACAACATTTTCTGTTTTTTATGAAGTAAGCAAAAATTTTGAATCAACAACGCTCCAT
GAGATTCCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTGCAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACCTGAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAACCT
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

69/161

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFYIDDHRSGK
IVVQLNGRLNKGCVISPRFNVKIGDIEKWTANLLPARQFGYVILTTTSAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGTGAGAAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC
TCACCCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAAC
TACTATAAACGTTTGT'TTTGT'FCC'TTACGCACAATATCCTTGCCTAGAAATCGTTT'TGA
AATTTAAATTTTATTACCATTATTTGATTTCGCCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTATTTGCGATAT
CAGAGTAACTTAACTAACTATGCAGGGCACTTTTAAAAAGTTT'TACCATCCCACGCTTA
CGCGGATGTCCTTCTTGGATAAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAAGCA
CCAAATACTCCCAGGGGAACTCTTTGAGGGATATGTTTGATTTCGAAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGCTCTTCC
AAAAGACAAAGGGGAAATTTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTTTCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCTTGGCGCCAGCCATTTTATTTTGAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGTCTTTTCTGGATACGTC'TTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGGCGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFIAPVSYWKEDKALFFPHLI
GTAMDGTKQONIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLTEADARLS
LNDSNVQIIIEVNLVENAVKSALVKTLARWANRVPFSWRQPFYFECSRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAAGTTATACCAGAACCATCCTTCCCAAGGCCCTTTTCCCGCAACATATCC
CATACTCGAAAGTAACTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG
GGCAATTGCCGCTACTAGTTTTCAGGCATCATAGTGATGTCATGTCATCACTATTCGCT
TGAATTATTATCTTCTTCATCGCTATAAATATAGGAATCGATTCTTCTTTTTTTTGAAAAA
GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTTCGAAATTTTGGATTTTGTATTGTTTGTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCCTCAGTATTAAAAATTGCAAGATATCCC
TAACTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCAC'TTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAACTAGGAGATTACATCTCGAGAGACAACG
TTAACTTATTGAATGACAAACTGAAAGAGTGCCAGTAATTGAGCGTCAAATTTGAAAAACA
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAAGTTAACAAAGAACTGATTGATACCAAGT
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGCAGAGCAGTTTAGCAGGGAACCTAACGGACCTTGAAAAAGATTTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTCTTAACTTGGGTC

70/161

AATTTTTCGAGGCCAAAAATAAAGGAAAAGACAGAAGTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAAATTCCTGTACACAAGATATTCAAACAACCTAAGGAACCTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACCTATATTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAAATGGAACCTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQOGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKEYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDIYISRDNVNLLNDKLKEVPVIERQIENIKLOYENMVRKVNKELIDTKLTDVTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLILLQDKKIDNDEREEL
FKVVQGGDDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPBKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTGTGAAATTTTCATGTTTGTGAAAAATTTGGAAAAGGGC
TAAATTATCCGTCGGGGTGTCTCTTAGCTCGGCTCAACCTAGGCAAAATGCGTTTACTGG
GGCCATCCAAGCTCATCCTTCCAGAGATTTCGCCTTTCAGAGGCAAAGAACTCGTCTCCGC
AGGCCCTCTTGTTCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA
TGGTAATTTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACATTTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTGTGTACAAGAACAAGGTTCCCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGTATGTTGAGAGAGTTTCACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCACCTCCGATGGAATAATAAACG
TCACGGGTTACCAAATACGAGGCCGAATTAACCTCTACGCTACTATAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGGAAAATACAATATATGACTCAATGCGAATTTAAA
AATTTTCACTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCTGACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCAGTGGTGTGAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACATCAGTTTGTGTAACAC
CAATGTGCGATGGTAACATTAATAATTTGTTTACGCTTTGACCACTATTAAGGGTGTGTCG
TCGTTACTCCAACTTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAAAGATTGTCCAAATCATGCAAAACCCAACTCATTACAA
GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGCTTAACAACGTCGAATCCAAGTTGAGAGATGACTTGGAAGATTAAAGAAGATCAG
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTIIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTTCTTTTCTTCCTTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCGGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACCTAGTTAGTTGTATTTCGCCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTGTTGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGCTTCGATATTAAAG

71/161

CCCCATCCACTTTTGAACACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCGAAGTTTGTGGCTGACTTGC
AAGGTTCTGAAGACCATTTCTTTCAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAAGTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCGAAAAATGGCAAACTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAAATGCTACCAAGGACATCTTCCCCTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTCTGGTTTCAAGGATGAAGTCTTGAAAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRNVGKTLVKNSTGLKNASDA
LKGRVVEVCLADLQGSSEHDSFRKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVKLLKQPKFDVGALMALHGECSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTTCACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTTCTGCCTTTCTCTATGACGCTTTTCCCAAAACAC
TACCTCTTGACACGACTTGTGTTTTCGTTTCTCTAAGAATATCACTATTTTCACTTT
TTTCACTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAACGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACATAAAAGAA
CTGTTAATTAAAGAGAAGAAGATGAAGCAATTCAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTTCTTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTAGCTAAGTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAAGTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTCG
AAAAGTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAGCAAGGACGAGC
TAGTTCAGAAAGTCAAGGAAAAACATCTACCGAAGTTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAGCTTGGATTGGCTCACCAACAAATATTAGACACATCGGGACAAA
TAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTTGACCAAGACCCAGAAATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTCTACAAATTTGTACTCCAAGTTTCAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGGTATTAAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTGGTTTGTGACAAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGAAGAGTTTCCAAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAAATACCTTTTCAGAGCTGGTCTCAAGAAG
ACCTATTCAGTACCTAAAATCATTCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVSNPNPGWFGYTGSSDHPVSDWLFDTWSTDLSLRNF

72/161

LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELVQVKENIYRTSEKAEQQRLGLLESLLDLAHQQILDTSGQIKDTPVD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTNDVINDTFLVLGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFQVVPVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVKNWSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTCCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGATATGTAGGAGAATTGATATATTTCACTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCTTTGGTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTCC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAACTTGTTCATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACCTTAACTGGTTATCTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTCAGGTAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG
CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAACACAAAAATGCCT
TTAATGACACTCACTTTTGTAAAGGTCGACAGGAATGATCACGTTAGTCCCAGTTGTAACG
TAACATTCATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT
TAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACGTGTTTACAATTGGCGAAA
CTGGTGAATCAATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCCTTA
TCGGTACTCACTTATCAAAGGAATATTGTAACAGCAAAACTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTCTCTGATAGAGTGACAAACATGTATTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCAACCATATTTACCAGAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCAGCTGG
ACACAAAAATTTTAAACGAAGACTTAGTTTTTGCCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTGT
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAT
ATGAGTTGATTGCACTATTACAGACTTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTCGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTTACACCA
TAGAAGACATCAATTCCACTAAAGAAGGAAAGAAAAAGACTAACAAATCTCAATCACATG
TATTTGATGATTTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAAACGTTTGAAGCATTCAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPSCNVTFNELN
AINENIRDDLALLKSDFFKYFRDLKYQCSFWDANDGLCLNRACSVDDVEDWDTLPEYW
QPEILGSFNNDTMEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNKTGKWEPNLDFMARIGNFPDRVTNMYFNYAVVAKALWKIQPYLPEFSFCDLVNK
EIKNMNDNISQLDTKIFNEDLVFANDLSLTLKDEFRSRKNVTKIMDCVQCDCRCLWGK
IQTTGYATALKILFEINDADEFTKQHIVGKLTKEYELIALLQTFGRLSIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNNSQSHVFDDLKM
PKAEIVPRPSNGTVNKKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACCTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTCTGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCAATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGT
TTAATGTCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAAACTTACTTTCA
CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC
ACTCCCTGGTGTATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGTGTAGAAAAAATCTATTAAAGTGTTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQPPDTPYADGVFNAKLEF
PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCCGATCAAAACCATCACTCATTCGGTC
ATTCCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATTGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAGC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTTATAAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPMSWYLSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA
GTTCTGCAGAATGATGTTTGATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTCTGAGTAGGCAGTAAATGAGTACGCATAGTGTATTTATC
CAAAGGAAAGAATTGTTATTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

74/161

TATCATATTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTTAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCATTTTTCTCTCAATGAA
ATAATTTGTTACTAACATTGAATTTCTCGTAACATAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACCTT
CTTACGACAGAACC'TTGTGATTGCTGATTCTAGAAGACCAGAACCAGAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQYVDEQSKNELKKAFTSYDRLLIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTTCTTTACACCTCGTACTGTATTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACCTCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGAGATAGATTAAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCAGA
GCTCAAAGGAAAAAATTGCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAGAAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACATATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDQKVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTGACAAAGTTTGCATGACTTCAT
GTTGTTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG
TTCTTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTCCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCTTTTAAACATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA
CCGCCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATCACCATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTTATATGTGCATTGCAAAAGCATAAACA
AATCTTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTCACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTGCGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCCACCAATATAATCGCAATATTTTTGTCA
CTTGGTGGAAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTACAGCCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCCAGAGTGCCCAAGGAGCCCCAAGGGGCTTTTACCA
ACTGGAATATGACATCAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAGAAGTTATCTCAA
AGGATATCAATTTTCATTCGTAATTTAGAATTTAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCTTATATTGAATTTACCA

75/161

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA
GTAGTGTTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTTCGAATACATTTTCCAAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCPPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLP SHFAFHD LK WFFHNR RAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDR TLISLSH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRG IARFDHFRPV PNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLR CFNSLGG LNQ
CSHSNSCKAYQNASNVT SKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDE TSA
YYMEKPGSYIEFTISEFNVNGTF SAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHF PNSTVVETEKL IAGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTT CATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCATTATTTTTTTTGGATTTAGATGTGAGACATAC TAAAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTTCGC
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAAT
AGTTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAAGCTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCAATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATTCATTATTTACGCGTCCATTTTTATAATGTTT
GAACTTTTGAGTCCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCGTGCTAAGAAGGATTTCACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAAGTTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACCTTGAG
AGAATACTTGAACCTGCCTGAACACATTGTCCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATT CATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTGCG
ACAAGACTGCCCTCCCGTCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCTCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTTCGTTGGGTGGTTTCTGCGACGGGTATCCCCTTCG
ATTTTGCATAATGATCTTCAATTCTACAACATAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCGAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTCGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTGCCCAACA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGC'TCTGTTTCATCAACTAATAATAAGTAACAATGCCCTAATCAACCACA
ACCCTCTGTCTATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTATCTCCAATAATATGCCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCCGG
CGAATATTTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCCT
TCTCCAATAACACGGCAGCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAAACAAAATAAGCCAAAAATAATAGAGAGGCCCA
CAATGCACGTCACATAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAAATGCTCCCGCAATTCAACCACACACGATAATGGTCCAGTAGCAAATGATG
GGCTGCGTATACCGAATCAC'TCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCCGACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATAATTTCC'TGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCAT'TGCTAAACAATAACAAAAAAT'TATTAAGCCGACTGAAAAAT'TCAAGACATA
TTAGCACTGGTGGCATAAT'TGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTGA
ATTCTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAAATTCGCAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTTCTCT
CTGCTAATAGAAATCTAATTTATGGTGACAACAAAAGGCCCTTTAGAACAAACAGATGTCAA
AGATATTTGATTCAAACCTTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCATGGTTTAAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGT'GACTCGTCTAATGTAAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACCTCCATGTTTATTATAATCATAGAAGACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTTACTATGGCTCAGCATCCAACACGCACGAACCTCCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAAACA
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATGTTGGTTACTCACCACCAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTTATCTTTCATGATTTGTTATATCATCACTATTGATGACAG
GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCGAAAAA
GTTCTTACCTGAAGTGCGATTTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACCTACGATGTGTCAGTCTCGAGTGTCAAGCTTTTAA
GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLLSNNSNVVAPNPSPSASTSTSPLHREIVDDSVATA
NTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNM

77/161

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNAPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKIIERPTMHVNTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKNINSKGKNERNDTSKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNNNKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNHLDLSSIKQEPHQLQQQQPPMDVQSVDSYTSNPDSDNVIKSPDKRSSL
VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNRPLRRTTVSKIFDSNPNNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPOHTNLQHEFI PEDNESDENDIHSMFY
YNHKNLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSRNNNDYY
DFMVGNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFI LGFLLATNKELQDVDVVMDNVIS
SSDELIFDITVSAFNPGFSSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVSVS SVKLLSPGSREA
KHENDDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
YEVFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTCACACGTTGTGCTTGCCAGGAAC TA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
GTAAACTCATGTGGTGCAC'TGGTGTGTTTCCAAAGACTGCACTATTAAGTGGGAATTTT
TTTTTCTTCTAGTGAATTTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA
ACGGACGGCAAACATGAAAAAAAATTACCAACCATATTTCTATTTCCCTTTCCCTTTAC
CTATTTCTCTTTTTGAAATAGTTTCATTTTCTCTCTCTGAAACGACAATAAACCAAACCTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAAACAAATTGAAATCCCAG
AAGGTGTTACTGTGACGATTAAGTCCAGAATCGTCAAGGTTGTCGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGGTGTCAACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTACTA
TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCACAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTF TKVNNQLIKVAVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVPRVDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICVRNKNKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC
AGTAATGGAAATGGTAATGATGACACCTTAATCAGAGAACCGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC
TAATGACACACTATTCAC'TTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCCATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTTACAAA
AGGATTTAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAACTGCTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTA AAAAAT

78/161

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAGATTCCGAAAGAGTAATCACATTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGGGGAGTAGAGATTGCCGAAGTTGGTCCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGGGAACTTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQQRQIIKQALAQGKPLPKELAEDESLQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIIINAG
NQSEVNPFLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVVYR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTTCCACAACCTTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTGGCTTAATTTCAATATTTCCGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGGAAGAA
TGGGCTCACCTAGGCGTTCATAATACGCGGAGGGGGAATACCAAATGCTATTGATTATGG
TAAAAATATGTGTTATTTGACTTTGTATATACAAACAGAGAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAAATCAAATCTATCAGAGAAGTATGTTAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGTTCTTTGCAGTAATTTTTT
CAAAAAAGAGTGATTTTGGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCTTTTTTGTATGAATGAACCAATTCAGTTACTAACTTTAT
TTCAACGCTGCTTGATTCCTTATTTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCAC
TCTTTTTTGTGTCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATTTGACCC
GTGAATTGGAAGAAATTTCCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTTACGACAAGGTTTTTGAAGACATGGTTTTCCCAACTGAAATTTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAAACAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGNGKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCAATATAGACTAATGCGTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTCATATCGGCATATAATAACAGTTTCTACCAAATGCTGTCCTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATTTATCTATTTTCTCTTGGCGGATTTAACACCTGAATTCGGCTAACGCCA
GGACTGATCCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGAGCAGTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCGGGAAGGCGGTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCTAATGGTGAATAAAA

79/161

TCAGGACCAATAAAGAAAAGCTAATTTTGATTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACTAAACGATGCGCAATAAAAGTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGCAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTTCTA
ATAATAAACTTTTTTACTAACATTAGTACGATGTCCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTTTGCCCAAGGTAAGAGACGTTA
TGACCGTAAACAACTCTGGTTTCGGTGGTCAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHKKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTTCTCTTGTTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCTTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTTGTTTCCGT
AACATCCATACCTTTCCCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTTATGAAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAAATAAA
ACAGCAAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGCTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACCTTTGTTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGCTTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTCGTGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTTGTTGTTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGCTTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAAGAAG
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRINELTLLVQKRKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKASRTGPKALPDAVTIIIEPKEEEPILAPSVKDYRPAEETEAQAEFVEA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACCTATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAGGAGT
ATGTGCTGTGAATTGAAGTGTTAGCGCGCGATTACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAAATTTT
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCCATTCCAAATATGCTTATTCTGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTTATTGCTCAAGCACAAAAAGCAT

80/161

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTC AAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTPCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTTGGTAAGACCCAGTATTGCTTGCACAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA
TCGTTAATCTGTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGAACGTAACCTACTAAGTGGCGGCGAAAATGAAGATTTGGATGCATATATGCAA
TGGGCCAACTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTGCATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTTGCGGAAATTT
ACTCAAAACAAATCATTAGAATATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAATCCAAAGGCAAACAACCTAGTAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA
ATGCCTATTTGGAGCAGGTCAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACCTATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTNTSGTIAVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMHYQSITKIKSILNGKYIITSGNDSRVIWQTVDLVSASNDPK
PLCILHDHTLPVTDVQVSSSQGKFLSCTDTKLFTVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKILKGNATVNLQ
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTL
IGDTEGKVSIAEIIYSKQIIRTIQTLLTSQDSVGEVTNLLTNPYRLERGNLLFEGESK
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDNSNAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTCAAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTAAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCTGTTTCTGCTG
ATTACTTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT
TTGTATTATTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTCTTTTGAATAAAA
GAATTTTCTTTAAGGAGTAACCTTAAGCATTTAGCTGCACATTAAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGGGAAGAACATTTATTTTTTTCGACCTTCTTTCCCAATACC
CAGCGCTTTTAAATTGAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATAACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATAACCGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATAACCGGTACTCACAAGTATGGTAAGT
TCAACAACAAACCAACATGACACTACCACCTTATGGTCTGGTGAAGAGCCCGTAAGAACA
ATGCCGCCCTGGTCCATCTAATTTCACTCCATAAAATGTTTGGTGTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

10/030019

81/161

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKGEHDFTTTLTLSSDGSLLLLTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTCATTTTAAATGTCTTAGCTTTTGTPATCTTAGATGAA
GTTTTAGTTCTGTATATCACGATCAAGATATCATAAATCAATTTATTCTTCT
GTTTCCCCTCTTGAGGCATCAAACGAGTGTGTTGACTGATACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCCAAAGCTGTGGCACGTATGAACTGCTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTTACTGTATTCGCATTTTCGCCCCGCTAGCATTTCTTCGTTTCATGCTA
AAAAAGAGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC
GGAAAAGGGGGCTGGTGTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAACGAATTCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGTCCAAACAACGGTCAATATGGTG
CCGACAAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGGCTACGTGGATCTAAGGTGTGCAACAACCATTTCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATACGGCAACTCAAACCTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCTCAGGAATTCGGGGGCCAAGGTTCGTCAGGATTCAAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLKSLGVLAGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSSEDKAHKDLLEVLVHKSLLVQVAKDSVVQILKNSAARWPRIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTTCATCAGCAATCTTATCTGAGTAAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTAAATATAAGTAATGAA
CTTGGGTAAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTAAATC
AGCTAGTGCATACCAAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA
CCAAATTTGGTGAACCTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCACAATAAAAAACA
TATTCGCCGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTTCAGAAAGA
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTGGAAATATGTTTGCCACGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTTTACACATATCACGATAACCGCCTACGTATTTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC
TGACAAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAAC
TGAACAAAACACAAATCACTTTCTCATTTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAAATAACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCACTGAACTCTGTTCAACAACAATACTAATTTTCGGGTGACTTATACTCAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVLLNLVFTDNILEICLPRFVSREDLRFVNNTFYTYH

82/161

DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPE
VQQTILISGDLYSIALAVTSIESALITLDDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCGGGTAAACGGAA
TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAAGTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCCAGTTCA
TTAATGAAAAGTTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACCCACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCATTTTAAACGAAT
TACCTGTCACATCCGAAGATCTTCCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAGAAATGCTG
AGAATTGGTCGTCAAATCTGCAAGAGTGGGCAAAACGAGTTCCAAGAGATGGTCCGAGACA
AAAGTATGGTCAATGAACTACATACAAGAACGTTTTTTACACCCCTTTACAACCTGAAGAAAA
TTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVAstilHSSIHVPSGGEIISAEDLKELEISGNSICVDNRCPK
IFEPHRDWQPILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA
NL SLNENLPLTLRELSTRVITSCLRNNPPVVEFINESFPNFKSKIMAALSNLNDNSNHRSS
NILIKRYLSILNELPVTSEDLPYISTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDFDLYNLKKIFKSDIT
INKGFLNWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTTTGCATTGATGACTTGTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGGCGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCATATTCAATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTTGTAGAA
CACTGGTCTTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTTAAGA
TTCCCGATTACTATTACGAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTGAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

83/161

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFTIVTIISSNTVGAAGWCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCCTGGAGGAAT
CATAGGCAAAGAAAGAAAAGAAGATTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCTCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTGCGAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACATATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGGAAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAATACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAAACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCCAGCTGTTGCTTCTTCCACCAAAGCCTCCGCCATTTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASAIQSISDQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTTCATCGCAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCTTCTGCTGCTGCTGCTTCTCCAGTG
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAATAA
GGACTCCTCATTAATAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAATTAATATGATTTCTGTTTGCCACAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTGGAAGAGAGAAATGAACAAAACC
TTAAAAACGGGCCAAAAAGAAAGGAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA
ATTTGCAATATTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAATT
CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCAGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAAGCTGGA
TAAAGTTATGGCGCCAAAGAAACTCAAAATAAATAAGGCTGAATGACAAAAAAAAT
GGTTTACTTACCCAGAACTTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAACGGAAAAAACATACGT
GGGTGCCCCAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTGTATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAAATAATTGTAG
GCAAAATTAAGGAGTCTGGTAGATGTCAATTAATGTCCATACTCCAGATTTCTTAGTTC
TTGCTACTTTAAAGCAGGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAGCTGA
CAGATGTCTTTCTTGTAGTTATCCGATTCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCGTTTCGAAGTGAATCTACAAAGAGAAGTAAATGAACATTAATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAATAACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAAATTTTGTGAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA
CAAAGTTTAGAAAATCTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAACTCAGTAGCTCGCCTACGTCCCAATCAAGTTTGCAACCTCTGTAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATCTTGTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCTTTTGAGGAAAGTTAAAGTGCCGGTGCCTTAAGAAAAAGTCAAACTAATGACTCCT
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG
GGGGTGGAGTTGGGATTTTAAGGTGTTTAAAGTGGAAGTCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTTCTTATTTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNLKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVNYTMEECYDDETSFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDSAPECTKEQKRKHKILQQKVGYPNP
KTIIVCHINGKKHTWVALDWTVYKFARNLDHIVITLTKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDFYILQLVKVKISVKITLIEIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNLNITYKSKKLTDFVPVSYPIPTFVVPKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKNTISDISSHISVDSYAEDFKRQGYIKKQFNSTNDSIPRKLTLGLAQHSRR
KITGDIEKLQDDEKDIRECTKEKLLLKKIDIIRESLKSSLAIETLPGKNVSQSSHGDIQS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFPDSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSFSTVNTFTGGGVGIFKVKFSGSSSGNKSSSRNSSSGDVFESEDDRNDRNDKKKKKKK
KKSFLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCCCTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCCGCAAATTTAACGAAGACAGCGTGG
TTAAAATTGCTTGTTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAACCTATTGAACATAAACGCAAGTTCAATATACATAATATTTG
ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTTCTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTATATTCTAACAGGTCCGCCTGTTATACTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAAACTAGCGAAA
TGATGAAGGACCCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAACCTCCATGCCAAAGGAACCGGAAACCA
GTAAAAGCACTGAACAAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACCACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

85/161

ATGAAGATGACTCTAAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTACAA
AGGCACGTCAATTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGAAGTGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTTGCGCGTATTGGTAAATGCCTATCACAAATTGGGTGACTTGAAGA
AAACTATAGAATACTACCAAAAATCATTTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCTTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTTGGAAACACTAGATGCGGCCAGAACCAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAGAAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTCAGACGTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADEYKQQGNAFTAKDYDKAIELEFKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAHLGLGLDEAESNYKKALELDASNKAKEGLDQVHRT
QQARQAQPDGLTLQFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGDQLFT
DPRLMTIMATLMGVDLNMDINQSNMPKEPETSKESTEQKKDAEPQSDSTTSKENS
KAPQKEESKESEPMVEDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEYKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTIEYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPEKAEERLEGKEYFTKSDWPNAV
KAYTEMIKRAPEDARGYSNRAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAV
KEYASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFPQGTSTNETPEETYQ
RAMKDPVEVAAIMQDPVMQSILOQAQQNPAALQEHMKNPEVFKKIQTLLAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTTCAGTCCCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCCTTCAAATGAGTTCACCTTTACGTCAGATC
GCATAACAACCGGTCAATATTTTTTTTCTTTTGGCTAAACCCCTACTGCAAGCACTTTTA
AGAAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTTGTCTTTTCGGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTGATTTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAATGCG
AAACCACGTGCACCTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAAACAGTGCGCGCGGTAATTTTT
TGTCACCTCAGTAACTAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTTACGCTAGCAATCATGTTCTTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACCTTGCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCCTTGGGACTTGGTATATATCTTATTTTAAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGAAAAATCTTCTCCAGAAT

86/161

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTCAAATATCACCTAATCAAACCTTACTAACATTTTC
CTTTTTTGTTTTCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAAAGAAATCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTGTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTTGAATCTTTCCAAGCTGTTTACAACAAATTTGACTGGTAAGCA
AATTGTTTTCGAAATTTCAAAGTGAAATCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAELRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHIVFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVL LDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCCTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAATAATCACATCACTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAACCTACCCTTTAGCGCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTGTGTCACCTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCCTCCTCCTTGTCCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGAGCCCGTTAC
CCAGTACGTTACAGTACCCCCAAATACGACTACACAATACGTTACTGTCAACGGGTGACCC
TTCTGTTACCCTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLC LHHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLLPLPLQVTVNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCTAATGCA
AACACACGTCCTTTAAAGATCCCCGTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTCCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCAGAGAAGTACAATTTTAGCGGGTTTCAAATTTCCCCTGTGTG
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACACTGGTAT
TAAGATTTGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACCTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACACGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

87/161

CGGTAAAAC TGT TTTACGCGGAGATCCAAC TTTTGATCCTTACCGAGTACCACGAATCAT
 CTATATGATCTTTTACTA ACTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
 CTCCTATGATAATTTCTTTT TATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
 CCAAGCCAAGCACGAAGAAATTGACACCAAGAAC TTTGTATGTCATTAAGGCTTTACAATC
 CTTGACTTCTAAGGGTTACGTCAAGACTCAATTTCTCATGGCAATACTACTACTACACCTT
 GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAAC TTGCCAGAACACATTTGTTCC
 AGGTACCTACATTTCAAGAAAGAAACCCAAC TCAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)
 MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTFQS
 WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
 915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTTCATATCTTAAAGGT
 GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGT TTT
 CGGGACTGTTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTT
 ATCTCTTTTCAAGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
 GCGGCCTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
 AGTTGTTCCGCATAGTCTGTCTAGCTCTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
 CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAAC TCTAATAGATAGATATAACCGTT
 TTTGAGGGCATTATTTTTCGAGAAGATAATAGAAGAGAACC GTAAACAAAGGAATCAAGCA
 AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
 TTTATATGGTGAAGTCAAATTTGAATGAACATATCGTGGAAATTTAAAA TACTGAAGAATA
 CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCTGAAATACGCCGAATACTGAATACG
 ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
 GTTAATATCATTTGAGAAGTCTTTCACATGAGGACTATAGA ACTACCATCCAGGAATTATA
 GAGGAAATTA ACTGAATCAGAGATCTATTTTGAACAATTCATTTACATGTAATTGTCTGC
 AATAAAGCAATATTTTGAATATGCAAGTTTACTAACAAGAATAAATCTTTTGTGATT
 TTTATCTTTAACAGTGGCTCATTTTCAAAGAATAACCAAGTCATTGGTTCGTCGTTTACCAAC
 TGAATCCGTTTCCAGAACCAAGTTGTTT CAGAATGAGAATTTTGTCTCAAATGAAGTCAT
 CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
 TGAAATTTGTTTCCATCAACCAATCAACGAAGCTCACCCAACCAAGGTCAAGA ACTTCGG
 TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
 CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC
 TAGATTTAGATCTATTACATCTTGAAGTTTGTCTGAAATTTGAAAAGACTGCTGATGTCAA
 GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCAATTACCTCACAGAGT
 CCAAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)
 MYLAHFKEYQVIGRRLP TESVPEPKLFRMRIFASNEVI AKSRYWYFLQKLHKVKKASGEI
 VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVA AVETLYQDMAARHRARF
 RSIHILKVAEIEKTADV KRYVKQFLTKDLKFLPHRVQKSTKTFSYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAAATTTCTGCTTCATGTATATA
 CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
 ACATCTTGGCATATTAAATGGTTATTTCCGGGTTTGTTCGGCTCAACGGTGATATAAAA
 AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTGTTTACAACATCTTC
 ACATTTCCATTGTGGAATCATTTTATTTTTTTTCAGAATACCTTACCCGCAAGCAAAC TTT
 CAAGCAAAC TTAACAATTTGCAAAAATTTATCGAATTCTCCGCAGGACATATTATAAAAGT
 TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCCTTGTTCAATTTGTTTTTCCCAAT
 TCAAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAAA ACTAGACT
 ATATATTTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
 CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTGTAGAA
 CCGCTTTGGTTTCCAGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
 GAGGTGAAGCTTTATTGGTTGTTTTGGTTCAGCTCTGTTACTGAAGCTAACATTATCAAGT
 TGTTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
 CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
 AGGTTGTCGGTGCCCTCGTTGTTGTTGTCAAGA ACTGGGGTGCTGAAACTGATGAATTGT

88/161

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTA EVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANI IKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCGCACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAACCTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCATGCGCAACCAAGGAAATGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAATCAAGTTTTCCTTTTCGTATCTTGGATTATTGTTATATATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATCTTTAGGT
TACGGGGTTTTCTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACACAAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTCGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTCACCTGTG
AGAATTGTGGCAGGGATGTGTCCGCAAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLSYYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAACCCGGAAGAAGACAAGAGGTTTCATTTCAGAGAAAACATCCGTACATTTCGAG
TTCTCATTTGAACCCATACATTTCAACTATTTTTTACATAGTTCGTTTTTTCATGTGTAAAAT
TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCCGTTCCCACTTGGAAAG
ATTGGCGTAATTCCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTATGATACTATTATTGAGGGGGCAACA
GAGAACTTTATATGTGGAAAAATGGCATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAAATTTTTTATGGAAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTTAAACAAACAGAGCGGGTTTACATATACTGT
TACTACAAACCGTGAAATTGAAGCAGTTTCATATACCTTGAGTATAGTCAATAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTTCATCAGAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVGDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE

89/161

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQKRHRQRALEKVRNAQAQREAAEYAQLLAKRLSERKAIEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCTCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCTATC
ATCATGCCCTTCTACTTTTTCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA
AAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAGCGTAAGAAAGAA
GAGCGTGTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT
AGTAGTCTTATAGAAATTGCGAATAACGGAACAATAGTCCACCAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTTCGATGTGCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCCTTCTACGTCGC
CAGCCTCCTCTTTCATCTACGTCCTCTTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTGGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAAATAGCGGTAACCGGAGCGATTCCCGTGACATTGATA
ATCCGGTACCCTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAGCACC
CGCCAATTCTTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTCGATTTTGGATCTTTGTTTAGCAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCATAAGAG
GAGTGGCACCACAGCTAGCAAGCCACAGACACCTATACCTCCCTCCCTGCACCTGCGAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT
CCGATCCTCCCAACAACCTTCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCCTTCTATTTCCGTTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTCACATTAAGGGACCGTTGTACACTAAGAAGTCTAAGAATATA
TACTCGCCCTGGAATAACAAGTTGGCTTAAAGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAAGCCGGCATTTGATAAGCCCATTATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTTCTATTGAAAAAACAAGGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAATAATTTACCCATTCCGCTACCCCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTFTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTTGTGATTTTATCACCATTGCTCCCATTCACACGATTGTTTTCG
ACAATGTAGCTTTTAAACCAGGATATGTTTCAAGATAATTTATTTCTGCTTTGGTAAACTCCA
CAGTTTTTGGACAAATTGAGTTTAAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCTTTTGTCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGTGAATCACTATATCGCCATAACATGGATTGGAACTTGTTTACTG
ACGTCTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAATGATCTGTCCACTATGATTAAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTCAATTTGAACAGCACTAATATTTTCGACTTCTTATGATT
TAGCTTTGCTCTTGAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTGGATTTGAGTA
ATTTGTGCGCAATGCTTTCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAGGAAGTACGCTGTG
TTTGTAAATATTTTGATTAAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCGTTTCAACAACTAACACAGACG
CGCATTTGGATGTTTCGAGCACATTGGACGTTTAAAGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTAGATTTTGA
ATGATTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACGGACCATGGATTCGACTTTCCAGTTAGATGAATTGGATTTCGCAAGATGATTGTGCTAT
TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAACTGAACCTGTAA
CGGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

90/161

TTGAAAAGTTCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTCGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACTATTG
ACGTTTTTCACAGGCAAACCATTGGTGTTCGAAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGGTGAACCTACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTATACCCTGAAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAATCCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCAGAAATAGCGCTTCGACATTTACACAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTCGCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKKGSRRTNTKPSRPSTSPASSSSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPD LKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDDNGSSTQFVRKKRSTSISNAVSSSKPRLASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKTKR SIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDP RVKEISSPMRGVAPTASKPQTPIPLPSPALAVKDLSTVSLKRVSFVDFKFESDPPQQL
PSRTPKKGNI LIPDDMISEVPSISVGISSNQSAKSTNSNIKGPLYTKKSKEYILALENQ
KLALREA AKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPPNVE
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKL LCKFLLNKS LNKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWM SQYNVQGVDLAFNDLSTMIKPMVGKLSALS YDNLRY
FILNSTNISTSYDLALLKYL SKLPNLIFLDLSNLSQCFPDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNLIKCKSLSHVSMTNQNVENFYLMNGTDS PVQQTN TDGDL DSSS
TLDVKGOFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKDTTKRYLLKKYIEKFHIL
HHNVQHTIDTMEKRKSGELPLQEKENLVRL LLLLEQNLCNILELFSHNPNLNDVLGSSRD
DSKESVDSSSEDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTI DVF TGKP
LVFKHTSSSTS SVGCKKQEEEEEGELHKWGFVQQQRS LYPENESTRQTPFASGDTPI NTET
AGKSTSSPSVSTSNNETATTSLSFPANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVDS DV SAPNTDKGSVETLPAVSTDDPNCEVKVPAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCTGTGTC
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCATTCATTAATATTAATATAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTAAATAA ACTTAGA
TGTTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTTAAACTACTAATCGTATATTTCAGCAGGTGCAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTCACTCTTCTTTTA
CGTTCCTTAAGTAACAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCACTTA
TAAAGCAAAACAAGACAATCACAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA
AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCTTATTTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTCTTTT

91/161

CAGAGTGGGAGAATATACCTAGTGAACACTACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSRRKKGSKKAAY
HRQPPEHEHTAPLIKQNKITIKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTIN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFPHPKEKSMNTNELIHVSARKNTLVDNKTSETLQRKMDEFKRRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2: 569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCTATA
GCTTGCTCAAAGTCTGCGAGTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCTAGTATTACCATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATAACAATGTATACCAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG
AAAATTTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAGAA
GATCTCTTTTGTGTTGATACTAACAGTAAAGTTGAGAGTTATAACAATGAAAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCCATATAATATCATTTAT
CGCAGAACTAATCGATTTGGGCCATTCTGTCTGTCATTATAACTCACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTTGTTTCATTCTCATGGTAGCGCTTCCACGTTTCGCTCACG
AGGAATTTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACCGGACCATTCACTCT
ACGGTTTTTAATAACTTAACGTCGATTTGGGTGAAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC
CAAGGGATCCTACTGGTGGCACCAAGAGAAAAACAAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTTCCGAAAG
TTTGTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTGTTGATCAATCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTCCCAGAGTGTACCAAATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFFYPQLGGVEFHIYHLSQKLIDLGHSSVVIITHAYKDRVGV
HLTNGLKVYHVPFFVIFRETTFTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRVTFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNCTKENMIVRTELSPD
IISVIPNAVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFNPNGSDLLTRIIIPKVCSSH
EDVEFINAGVDGPKFIDFQQMIESHRLQKRQVLLGSPHEKVRDVLQCGDIYLHASLLEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWMMDVAKRTVEIYTNISSTSSADDKDWMMKMANLYKRDGIWAKHLYLLC
GIVEYMLFFLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGCGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTTCTATCGATTTACGGGTCAGGTAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACATAAATTATGGTTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTTCGCTAGAGTTTTTAACACATG
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCATTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAAATCAAGGAAAAAGATCAGCATCCTTTTCATAGTCCGGTGCATAATACAGTGC
TCAGTCCAAAGAACAGCAGTCATTTCTAATACTGGAAGTCTGGTTTCGGCCTGAAACCAC
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGTAAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAATTTGA
GGGCCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATTTCTGATGTTGGTAATACCTTAGCTGCACATAAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGTTTTCATCAGGAAGATCACATTGATGCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTATTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGTTGAGCATATGGCTTCAGGTGATACTTTAATGAAGTGGATGATGGCAAAATGTC
GCAAGAGCAAAGAAAAATGGTGAAGATCTCAACTTGGCCAAAATATACCGAATCTCAGT
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAAATTCATGCAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACAGATCCCGTAGCGATGCAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG
ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTCAGGCAGTGT
TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGCCCGATGGGTTCAGCAGCAGCTTTGCACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPEEKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQDGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHSQNLRLASLVKA
GDNISEAPYDKEKKILDVGNTLAHKSNOQKPSHSDQFDQEDHIDAPRSNSSRKSDDSSFM
SLRRQSSKQHKLLNEEDLIKPDIDISSAGTKDIEGHSLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNIEHDSGEHMASGDTFNELDGDKLRKSKKNGGRSQLGQNIIPNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNQNLRLSNDLKN

93/161

SAAPASPLSNEHITSSTNSGSDANRQSNNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLLFTNYDKKFDDLYPHILASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGYMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTCAATT
TGTTCCCTCCCTTATTTCTTTTCATAGTATTTATTTTTATTTATTTATTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATTCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAAATTCGCGCTCAACATGGCCGATTGTACATTATATCGTCTATCATTATATC
GTATACAGCTTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATPACTTGTCAAAATAGTTATTGTAATGGA
TCCTCTAGAAAGGCAACAGTAGATTTATTTCTTTCTTTCTAGAAACATCATTATAACT
AACAATATATAATTGGAATAATGGCTGGTGGGATATTTTTGGTTGGTGTATGTTATCAC
CCTGTTACAGTTTTTTCGGATACTTAGTTTTATTCATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTCTAGAAAGAAATGCGTCTTTACTAACTTTATTTTAC
TGACAGTCTAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TTCTTGGGTTTGGATAATGCCGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACTTTCGATTTGGGTGGTCATATCAAGCTCGTCTGTTATGGAAGGATTAT
TTCCAGAAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCTGAAAGATTTGAT
GAAGCAGTGTGCAATTAGATGCTTTATTTCAACATTGCCGAATTGAAGGACGTTCTCTTT
GTAATTTCTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACCTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTDFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVPFVILGNKIDAPNAVSEAE LRSALGLLNTTGSQRIEQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAATTCACCTTGCAATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCTTGCAGACAGCGCAACAT
CCAACCATCCTAAAGGTATGGGTGTAAGTACGATGCGATTATTTTCATTAAGTTCTGTCTT
TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGTTACCGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMDLKIIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCGTGVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTATTTCTCA
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT
TTTCGATTTCAATTTTCGACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAAATAGTA
TCATAAATTTCTTGCTTTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTTAACATTCCCAGTTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAAC
TACGCCCAGAGAATTGGTTCCTGGTGCTCCAGTCTATCTAACTGCTGCTTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAAATGCTGCTAGAGATAACAAAAAACAGAAATTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAACCTTGTTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAAGCTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIPRHLQLAIRNDELNKLGNVTIAQGGVLPNIHQNLPPKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCTCGCGATGTAAGAACTACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAATAAAAA
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC
AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG
CATCACCAGTGAAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTTACACCCCGGAATAATACTAAAAACCAAACCTGGTAAATAGGGCT
ACAGATGAGCAGGAAAACGTTGCCGGAAGTTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTACTCTGGTGTGCACAAGA
GTGTTTCATCATTTTTTTTACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTCGCATTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPEKVYLSERIIDEEVAVCTVAAEVLAIFTLVCTR VFIIFFTARICHGIWPSSPSER
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIAKAPLLIAQRCEC
ASNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACCTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCCTCACTGAAGATCCTCATCTT
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCCGCGGGGGGCTGACA
ATTTACTTTCATAGAGCAGTAATAAAAAGGGAAGAGATGTAAAAGCTTGGAATAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAACCTGTAATTAAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCCGAGAATTGGTGACTATATTTTGAAGTCACCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTTCATTAACTCGCAGGTTACAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCCCTTAC

95/161

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTCCTGTGT
AGCCTAATGTTTAAATGCCTAATTTTTTCTAAAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCATAACATTAATTTTTTAAATATTCTTTTTGTTTTTACCAGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGGAAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGAGAGGCATTTCATTC
GTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATATACAAAAATACGCGTC
CAAGATGTCTACTAAAGCCCAAAACCCCTATGCGTGATTTGAAGATCGAGAAATTTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAATTA
TCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGGAAA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTC
GGTTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTT
CGGTATGGATTTCTATGTCTCATGAACAGACAGGTGCTAGAGTCACTAGAGAAAGAGAT
GTAAGGGTACTGTTGGTAACTCCACAAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACCTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCCCTCTCATATGTC
TGTGAACCCCTTTAGTAACTATTAAATGTTTATTTCATGAGACTAGTCAAAACATTCAATAACA
GT'TTTTCTATATGAGAAAAAATGAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTCACATTACACGAAAGAAAGAA
AGAACGCTATTTCTTATAAGAGCAAACCTGTTGATAAGTTTATAGCAAGAATAAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTC
AACTGTGCAAGCAGATTTCATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATTATTGGACAACCTTGATGATTGACGAAGAAT
ACCCATTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTTCATGACGATTTCGCCT
TTGAACATCTCTCAATCATTTATCTCCCATTTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTTAAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTTCAATTTGATTGTTGCACCTTCTTGGATATCTAATTT
GGATATCACATATGGTGCCTTGGAAAAATCAACAAACCAATAAAAAAACAATTA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEEYPFFNRFFANDVSLTVHDDSPNLSQSLSPIMEQFTVDELPES
ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVVINSLGWAFED

96/161

EDGDDEYATEETLSHHDNNKGKEGDDDLSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKKNN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTTCAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT
GTTTTTGTGTTGTTACTATCTTTGCAGGTGCCTTTGTTTCCAACTGTATTTGATACTGCTAT
TACTTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTTATTTTATTTT
TGGCTGGTGTTCATGTTCAACCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTTCTCGCCAAAGCGCATTCAAATTTTCAGAAATGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTGCAATACTGTTCTTCGACGTTATTAAACGTAATAGCATTTTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDGVS

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC
AACTTTTGAACCTCCCAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCTTTCCCTAATG
ACATCCCCTCTCAAACCTTAGCTTAGCAGTTGTATTTAATGTCTGTACGGATAGTCAATA
ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC
TAAAAATGGTATGTTGGTGTGTGTGTGTGCTGCTTCACATTTTCAGGCTAAAAATGTTATCCGT
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGACTAGTCTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCACGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCGCTGAGCTGGGGTCTAGTTCCACTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCCACAGGCCGTTAATGGCCTGAAACAGTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCAATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTGTTCATCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCGGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCGCGCGTAGCGTTCTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCCTGGTCAAAGGCGAAAACGCTCTACCTCGCTTTCACTGCTGCTTTCCG
TTTCATGACTTCGTTTCAAAGCGGTCTCTTTCGCTCTCGGTTGTAAACACACTTGTAGCCTGCT
ATGCTTTTACCCTGACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGTCTTT
TTTGCTCATTTTTCGTTTTGACGTTGCGATGGTTTTCGCGGACCAATCGCATGGGTGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAAGTCTTCTTCTCCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCTGTTGTCGTATCGCTGTTTCATATAATCGTCTGCTCACTCA

97/161

TATCGGCGCTTTTACTGCGTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAAGCTTACATACGGAAAGAGAAAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSMTSCTNALSFLFFLLTLRRIHRHWKPYGAFL
LIFVLTLRWFRGPIAWVVVDVVFASCNVVFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI
GAFTACCLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCCTTATCTTGTATGCCCCGATATAGCAACCTTGTGTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACCTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCCATTACGGAGAGAAGCATTTCCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCCTACCCACTGCTTGCTGTTTCTCACTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTCTGATGCATACAATCTTTTAGATATTTATCTTTTAAATTTATTTTAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAATGGCTCCATCTGGTATGTGAAC TGCAATATTAATAGCACGAGAAAATTGAGAGGAAG
ATAGATGGGAACTAGTAGAGTTGATATTTGATGAGATACGAAAACCACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTTGATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTTCGTTTCGTTTTCTGCTCAGATTCAA
GAAAATTATTCCATCCTCATTATACTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCCAAGTTTCCATG
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

```
AGAGAACGTATTGAAGAGGAGAAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCTAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTGGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAAATCATATCAATTTTATGTAATTTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAACTCAACAATCTATT
ATTCTTAATTTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTGAATTTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTAACAA
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCAAGTAGTTTGTGCT
CAACAGCAACAACAACAACAACAACAACAGCAACAGCCGCCACTAATTTCATCAATCCATGATTCCT
CCAACACCACATCATCATTTTACCCTTCAACAGCAGCCACCACAACCAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC
```

YBL051C_homolog_1 409aa (SEQ ID NO 286)

```
RERIEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLTYQLVLYRDDITKSTFELAI SPANLNISQRKII SILCNYLNLLELFD
NGLIIIRRKPGYIAQCITQQSIIIPNSQQVSGPTHQQHQONQLQQQQQQQHQQHPSHSSSMMNLH
QLGGT LAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQVQHQNQPPQQQQQQHVQPPQYNYNQ
QSIQSQPHSARPYSSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL
```

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

```
ATAAACAAAAAAGAAGCACGAACTGTGGGCAACAACAACAACAACAACAACAAAAAATTT
CTGGAAAATCAAAATTTGAATCTCAACCAGCAGCGCGCGCGCAGAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTCTATATACACTGTAAATC
AATCAACAATAGCAGGATATCCATTTCATATACAAATAGATAAACTGTTTAATTAATTAATTAAGT
ATTTGATTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAAACAATTCA
AAGCTTTAATTTCCACCTATCAAATTTTATTATTTTGTGTTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTTTTGGAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACGTGAATGCAACGTCGTCCCTCTCTATCATCATATTATCGTCAGCCTCGGGCT
ATTCTTTCTTCCAAATTATGGTGGAATCCTACACCCAATCCCAACAATTCGAATACCAATAACAATA
GTAGTGGAATAGTAATAACAACACTCATGGCAATAACACTCCCAATPATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAATGTTAATGCAACACAACAGCAA
CTGATTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTTGCCATTAAAAAGGAACAATGTG
TAGATGTGATGACAAAATTAACTTGCCATTGACCATATGCCTTTAATTATCATTTTGATAATGGTG
```

TGTTTCGTGGATTAGCATTGCGCAATTTACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT
TGAATGGAAGAGAAATAGGTGGAAGAAAATTACGTGTTGAATACAAAAAATGCTTCCGGCACAAG
AAAGAGAACGTATTGAAAGAGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTG
CATCAAATGCTTCTTTGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGA
GTGTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATT
CCCTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTC
AATTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCATAT
TTGAATATTTCTCAACGGAAAATCATATCAATTTATGTAATTATTTGAATTTATTAGAATTGTTTG
ATAATGGGTGCTACTAATTAGAAAAAAACCAGGATCCATTGCTCAGTGTATAACTCAAAAATCTA
TTATTCCTAATTCTCAACAGGTGTCTGGGCGCAACTCACCACGACCACCATCAAAAGAATCAACTTC
ACCAACAGCAACAGCAACACACATCAACATCAACATCCTTAACATTCATCATCGATGATGAACCTT
CATCAATTGGGTGGTACATTAGCTGTTCCAGCGCACCATGA

YBL051C_homolog_2 550aa (SEQ ID NO 288)

MDFRNLSTTPNQMGTVMQRRPSLSSLSASGYSSSNVGGNPTPNPNNSTNNNNSSGNSNNNTHGN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQLDLSLENNTKTDSSNDASATNNNNVN
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNNTNNSSTGSSNIANMLPSVSNATTTMNSNSINSTNNNTTINEADDDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKMLPAQERERIEREKREKRGQLEEQRHSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER
MFLNLPFNNSFNPAPPVEINFNDLEVLQVLYRDDITKSTFELAISPSIFEYFSTENHINLC
NYLNLLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQOHTSTSTS
LTFIIDDEPSSIGWYISCSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:
95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAAGAAATACAATTAAAAAAATTTTCTTCTGTGAAAAGGCAATTTCTGGGTCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAAGTAGTTTTCAAATT
CAGTTTCTTTTTCTTTTATATATTTTTTCTTACTTTCTCTTCTTCTTCTCTGACAGTATATTAATA
AATATTCCTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAAATAACAATAATTTTTTTTTTATTTCATTCCAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAGAAAGGTAAAGTGAGAA
TTTTGCCTAAACCATCCCCCTACACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGCTCAAA
CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAACAGAAATCAA
GAAAATCAAATTTCTACAGCTTCAACACCCCAACAGTGTACACCAACATCAGTCGGAACACCTCCAC
AGAAAACCTTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTGTGCGTCAACATAAAA
TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAT
GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGTCACAAATCCAATCATTGAAACTGGATGTTG
ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC
AACACAATTTGAACCACGCTTCGCAACAGCAACAACCTGTCTGGATCGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTCATTTGTCATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA
ATGCATCGCCAATTCCTTCTGTGACAAGTATTCACAAAAATGCACCGTTGACTCACGAAAAATCCG
ACAATTCCTCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA
TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC
ATTTACCATTTTGGCCAATAATAATATCTCGATCTGCCACCGAATTGTATCATAAATCTCAATTGC
TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCCAGAACCCAAACTTTATATGTCGTTGG
CATCCTTAATTAAACAATTAGCAATTGAACATGTGGATTAAACACCAAGATCAACTCATGTGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTACCTAATGAAAAAGTTTTGGATGATTGCTCTT
ATAGATTTGTTGGATTGGCAAAGAACTTGTCAATTACAATTAGGTCTACATCGTGGTGGAGAATTCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTTCAT
GGTTAGCAGTTTTCTTTTGTGAACAGTTTTGGTCATCATTGTTGGGGTTGCCACCTTCAATAAACA
CTACTGATTATTTATTAGAGAATGCTCGTGTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

100/161

TTTCGCTATCTATTTTCCAAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGCTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTCAT
ATTTATCAGCAACAAGATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAAATCT
TGCCCTTGCCATTTTACAACCAAATCATAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAACACTATTACTACATTAGTTCCAACTGATCAAGCTATGAATCAAGCAAACTGAAATCTT
TTGATTTCCAGCAAAACCACTTGAAATAAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAAGCACCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAACCTCACCGTTACCACAAAACCTTATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAAACCTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTTGGGTTGGTTTGTATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLP AQTKPVNSKRKSAASTPGNESKSKSRKSNSTASTPNSA
TPTSVGTTPPQKTSKPTGHRPVTSTFCRQHKIKCNASDNYPNPCRCKKMKGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSNDNSPYALNTPENIEELQPISEFILGDVTLPLNRRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIEQFSRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLNARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLDRELERLRFKLQFEEGPIEVYLYIKLMICCFALPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITRMRSHLTAS
LFYDLVWCVHEARRRSVLDKGKRQAQPNKKILPLPFYNQITKDDFKITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLLQQYPMQQDQQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQF SMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTCTTATCTACAAAAAATAACAACTCACTATAACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAACCTATTATCATTCATCTATATA
TACATCCCCATCGATTTCATCTGACATAATAGTATGTATGATCATAACAGAGGGAATACCCCTTTT
TATTATTACCAAGGTCATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCCTTTTGGTATGTATTACA
TGATTTTTTAGTCCTCTGAATCTTCTCCGATCATCATATACTAACATTTTCGTGGGTGTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGACAGAAATGTCTCAGAGGTTCAAGGATAGAGTACCACTCA
TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG
CAATTGACATTTTCATCATTAGATTTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIIYEEHKDEDGLYVLYSGENTFGEKLAI DISSLDIFS DIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA
AAACAGAAACGAGAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT
CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGFACT
ACTTTTCATTTTCCATTTGTTATGCTTACGACAACCTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTTGCCTTATTTGGTTGCCTATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGCAATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTTATAGTTTTAAAAAATTTGTTAATAATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAAGAATTTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGGTGCAGAAAGTAGTAAAACGAAAATTGCCCCTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAGAATGGGGCATGCGAGATATCTATCA
AGAAGTCTGATGGCAAACCTATGGGGAAGAGTGTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCTTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAGAGTTGCTCCTCCACAGCTAGTAGTCGGAAACCGCTTT
ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAAGTGCTTCGTCCGCATCAGGTTGAAGGTGTGAAGTTTATGTTATG
AGTGTTTAATGGGGTACCGTGGGTTTGGCGGGCAGGGTGTTTGTAGCAGATGAAATGGGGTTGG
GGAAAACGTTGATGACAACTCACTACAATCTGGACGTTTGTCTCAAACAAAACCCGTTTATGGAAAAG
GTGCACTGGTAAATAAGGTATTGGTGGTGTGCTGTACGCTTATTTCCAATTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTAGTGGTGAATTATGAAAAC
TTGTGGCACATTTTGATGAACTCTCAGCGGTCAAGTTTGATTTGTTAGTGTGTGACGAGGGCCATC
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAACGAGTTGGTAGAGTTTACACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCGAGCTAAAATTGTTTTCAGCGAACTTTATAACACCTATATCTAGGGCCCGAG
ATATCAACTGTTTTGACCCTGAAGTGAAGAAACGCGGTGAAGAGATATCGCAGCAGTTGATTGAAT
TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACCTG
ACATTTTGTGTTGTTTGTTCACCTACATCGTTGACAGCTCAAGTTGTTTCGACTATATAACCAACTGA
AGAAATTTAATCAGTTTGAAGCATTTACCATGATCAATTTGTTTAAAAAGATTGCAATTTCCCTTT
CGTTGTTGGCCGACGACGAGTTATTTTAAAAAGATTTGTTGAAGAAAAGTTAATTTGGGGATGGCAT
CCGGTAAAAATAAACATTTCTTGTGCCGTTGCTATTGGAAAATTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTCGCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTCGACCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAAACACGA
ACCCCGACATAAACGTATTTTATTGTCGTGAAATCTGGCGGGATGGGGATCAACTTGGTCGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTGCGGAA
TTCACAGAGACGGACAATTGAAACCGTGTTCATTTATAGGCTATTACACCGGGGTGATTGACG
AGAAAATCTTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA
CGTCCAAATCTGATGTGTTTGAACAATGATGATTGGAAGAATATTTTGGAGATAGATACATCGACAA
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGTTCGATGTTGAGTCAGCCAA
CCATAGAGGAAAGCGAACCACCCCAAAACAAGCATGGGTACTGCATTAGAGCTTAAGAAGAAGA
TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTGATTCTGCGCTACACCGAATTGCTAACAAATTCAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRPKGGVAVVQKVVRKLP TTTNPKPAKILTTDPGSTKYVIQW
RKKTSSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLKQNPFMKGAVVNKLVLVPCPV
TLISNWRQEFKWLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQRN
DLLVCDEGHRLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQRN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPSTLQL
KLFDYITNLKKFNQFEAFTMINLFKKICNSPSLLADDELFFKKIVEEFNLGMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSFTFSRLDGS'PNNVRSKLVNQFNTNPDINVFLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMRIHRDQKPCFIYRLFTTGCIDEKIFQRQLVKNL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDGGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAATTTCAAATTTAGT'TTTAGGTGATAATTATCGTTCGTCTTTCCTAACCTACCAATTTTGA
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGT'TGCTTTGCTTTTCAATTTCAATT
TCACAATTGAATTTCAAGAATAGAAT'TAGTTTACCTTTTCTTACAATCGGCTAAGATTTT'TTCA
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGCTTGT'TGCTCATATTTACAATCAATT
GGTTAT'TGGTGT'TATTATTTT'TTGGTTTCTCTT'TTACCCCCCTTCCGTCTAATTGAGTTA
TTGTTTGGGAATAATTTATTACTTATTCAATATATTTT'TTCTTCTTCCCTTCTTCAACTTCTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACTTACCTTCTTCAATTGGATTA
ATTGGATTTGAATTTGTTACAATTTGAAT'TACTTCAACGAGATGACTT'TACCAATTCAGGATTTAGAAC
CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCACAAGCTGAAA
AATCATTTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCCAAAT'TAGACCTGGTG
ATTTAGACCATTTGTTAGTCTTTGTTAAATTTGCTTTCATACAAGTTT'TCTGAAGAAGCTGAAAAAG
ATTTAAATTTAAAAAT'TATGAATTTGGTGTACACGGGTAAAGATGACGTGTTAGCTTCTAAACTTAGAA
TTATTTATCAATACTTAACTTATCCACACGATTTGTTTCCAATTACTTAATGCCTT'TAATGAAACCACTTTAGTTGAAG
ATTTGAAATTTGTACACGATTTGTTTCCAATTACTTAATGCCTT'TAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAAATTTATCAAT'TGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTT'TGGTTATTATTGCTT'TCTATTATTG
GTCTTGTATCTCATTTTAGAAAAGATAAACGATTCCTGTTAACTT'TTGCCTTTATCAATTTGCTTT
GGGGGGT'TTTATTTCTTGCATCATGGCATAGAAGAGAACAACTTGGTTAATGTATGGGGTGTTC
AAAATAGTCATTTAAT'TGAAGAACATAATTCGAATTTGGCTAAAGTCAATGAAAGATGAAAGAAA
AATCAACTTATTTCCATGCAAATAATAACCAATGGATTGAGATTT'TTAAAAACAATTGGCATTTATCC
CCATTGCCTTGGTGT'TTGGTGT'TTGGATTAGTTATCAATTGAGTTGT'TCTGTATTGAAATCT
TTTTAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTAAATCA
GTGTATTTGTGCCAATTTTGACCAT'TGTTTATAATGCTGTCACGGATATTATTAT'TAAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTCATTTCTTGT'TAAACCTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTTCATATATTTACCATT'TGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTTAAACCACTATTGGCCACATATGCTGGTGAAAATAGATTCTACACCAAATACT
TGTGAAATTTAAAGAGTCAAGAAGAATTTAAAAATCAATCAAGGTAGATTAGATGCTCAATTCTTTT
ATTTCAATTGTCACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTTGGGT'TAAGAT
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCCTGAATATAATGTTGATG
ATGATTTTAGAGGATTAGTTT'TACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTTCAATTTAATTTT'TTCAAGTTGGATAATTTTAAAT'TATTGAATG
GTAAATATTTCAAACCACTT'TCCAAGAAGAGTTGAT'TCTATTTCATCCATGGAATTTAGCCCTTT
TCTTGTTAGCATGGATTGGATCAATTATTTCCCCCGTGGTACCGGCATTTTACCGTCATGGTACTG
CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTCATGTTTTCATCCTCAGTTT
TCTTGGTTTATTATATGTTTGT'TTCAGAACATGGATTTT'TGATTTTGAAGTTATCTTTTATTGAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATAATGATAATGA
GACATGATTATTATTCTGGGAAAGTAAACCAACTATATAAAGTCCACTCGGATGAGT'TGTGGGAGA
AGTTTACCCCAACAATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAAACTGATGATAAAG
TTGAAAAAATGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLPIQDLEPDYIISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHDHLLVFKLSS
YKFSEEAEDLIKNEYFGVTGKDDVLASKLRITTYQYLYTPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRRQHLVNVWGVQNSHLIEHNSELAKVNEREYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGP GKSLTLLPTVLISVFPILTIVYNA
VTDIIKWHNHDNQYSKNNSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLSQEEFKINQGRLEDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRSLKLPYNNVDDFRGLVLQFGYLMFGPVWPLAPLVCIIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVD SIHPWNALFLLAWIGSIIISPVVTA FYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYS GKVKPTY
KVHSDDELWEKFTPQSTLNF TGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399.1781 (SEQ ID NO 297)

CGGTAATTAATGTACAAAAACAACAATCAACATATTAATCGTTATCCCAACTTTGTACAGTTTTA
CTAACACCTTTTATTTTGTGTTATACAAATTGCACAATCAATTACTATAACTTTTGTGAAACGT
GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTTATTATTCGATTGGGTTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATTCATTTCTAAATTCGATGAACCGAACACACAAAAACATCCAGTTCT
GGAGAGATTTTCAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATTCATTTGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTTCACCAATTTTCTTCTCTCCAAAAAACACCTTCT
TCATGGTTTCTGTCTTCTAAATTAATCAATAACGGGTGTTATTAACTAGTCAAAGTGTTTTCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC
AAATTCATTTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAACACAAAGGTACTTTTAAAGGTGATTTGTCAATCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAACATATGCTAAGGAACTAGCCCAAAAAATCTGAAGGAA
CCTATGCCGGTACAACCAATGCCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACCTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT
ATTTGCTAGAGGGTTTTTAGGTGATGATTATGAAGAAGGTAAAACCTGTCAAGTTTAAACATCATCT
CTGAAGATGCTGATCTTGGTGCCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA
AACCAAAACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAAATTTATTCAAGTTGGTGTGCTTATG
AAATCAACGTCAGAGGAAGTTCACCATCTGTGATTTATTACCAATGAAGAATTCATTAAGAAGT
CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG
GTTCAAGTATTTTGAATTCATCCTTGGAACTTTTGAAGGACACTAAGAAGTCTAATCAAGTATGGT
TATCATTGCTCATGATACTGATTTGGAAATTTTCCATTCTGCTTTAGGATTATTGGAACCAAGT
AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTCTATTGTTCCCAAG
GTGCCAGAAATATACACAGAAAACTTCAATGTGAGTAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTCGTGCCAATTTCCAAATGTGCTACTGGTCCAGGGTCTCTTGTAAACTTGATGATTTTG
AAAATTTGCTTAAAGAAAGAATTGGAGATGTTGACTTTGTAAACAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCATTACAGTGTCTCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTFKGDL SFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLEYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLLELLKDKTNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;

CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT
TTATTTAACGATGCAATAATTATTTCAATGTGAGTAATCCATGAATCAGTGAGAATCTTTATTATG

104/161

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGTACATGAAAAATACGTAGTTAAATTTTGTCTTGTCTTTATTTATTTA
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTCG
CGACTCACCCACGTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTTGAACCCTAAAATATC
AACTTTTCATAATAAACATAATTTCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTCAAGAGATATGGTG
AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTTATG
AAAAGGAGACTACTCCTAAAACTCAAAGGTCCATATTTTGAACACTACAAATTTATTACGACATG
GAGCTTATTTTTAGAAAAAGATATCAATCACTATTTGACCAAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCCTGGAAGGTGTTATCAAAGTGGTGTCTATTTGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAATACTTTGAATCAAGATTTACACAAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGCTCTGCTCATTATTTCTTTGGTGTGCTTTGAGATTAAACGTTAGGGGTATTCTCCATTTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTTGGCTCACCTATGGTGGAAGCGTCTGTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCTCAATCCATATA
ATGCAGCAGAAATTTTCCCTCAAGGTGCTAGAATTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCTTGGGT
TTACTTGTGAATTTGAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGACCGACCGGAATTGACATTTTATTTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHGERFPSKGDGKYFNSVMEVFKRYGEFHGDLNFLNDYEFVTNPDPYIEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRQYQSGVYFARGFLGDDYSEDVFEFVVDED
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPLDLSDQVSSSLFLWCAFEI
NVRGYSFPCNLFKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH
DTDIEMYLTSGLIVPPGDLVPDRVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHVDVYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATACTTCGTTCTAATTCATATACACAACCTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAAACATAACTGTTAATATGGAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAATAAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAATTTG
TTTCTTAAACAGCAACAACAACAATTTGAAATTTCAAAAATGGTTTCTGTTTCTAAATTTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTTCTTGGCGGTGATGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAAATTGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAGTAATGGTAAAAGTTTGAAGCAATTTATGCTAAATTTGAAAACCTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAACAATTA
CGAAAAGGAACTAGCCCAAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTATAGGTGATGACTT
TAAAGAAGGTAACCTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAAATAGTTT

YBR093C_homolog_4 461aa (SEQ ID NO 304)

106/161

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENS'TLPIFTSN'SNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNDSLKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNOVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYPFPNPYVHSSIVPOGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSSELTIFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAGAAGCTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAGTGGAAAAAAGTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAGAAAGAGCATA
AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTATAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAACCAATTTTAGTATCTATCAACA
AATACAAATCAATTTAGTTAAGTTCAATTAATGACAATAATTTTAATCACTGAAAACAATAAACAT
GCAAAACAGCAAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTTTGTTC
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAGAAAGAAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAATCACTGGTGGTAACGATAAAACAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACCTTGTGTTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTGTGCTAGTTTGGCT
TTGTCTATTGTTAAACAAGGTGACAATGAAATGAAGGATTAACTGACACCCTGTTCCAAAGAGA
TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATCTTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTCGTTGTTAGAAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMIDDDTKLRVSTEKRMQVEGEDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIQAQDLVLALSIVKQGDNEIEGLTDTTPVKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVKNA
QQORDAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAAATAGTTGTTGGTGTAGTTGTTGGGGTTGGTGGT
TCTATATTAATTGGTTTGGTGGCCGTTTTATTTTACTTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAAATGAGAAATGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTGAGAGACAGAAATATTAATCAAGGATCAAATTTTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAAATTTTGTACCTTAAAGTCTTTTAAATTTAAT
TTTAATAAAAAGTGGTGATTGTCGAACTTCAAGAGTATATTTGGTGAAAAAATTTTG
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTACTACAGCTACCATCAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAAGTATATAAATCTGATATCAATTTCCCTAGCATTAATGCA
CTGATTTCAGAACTTTCAAGTTACGACAAATGAACCATTTCCAATACAGTCTTGCTATTGAACAAAG

107/161

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTGGA
TAGCATTGGAAGATAATTCGATTTGTTCACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAAATTGATAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACATTATATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATACACAAATTTTGCACATATAGAAAAGTGAGA
AATATCAATTGAATGATTTAAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTCTTATTGAATTGGAAAACCTAGTTTGCCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAACATATGATGAGTTTATTCCATTCATTA AAAAGTTTGTTCCTGCCGGTAAAAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSY EYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYND SMVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHMTDISEFLLNWKTS LPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTTCCCATTTTAATTTAAAAAAATTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTTGAAATGGGGATTAAATGGGGATAATTTTATTTTGCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCTTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCCGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCCTAATCATGGTG
AACAAATTGAGAGAAAAATTAGCTTGGGTTTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAAA
GAATAACTTTATCTATCCCAGTTATATGTCATTCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTTGTTGATGATGATGCATTGAATGATTTGTTTGATA
TAACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIASLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKLSIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAATGAGGAAAATGAGGAAAATGAGGAAAACGAGGAAA
ACGAGGAAAATATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTTTGGTCAGAA
CACAACTTTGGAAGAAAGAAAAAACCGGAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTC
TTTTTGAATTATATCGATTTTAAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAACGGCCTTTGTCCTTGGTTTAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTCATGCACAAGCATCAGACCAACAACCAACAACATAACACCAAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAAAGTCAAACCAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT
CATTATCACCAATGACAAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKEYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313).

AGTGGTTGTTCAATAATGGTAAGTCTTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAAGTATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAATTTTGAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTATTTATCAAAATACGAAAGGAAAGGCAATTAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTTCAACGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAAGTATTTACTAACAATTTACTTTTGTCTTAGACTTTTGGTA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAAATTAATAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATGACTTTGGTTG
GTTTAGATAAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTCGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTAGTTGCCGACTCAA
GAAGAATGGAACCAAGAAATTCGGTGGTTCGTGGTGCCAGAGCAAGATTCCAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTTCTGAAGTTGATCACCAGATCCTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAAACGTACTACAGTTCAGTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACTCCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAGAAAATTTA
TTACTCTAAGAAGTTTATATACCTCCACAACCTCACTTTTTCTTTAGTTTCATTCTGCTTTTTTTT
CTTACACATCTTAAAGGTCAAACAATTTAACTTATTAAGTTCAGTTGTGAAAATCTCACTTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAAGTCAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCACGTTTAAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTACAGAACACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCCCTAAAAGGATGAGGCTACAGGTTTAG

109/161

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGTATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIKGEIPSFKLIE TAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNI PDDYLS DILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)
CATAATTATTTACATAAACTCGCACTATAATTTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAAAGTACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTCTTTCTTTCTTTTCTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
MRDKWRKKRVRRLKRRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTTCTA
TATTTTCTTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTTGCTTTTGTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATTCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCTGGTGTCTTCTCACTGTTTTTCTTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTGTTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCAACAATGAAACATTAATACTAATACTAA
CTTTTTTTTATTTATTAGGCCGGTGTGTTAAACTTTGCAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATACAAAGACC
AAGTTTACCAAGAATTCACACTGTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAAGTTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATGACTAAATTTGAAGCTTCTCAAGAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)
MAGVKTFELRTKSKEQLESQ LVELKQELATLKVQKLQRP SLPRIHTVRKN IARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLT KFEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)
CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTTAGTTTTAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACCAGTTACATCCCACAAAATCCCTTAATCTTGTTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAAGTTGACTGGACTTGA
ATACTTTGAGGGGCTTAATCATATATGTACATTTTATACCCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTTATGAGTGATATTTATATTATTATTCATA

110/161

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCCTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTTGGAACTTTTATACAAAGGATCAAACCTTGGTTCGTCCAA
CCAACACACCTTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTTCGTTCAAAGACGCCATCACAAACCTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAATTTGAGAGTTCAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTTACCCCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTTGGCAATCTAGCCACCTGAAACATTATCATACCCCCCACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAAACTTTTCTTCCA
CACCATCACCATCAAAGCTTCAGCAACAACGACGACGACAACTGCAAATGTCACAGCCATTGACG
TCCTTTCCAGTGAAACAGAACCAAAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTGAGAATCACCCCTAATGTATTTACAAGACCTTTTGTATTCGG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAGTACTCTATCTTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCCTCAGTATGGTGGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAGGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAATGGGAGAGTGTGAAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTTGATATGGCCATGGATAAATTTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTATCTTGTGGGTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT
GCTCTTTTGGCGCAGTGGCGTTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATACATAGGTTCGTTCCCATTAACAATAGTGTTC
CATTTAGAGCAGGTGACTGGAATGTGAAAATTGCATGTATCACAATTTTCGCCAAAATTTGTGTT
GTTTAAAATGTGGTGTGCGCCAAACCTGCTATTTAACAATCAACAAAATAATACAATTCATTCGGTGA
ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAACTTTGAATAATAATG
CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCCAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGTATGATTACACAATTTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIIIHISTTCDSDPTFVTKDSSSELIEFAWETVDSVTLETLYKGSNLVLRPTNTPTIPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKEFSIVMFDISKLRVQLVREARDKSVVLPSTYQLH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTVIDVLSSETEPNGKVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDQAQDITAFTSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYQNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSSKVFDMAAMDKLLLSFPLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPNTGNVTLNHLNNSETNLSNNTNLNNNNHNSNNYHNNYHHNNNNNNHNSNGNTIH
GRSHYNNVFPFRAGDWKCENCMYHNFKNLCLCKGVAKPAINNQNNNTIHSVNSTAAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSQPQGHYHNSRNNNNSGASKFNNGYNPKNQYNNNSKNLSNNF
GLNGMHQQNQNQILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,
PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
GATAGTGATGACAGTTCATAGACAATTTACAGCCTTAAATGGATATATATGTATATTTAATAATAA
AGGACTTGTTTTTTTTTAGTAAGTGTGATCTCTTTTCTGGGTGTACATTTCCGATAGCCAACCA
GGTTATATTTTAGCAGTTTATAGACAGTGTATTCGATGGGTAATATAAATAAAAGCTCATGAAATA
CTATCTAGTGAAAAGTCGTGTGTAATCGATTGTGAAAAATATAAAACCATAACGTAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAAAATGTTGTCCGCCAAAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG
ACTTGTTGATGCATATAATCAGATTTGTCATGCCTTCCAGAAATAAAGAATTGAAAAAGTTGTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAAATGAGACATGAAATGATTCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTTCGAGGCAATACTTTGAGAT
ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAAACGATTCTGTTT
GTAAAAGAAATGCTTTTGTCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG
ATAATATTTTCAGTTATTGAGACTTTGGATCCATTGATACAAATTGGCTTTTATTGAGTTTATCAAAA
AGGACTCTATTTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTTGGCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTACAAAGACTTGTCAT
TAGAAATTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAGTCTA
CAGCTTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTCCCAGATT
TAAGGGACGCTATTTTGAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTTC
GTGGTGCAATTATGGGTTATTGGTGAGTATGCCTTAGAGGAATCATTAATACAAGAATCTTGAAAT
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAACTGAAAGAGCTGATG
ATACTGAGGAATCACAAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACGACTCTTTGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAATTCCTGCTGGTGATTTCTACTTAGGTGCTGTATTAG
CATCAACTTTGGTGAAATTGATTCTCCGATTGCAAAGTTTGAAACAACTCAAGAAAAAATTTTGA
ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG
TTTCTAAGAAAATGATGAGGATTCGCTGACAGAATTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTTTACAGAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAGAAAGAAAAATTTGTCGTCGAGATTGAACAAA
TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG
ATGTTGTGTTAGATGCTTGTAGTGAATCAAAACCAACTACTTTAAGAACTTTATCAGTTGAAT
TTGCTACATTTGGGTGATTTGAAAGTGGTTGATAAACCACCACTACCGCAAAATATTGGACCTCATGGTT
TCTACAAAGTTTCAAACAACATATAAGTTACTTCCGCTGATACTGGTGTGTCATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTTCAGAAAGTCAATTCCGTAAAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGGGTAATTGGAGAAGAATGTCATTTTATCAG
CAAACCTTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCAATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLLEKGGKDDVKVDTMKKILITILNGDPLPDLMLHIIRFVMP
RNKELKLLYHYWEVCPKMDSESGKMRHEMILVNCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRCLEHRHAYVRKNAVFALWSIHKVLDHNLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQOYAQLMTEIIESSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNNVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLQFITTRNVEDVVKLLKKEQLSTALSNDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAVEVITFVKEVVEKFPDLRDAILRRLILALPHVKSQKVFGRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASSELKSKRRDDTEESQEEETEYDGPVLRKGPVLPDGTAYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLIILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELALA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFSDPIYA
EAFVKVHQYDVVLDVLLVNQTTTTLRLNLSVEFATLGLDKVVDKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDQGHSDDSRIVILNDVHVDIMDYIKPATCSSESQFRKMWNFEFEWENKITIKSPIET
LKEYLDELKMGTMQCLTPGAVIGEECQFLSANLYSRSSFFGEDALANLCIEKQSDGPIIGHVRIRS
KGQGLALSGLDRVASISRKGGKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGTATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAAA
AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCATCGATCCGAGACTTCCAT
AGCAAAGTTAACAAGCACAAATTGTCAATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT
TGTTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTTCATATTAACT
ACCAATTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTTCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT
GGAGTTTTCATTGAACATAATATTATTAATAATATTATTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTTCAACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTTC
TTGCCACATACTGTGCTCAAGGATCAATTTGGCTTGAACGGTTCAGTCTGTTTAGCAAGAGATATTT
TTGTTGGCTATGTTGTATACACTCAATTTATTAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTTCGAAGGTTATACCTATATGTTAGTCTACGGTGTCACTCTCAATCTTTTCACTAC
CATTTATTAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTTA
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
TTTCTTGGAGTTGGATAAATTACAAAACCTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG
GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACCTCGG
TGGCCAATCAATTGCATCCCGATGTTTCCCGAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTTCATA
TGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACCTCGGGAGGTACTGAGT
CGTTATTGTTAGCCGGGTGTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAATAACTGAGCCTG
AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGAATGAAAT
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAGATTGATCA
ATAGTAATACAGTTTAACTCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG
AGTCTTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT
TTATTGTTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC
GATTACCAGGTGTCACGTCAATCTCATGTGATACTCACAAATATGGGTTTGTCTCCAAGGGGTTCAT
CAATAATTATGTACCGTTCCGCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG
GTGGAATGTATGGTTCTCCAACCTTTGGCTGGTTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG
CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTGTGTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAAACTGACCCGATACATCCAAACATTTACAAATTATTTGGTGATC
CAATTGGGTTCGTAATTTTCGTTTCAACTTGACCTCAGCAATCGGGAATTTAAGTATTTACGAGA
TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT
TTGCATTTACAAGATTGACTGTCCCGGTGGTCGATGAATTGATTGCAGATTTGGTTGAAGCTACAA
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGGTACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL
YRVLRGYGIIVDSIRRLYLIVSVSSQIFSLPFIKSKIDKELQATIGKVEEIEIMKNPQLLQFP
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVPV
RKMEAEEVHMLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDFRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC
QYYIASDWTGMYGSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTPVPVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)

TTCAATTTTTTTTAAAAAATAGCAAAAAGGTATTTCTTAGAAATTGAAAAAATCACA
AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTGTGCAATAGAGAAAA
GCATGATATACTATCGATAAATATCTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAT
AAAACCTCCCTTTTCTGCTGATATAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
CTACTCTCTAGACAAAATCAAAACCTCGAATATATTTTTTGGTGTTCCTTTTTTTTTTTTGCCT
CTCGTTGAAATCATCTCCATTCTTCTTTTCCACGTCTTTGTTGAAAACCTTGCAACCTAAAAAAT
AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACCTAGATTAAACAAAGCA
GGGCCATAAGTCGGGTGTGAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT
ACCCAGTTGGTCTAAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCAGAATTTTCCC
TCACTGCTGTATCATTAATAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCTAATG
ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCATATA
TTTTAGAACATACAACTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTAAATGA
CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAACCTAATGGATGTGTATTTATCGTCAGTGTGTGAACCGC
AATTAAACCATAACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACCTGTCAT
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGGTGATCCCA
AGAAAATTTGTGATTTGCTGTACGAGGGTTTACTAGAGTTTCACCTGAAAAATTTATCATCCATCAA
ATGCAAAAACATTTACTTTATGGAAAAATTACCATTGGAAGACAGTTTAAGTAAAAATAAGCAAATACT
ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT
CAGAAATCTTTGATGTCACCATCCCGGGTCCAGTTGATCAAAATGAATGGTAAAGAGACTTCAGAAC
AGTACTGCACATCTATCACCTGGAACCTTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT
TTAAATGGAAAATATTGAGCTCATTATTGTTTGTATGGACACAACCTCTCCTTTCTATCAAGAGTTAA
TTGAAAGTGGATACGGTGACGATTTTCTGCAAAATACTGGGTGGACTCAACCACCGCGTTGCTTT
CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTTAATGAAAAAGTTATGG
AAATCATTAATAATAAAATCAATCCCGAATTAAGTAACGAAGAGTCCTCTCATATCATGGTAGAA
TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAAGACACAAGCCCGATTTTGGATTGGGAT
TATTGAGCTCTATTGTTCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGAAA
AGATATTGTTCGATTTTAAAGAAGATTATAAACAAAATGGTTTAAAGGATCTTTAAAGAATTATTAG
AAAAGACATTTGTGTAACCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA
CCAAACAATTGGTAAAAGATGAGAAATTTGATGATCGAGAAAAGAGTAAGTGAACCTCACAGAAGATA
ACAAGAAGGCAATCTATGAGCAAAAACCTTGGAAATTAGCTAAATTACAATTGGAGGATCAAAATACAG
AAGTTTACCCACATTGACTATTGATGACATTTCAAAGAGAGGTGATTTTATGCCATTGATTGGG
GCCAAGTAAATAAGAAAGTTGTACATGAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
CTTTAAAGATATTTCTTATTTACCCACCAAACTTTACAAGTACCTTCCATTGTTTAAACAACGTGT
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGGAAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTGTATTAAAA
ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACCTCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCGGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA
CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACCTCATTCAATTACAATCATACAA
GTGAAAATGTCTTAGTTAAGTTAAGTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTGAACGGGA
CATTAACCTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTC
AAAGCGTCGATGCTCCAATTAATATCTCTTCTCAGGTGCTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTGGGTACCACCTTAAAGGATCTCAGAGATGTGA

114/161

CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCACCTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSRASRVVRRYACSHPISPNLDKYPVGLKLHGYEVTQTSPPIPEFSLTAVSLKHTEGSA
THLHLDSPNDSSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDYTFYFPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYIKFLESIIYPSLNNSGGDPKKIVDLSEGLLEFHSKNYHPSNAKTFTYQKLPLE
DSLSKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSIWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNLYLTKQK
VDNFNEKVMEIINNKKIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTVEVLTTLTIDDI PKRGDFY AIDLQGVNKKVHERVV
DTNGLVYANALKDISYLP TKLYKLPLFN NCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILT TTKFDTSDDEVLEKLSVLIK NMGNQ INNIADR
GHSYAAA VSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIVENEKLIKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLHHSKIRESN GAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDSLSYGLDANWNDKDLQEA KLRVFSVDAPINISSQGASAFFENIDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAATGTTTATGTCAATTATATAATTTGTAAATACATGTATATAGATT
TTTTAATGAATGTATCCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACCTGGTTTGAG
TATTGGAGAAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAGAATTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCCTGCTAGAGGTTTTTCTTTTGTATGTCTGTAACAGTGCGACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTCCTCAA
CTTCTCTCTCTTCTCTCTTTGCTTTTCTCTCCTAAGGAAAAAAAAAATTTATTTCAATTTGTTGAAAAT
TTTTGTATAGTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTATCCAAC TACTGTTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA
AAAACTTTTTCAAGAGATGGATATGGAACAAGATTTCGATTGTTATCAACAAATATAAAGAAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTAAACCATCACTCTATTCAACAATCATTTAAATATTAAAGACTTTTT
TTTCCCTGTTTAAAGTATTCGATTTACTAATCATTAATTAATTTATTATAGTTTGTGTAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTA AAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAAGAATTGTCACCATTTATGCAAAACCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACTTGGAATCTAAATT
GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAAAC TACTTCTCGTGGTCGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKL RDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)

ATAGTTATTACAATATAATAAAGCAAATAAATAAAGAAATGATAAAGAACCATATTAACAAAGTT
TGAACGTGCTGTAAGTAAATCTTGTATACGAGAATATTCATCTTGGAATATTTCTAAACGATACTG
GTAATACCTAATTTCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTCACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAAATTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAAATTTTTTTGAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTCATCAAACTCTGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACCTATGAATGG
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAGAGAGAAGC
AAAGAGAAAAAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAAACTAGAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCACAACATTT
TTATTTATTTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC
ATTATACTAACTAAATTTTGTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAATCTCACCCATTCACCATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTTAAATTAGTAAACTACAACCATTTAATGCCAAGTACTAGTACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)
MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTSHPFPHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKKAFFEEKHQAGKNKWFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)
TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
AATACTTTGCCATGACGACCCACTGAAGTAACAACCTGCATTTGTTAAGGCTTTTCTCATCTTATTCA
ATTCTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA
CTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTAAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTAAAGTCTGTACCTTAAGCGTCAAACGTAACCTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAAGTACAAGCTACGAAAAA
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTCTCTTT
GGAGGTTTTAGAAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGAAGTCGGCACTAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAAATATGACACAAGCTTCCATGACAACAGATACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACGCCAATAAACTGTTGAAACAAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTGATTGATAAATCAA
ATGAACATACAGGAGGCCTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCCTACAGCAGCAGATAAATGCCTACATTTATTGACG
ACAACCAAGAAGCTCAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)
MNRLFGTKSTAPKPSLNDAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGPGRSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTDNLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELQELSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS:
501..4547 (SEQ ID NO 335)
GAATGAGATTTTTTTTTTTTACTAAGGGTGCCTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTATTTTAGTTT
TTGGTTTCATAAATTATTTAAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTTGGTTTTT
TTTTCTTTGGTTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTGAAAATTTTCTCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAACCAACATCAATTCCAACTTTGTTFACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCTGTTATTTTTTCCAAGTACTACACGTCTTTAT
TTTTAATACATTTATCATAAAACAAAATTTATATCAATAATGCCACATTCAGACAACCTTCGATAT
CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
AACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACCTACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAATTATTATAATGAAATTATTAACATCATCCTAATGTTTGTAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTTGGTGGAAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA
TCATATTGGGTACGGCTTATTTGTTCATGCTCTTGGTATATGTTCACAGAGATTTAAAACAGAGAATT
TGTTACTAGATTCTCAATTGAATGTAAAATTAGCCGATTTTGGAAATGGCAGCTTTAGAAAGTAACG
GCAATTATAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA
AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGTTATATTATTTGCCTTGTGACAGGTA
GATTACCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA
TGAGAAGAATATCTACTGAAAAATCTTAAAGACACCCATTTGTTAAACCAATACCCAATGTCAAACG
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
GAAACATTGATAAACAGATTTTATCAAACCTTGACAAATTTTATGGAATGATAGACCCGAAGAGAAA
TTGTTGATTGTCTTTTGAAGATGGATCCAATCCAGAAAAACATTCATGCATTTATGATGAGAT
ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA
AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA
TAAGTGTGTCAAGACCAACATCTTTCCAATACAAGTCTAATCCTGGCGCTGGTGCAACAGCAAATA
GAACTCCGTTGCCAGACATTTCTGTGGCTTCCTCGGCCAACAATTCCTCGTAAATCACCATACA
AGTCACCATACAGATCACCTTATAGATCACCATAAAATCGCCTTCTAAGAGATATTCATATAATC
AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAAATTCACAAAGACAATTTGAAAATGAACCAT
TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC
CATCGCTTCCACCTTCCTTACCTTCAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA
TGCAGTCAGCAAAAAATTTCTAGTGGAAGAGAAAATTCATAATAGGAAAGAACAAACAACAGCA
ACAGCAACAAGAGAATGTCTAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAGAA
ATTCCATAACCATGAAATTGTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA
TGGATAAAACAAACAAAAGAACATCGGCTACTTTTGCAGCATTGTGTGACAAAATATTTAATCAAG
AAGACTATGACGAAGAAGACGAACAAATAGTTGATCCTGAAGAAAAGGAAGCCAAGGAATATGAAA
GGTTAATGGAATTTGGAAGAAAAGAACATGAAGCTGAGTTGAAAGCTAGAAGAGAATTAGAAAAGA
AGAAAAGAAGACAAAAGAGACGTTCCTATTTTGAAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG
ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTTCGATGAAGGTATAAAACAACCAAAACGTCAAT
CCAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAATCATGCATCTGAAGAATTGACATTTGG
AAGACGTTGAGAAATTTGAAGAGACGATCAGCATCAGACCCGGTTCCAAAAAGAACAAAACCTCCGG
TTTTGACAAGAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG
ATAGAGCAAAAGATGCCTTGGAAACAAGAATGGAGGGATTACAAAAGAGAGATTCTACTGTTAGTC
GTAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC
GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAGAGACTATGAATTACCAGAAC
CAACTGTGGAAGATTCCAACCTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAGAAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTTCTATAATTAATCAACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAAGAGAG
CATCTAGAGCTTCAACAACTAAACGTTACAATGTTTCATTCCAGTTTCAGAAAAAGACCAAAATCCA
AAGTTCTGATTTTGCCTAAAGAAATGATTATGATGACACATTTGTGAGTAATAGTGTGAAGTTTATA
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGTATTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTTGGCTAACGGCACGCTTACAAGTG
GTCATAGAAAACCAAGATAAGACATTTCAACCGGGCCAGAAATGTTGATTCTTCATTTGAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTCGTGGTAACAATTCAGTGGTCATGATGATA

117/161

GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTGGATGATAAGACGAATTTCC
 CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTCATTTTTTAGAAAACTTTCTTGGGGATCCAAAA
 AAACCATTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG
 CTGAATCAAAAAGAGGAGAAACCAAAAAGTTCATTTTTTTCAGATGGTTTTTCGTCATCTAATACTCCAT
 CTGCTGCTGAAATTAGAAAAATTCACACCATTTTTACCTAAACATGAAATGTCTACTGCTTTATTTG
 CTTTATTGAATTCCTTGGTCTAATTTTGGTTTGAAGATTTACGGAATGATCAAGTTGGATATTATA
 TTACTGGTGCTATTTCTAAACATAATTCCTTTTAATTTAAAGAGTTGTAATTTAGAAATTAAGATTA
 ATCAAAGAGATTTTAATCAAAAATCAGAAATTTGTTTGTGTTTAGAGTGAAAGGATCTAAAGTTACAA
 CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGKTLGRGATGRVLLATHQTGQKAAVKVSVKSELQD
 EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
 VEAIKYFRQIILGTAYCHALGICHRDLKPENLLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
 AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLVQAGNFEMPVDEVSRARDL
 IARMLEVDPMRRISTEKILRHPLLTKYPMSEDLISEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI
 LWNDRPEEEIVDCLLKDGSNPEKTFYALLMRYKHNQDDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
 TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK
 SPSKRYSYNQSPTKSPYGRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPSPSLPSPSKDSR
 YMIDEPNQPLQOPALSQVNPENIVDESPDLMSAKISSGKRNSIIGKNNNNNSNKRMSKRKSIR
 ASMTTGLKRNSITMKLLSTYAKLSGDDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
 EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRSILSSKKLSIIVKNDADPNNSEQELVD
 EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPKRRQTPVLTRRPVSRDLPL
 WQAHENEQLDRAKDALEQEWDRSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE
 RERDYELPEPTVEDSNLTDYMTAIRKSRLNLSQNLVRDPLNEKRKSEPKTLISNVQIPSVTRKSR
 NFTTSNKRSLSVLSMYSTKESYRDLNSIINSPDENPEQHONMKNPALRTSIADRLDKAGLAEPEYET
 ETDGEDKVSVIDLDDHLADRRTSYDGSQKRASRSTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
 FVSNSDEVHVRQYKSMVSESSASDDVDFDIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
 PEMLIPLHNGGIESSQPMKSVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGSF
 FRKLSWGSKKTIENTNTAATNTTTTQQQLPSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP
 KHEMSTALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSKCFRIKINQDFNQKSEIVC
 VRVKGSKVTTDTLFCIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
 (SEQ ID NO 337)

ACAATACTAGGCACGTGTTGAGTGAGTGAGCATTTTTTCTGTTTCTCACTCAGTTAACAAAAATAAAA
 AAAATTTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA
 TGTAAGACAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG
 TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
 TGGTATACAACTAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA
 TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAGA
 ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA
 TGGAACAAAGTTTACTAACAACATTTGTTATAGGTAAAAATGGGTATTTCTAGAGATTACAGTCACA
 AAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTACAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC
 AACCAGCCAACACCAAGATTGGTCCAAAAGAATTCACTCTGTGAGAACCAAGAGGTGGTAACCAAA
 AATTACAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTGTTCCAGAAAAA
 CCAGAATTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
 AATCTGCTGTTGTTCAAATTGATGCTACTCCATTACAGACAATGGTACGAAAACCACTACGGTGCTA
 CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGATGCCAAGAGAT
 CAAGAAAAGTCAAGAGAAAATTGGCTGCTAGATCTGGTGTCTGCTGCCATTGAATCCGCTGTTGACT
 CTAATTTCGTTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
 ATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFS
 WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTSAVVQIDATPFRQWYENHYGATLGKKKGGGAHAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACAGCACCACAGCAATATAGCAA
TCATAAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGAAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAGACCCCTTGCTGAAACAGCTCAAGAATATGTTCGAGGTTGCCAAAACCTG
AAATTGGAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TGTAATACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTG
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACAGCACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTTGAATCTTGTTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGAAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAAGCAGAGGGCGAAGCAAAGACCCCTTGCTGAAACAGCTCAAGAATATGTTCGAGGTTGCCAAAA
CTGAAATTGGAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTTTCTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAACCTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAACAAACAAAAAGAAGTAGTAGTTTGTGAAATTTGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATAATATGAAAGTGAGTGCGACATAATGTAGAAAAA
TGTCGAATGCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTGCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTGTAGTAGAC
ATATCACTATTTTTTCTCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCAGATAAGTTATTAGATCCTAAAACCGTGTGCATATATTTTTTAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAACGAATTCAGAAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANTSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTORAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQQEAT'TYLEKKFKKTDVAVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGGCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAACA
AATTAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAATTACAAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTCATTATGTCAAAAAATCTATAGTTACCTACCTACATCAATTTATG
GTCTGAAATACTAACATTTT'TTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTGAGAGGTGACTCTAAAATTTTATGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCCAACAAAGAAAGAACCCAAGAAGAATTTCTTGACTGTTT
TGTACAGAAGACACCACAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTGCGGTGCTTCTTTGGAATTGATCAAAGAAAGAAGTCAAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCA AAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAQKGSFQVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTGCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATAACCTTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAATATAATTATTTAACAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTT'TTTTCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTTATTTATTGTGTTTGT'TTATACTACCC
TTTGCATATATTACTAATATTTATCTTACCCTTTCATCATGGATACAAAGGAATAAGATCTACCG
TATCTAATCTTGAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTTAAACCATCCGAAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCCCATCATCATCGGGTCTGGAAGTACAACACCAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAACTGACGGTGTAATACTCAATTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTAAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTTGTGTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAAGCACAAGA
AGGTCAGTTATTATCAAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPKSEKLLRETKVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNLRSF
TMNLRNKKNPRLRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTD
FTCGKCKHKVSYQQMQRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTTATTGTTGGCTATACCTTCCAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAATAAAT
AATACATGCAAAATACTGCATATTAGAATTATAAGGGAATGAAAATGAAAAAAGAAATAATTT
TGTAAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT
TTGAGTTTTCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACTAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAAACA'TGGAAAACTAATCGAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACAACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAATTATTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAGCTGGTGGTCAACATCATCACAGAACCAAACTGGATA
AATACCATCCAGGTACTTTCGGTAAAGTTGGTATGAGATACTTCCACAAAACAACAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHRGNVSAGKGRIGKHKRHPGGRGKAGGQHHHRTNLDKYHPGYFGKVMRYFHKQQN
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEPVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)

GCTATCAAAATCACTGTTTCAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAGAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTT
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACCTTGGAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTGTCAGAAACAAGGATATCCGTAAATTTCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKSILIANLITGVTKGYKYKMRVYAHFPINVNIIKKDGQDYVEIRNF
LGEKRVREVKIHEGVTMEISSTQKDELIVSGNSLEAVSQNAADIQQICVRNKNKDIRKFLDGIYVSE
RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAAATTTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAAATGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAAATAAATCGGTATTTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTTGCTGTGTAAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTTATGAGTTTTGATTTCTTCCTGATGTTTTTTTTCTTTGTTTTCTT
TTGTGCTGTGTAGCAAGAAGAAAAAAGTGTCTTCAACAAGCTTTGGACTCAATTTTCACCCCT
CCACAAACTCAATTTCAATTAACATCAATAATCCAATATGGGTAAACAGTATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATTTCTTGGTGTAGCTATTACCAATAAGTTCAGTGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGCTAACTGATGATATAAAATCATTGTGAAAGCA
ATTGTTGGACCCCTGGCTTTTTATCGCGATCCAGAATCCAAACAAGACTATTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTTCATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTTAAAGGAACTCTTCTTTTCCCAAATTTCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTTCGTTTCGAGTGATTTGGTGACCAGTAGAAATTTCCCAATCGACGCTA
TACCTAGGGTGTGGCATTTTCCCTGGTGGAACCTTTGTTGGCTGTGGCAAGACAACTCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGTGAGAATGTGGGGTCTTTGGCCACACCTCAC
ACTCGGCCAAATCTGTGTTGGTGGGTTTGACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTGCTTCTGGTGTTCGTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTLTLLAFACFNLSIIIFRYIINDDFSTIESLTDIISFESNCWTPGFRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFNPNSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCI RVWNLET SEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTGTAAATG
TAGATGGATAAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCAATTAATATAAAATTTACAAATCT
GATAATAAACTACAGTAACCTATTATGCAACAATTGAAAGTATCCTGTGTACAGTGATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCCTGCACACATTTGAGTTTTTTTTCTA
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAATCTTTTCGTTTGAAGGTTTGAAGGTTT
GTTTTCTCAATAGTATATCCATACATACTAATACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTCAATAAGATTTTCAAGATTGGAATCAAA
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAAATTTTATGTAAAT
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAGT
GATTCATCCCAGTGATATAAATAATGATATTCAATTAATAAACAATATTAAGACATTTTATTATTTAT

10030019 . 122601

10/030019

122/161

GTATCAACAAAAATACTAACTTATCTTTCTTTTAAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTTAAACATTTTGTGTGGTGAATCCGGTGATAGATTAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTCCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG
AAGAAATCTTGGAAGAGGTTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA
CCGGTAACCTTTGGTTTTCCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)
MSDKSQNVMMRELRIEKLVLNICVGESGDRLLTRAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRRRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCACGACTATGAGTACGCACCTACTAATTATAGCCTGAAAAAAAAAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCCTAAGACGTCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCACCAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAAGTCTGCTAGAAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTGGAAAAAATTGGTATTGA
ATCTAAACAACCAAACCTCTGCTATCAGAAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAACCTTTGTTGACGAAAAATGACGAAGTCTTGTT
GGCTGGTTTTCCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTTAGATTCAAGGTTGTTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAAGAAAGCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)
MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGSSSHAKGIVLEKIGIESKQPNS
AIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTCCGACTTCCACGAA
ATGTGGTTTGAAAAAATTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAAAGAAAAACC
ACCAAAACCCCCACCACCAACCTAACCTTTTCCTTCCATCCATTCTCTTTTCCTTACTTTGCAAATG
TTGAATCCAGTTATATTCAATTAAGATCCTATAAAATACGATTATTACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATTTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAAGTGTCTCTTTGCCATTGTCAATAACACAAATATCAAAACATTGAAATTT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAATTAATTATTGGTATAACTGGT
TCTAATTTTATTAAATAAAAAAATTTAAATCTCAATTACAACTTTTAAATCAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACCAGTGTTATTTTTTTTTGAAATTTATGAA
ATTAATGATGTTTGTGGTCCAACCTGGTTATATTAATGATATTGATAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAATTTTCGTAAAGATCATGGATTTAAATTTATTAGATATT
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

501..1781 (SEQ ID NO 383)
AATTATTAGTTGTAAGAAACAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATTGTCTGCCATAAAAGAATAAACTAAACTAGACAAGTGTATAGAATCTTTTTTATTAATA
GATGCTTATCTTAGTTATGTTCCGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAATAAAGCAGAGAAGATGAAGAAGCAAAAAGAAAAATTTTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTTCATACCAATAAAGAACATGTCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGTCTCCAAATACTCTGCCCCAGTGCCTCGTCCAATTGAACCAGTTGGTC
GTTACTTCTTAGCCCAAGCCCTCAAGAACTTTGCGTGGACACACTGTTGTTGGAATTGAAAAATCG
AAGCTGAAAAGAATGTTAACAATAAAGTCAAGTCAACGAGATGAGGATTCTGGAGATTGAAGAACAAA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCCACAGAAAACAAGTTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAAACGATGGATTTTTCAAAATTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCATTGTTGGGAAATTTAGAAAGCACCAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAAGAAATTGAAGCAAGAAGATCACAAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACCTCTAAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAIVSKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHDPDKKSASGGL
ENDGFFKIIQKA FEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFFEAWGPVFESEARFSTKQVP
LLGNLESTKEEVD AFYSFWGRFDSWKT FEFKDEDV PDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKA AKKWEKESGRKAAEEAAKKAEEAAKKAEEAAALK
ANSKKAKEA AKA AKKKNKR NIRA AVKDN NYFGDSAKSADIDADVDLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYPN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTTGGTAGTAGAAGAATTCAACCTTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTGCAGTTTTAGTTT
TGGTTGTTTCACAATTTGAAAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTTGAGTGAAAAGTGTACATTTGTACACACACAAACAAAAAAACTAACTTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTCTTGCCATACTATCGCATTTTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAAGAAGAAAAGAGAAAAAAAATTTTCAGTTTTCATAGATTTTC
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTACCATGAG
TTATGGAGGGATATTCCTGGATGATCAGAAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAAATTTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTCAAATAAAACATGTAATACTAACTATTATTTTTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACCTTTAGTTCAACAACCAAGATCTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCAAGCTCAAACCTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTTCAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSATEAKQHKLKTLVQQPRSFMDVKCQGCLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

125/161

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1: 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTTGTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTTGTGGTCTTCTTTGTGTTTTTGATATTTTGCAGCTGGTCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGAATTTCTTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAGAGCTGGAAAAGTGTGATTAACAACAACGAGGGAAGAAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCACTAGTAACTTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAATGAGATACAAGATATTCTTCCAATACAAAGAGATTAATGGTGTTTTGTATAGAGTGTAAG
CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAAATTGTTGA
AAGAAATAGCCAACTATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTCGCTCAAGGTAAAGAAGATATGAC
AGAAAACAATCCGGTTATGGTGGTCAAACCAAAACAATTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTTGAAAAGATGT
AAACATTTTCGAATTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHVKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLCEVVCCKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGTTTGAACGTGTTTGATTTCAGAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAGAAGCACATAATTTTTTGAATGATTTCACGAAAGAGTTC
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTCACGGGAAAGCAG
CAGGCGAAGTTCAATAATAAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTTCAGAGTCAACCAAAACCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCACTGATTACTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACCGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA
TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAAACGATTCAGATAAATCAGAAACGACTCAACC
AAAACCTTGCCCGCTCAGAATCATTTGCCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAAGTTGTGGCAGCAAA
TGTGCTGGAGAACATTGATGAGAATGAAAAATTTTCAGAAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAAGAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAAT
GAAGAAAACAAAATTGAATACTATTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCCAAGAACCAGAAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAAATTTCAAA
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAAAGAGAAAATGCGGTCCGAGAA
TGCAAAGACATCTGAAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTCGAAGAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAAATGAAAAGGATTTCTGTGGATT
CACATGCTTGATGAGGAGCATTGGAAGGTGATACACAAATTTGTGAAATATCTCATCGAAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGAATTCAGAGACACCATTGATCGATGCAGCTGA
AAACAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACCTATTTTGCAGAGCT
 AATTAAAGGTAAGGGGAATATATAAAATACGCTGCAGAGAATTCAAAGAGAAAACAGCAGAATATTT
 TGGTGGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC
 AGAACTTGGTTGATATTATACTAGGGCTAAACCCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
 TGGTGTACTGCATTATTGGCCAGTATTGGACGCGGTCAATTTGAAGTTGTCGATTCCCTTGTGTGTC
 CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTGAATGCTTTAGAAATTGCACAACA
 CTCGCCACATTTTGATTACGCGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGGAAC
 CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
 CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAAATAAAAG
 TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
 CCACGAGTCTACAGGTCGAAAACCTGAAAAGACTCATAGCAATGAGGAAAAGAAAGCGGAAACGTGA
 ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA
 ATCACTACATAGAGAATTCACCTCTGATGATCACCACACCAGTGAAGCCATTTCAGATTCTTTTGC
 AGAAAAAAGAAAAACATTTATCGGCAACGCCACTGCTCCTCCGCCACCACCACCACCACCTTC
 TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
 AGAAAAGGTGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA
 GCAGAAACGGAAAGAAGAAGAATTGCGAGCACAAAGAAAGAAACGAAATGCCAAAAGCAAAACA
 GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAGAAAGT
 GGGGTTCGACACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG
 AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA
 GTATGCTGTTGATTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT
 ACAACCTCATCAGAAGAGAGAAAAATAATGCAACTGAAAAAAGCAAATTGTGGAAGCTCTTTTTCAA
 GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
 ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
 TCCAGAAGTACACTCAAAGCAAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGT
 TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTTCCAAGAA
 AATCGAAAAGTTTATTCCTCCTCATTTGAATAC'TAGGAAAGACATTAT'TAGGACTGTCAGTACTTT
 AGCACACCCACTATGGTGA

YIL112W_homolog_1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSFTDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
 SEQLLTDKKDNKSEPNSEVNLKDNNDISKATAGCALGPDKNKGKNDSDKSETTQPKLARSESFADT
 SLLSPVNESDTEFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEDEGKKLLR
 EQTADVCRHKLKKTCLNTIFSSDEEEEEIEQPDFKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
 VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKLPYKVKRDSGR
 SLLQRAKCKGNFADVQDYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
 DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTAKIYNEHEGEEGYDEIIQVLEEATANY
 NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIKYAAENSKEKTAEYFVAGHNLEGKPD
 ILILAARNGHTLVLDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
 DGLNALEIAQHSPhfDSREVSVMKFMKKSgtKILSGIPSRVVSrATSRAPSVPVSSDEDDVVEE
 KEITAHTENKSAEKKSedKITKTVNEHVSnrKPHESTGRKLEKTHSNEERKRKREWSdDEPKPHL
 LKKSksDLKLKSLHREFTSDDHHTSeshSDSFAEKrkHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
 IKDAEEARLWQEKVEAKKRARREmFLKSEKEKEQKRKEEEELRAQEEKRIAKAQEEQERLAREAE
 EKSKELEEKVGLRQQLTLdHYpVGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT
 STVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCdQRSSITNGQKQFQNLHLHFVE
 VDLAEFLKEFPEVHSAKDNQIDVSLSLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT
 RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog_659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGTATTTGCCCACTAAAAAGAAAACCAAT
 GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTTGT
 TCGTGTCTCGGTCAATTGAGGTGGGTAAATGTTTTTCTTTTGAAGATTGTGAGCATGCAATGTGCG
 CATGCAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

TAGTTTTAAACCTAAAAAAACAATTTTGTGTCAGTCGTGCACCATTTCGTTCTATTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGGAAATC
CCCTTTTTGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAATAACAACCTGTGAAAAATCCATTTGTGCGTAAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACCTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)
MIEPSLKALASKYNCEKSICRKYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)
ACTCAGCCTTTTGAAATTCACCTTTTGGTAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCCATATTGTTGTTCCCTACCCTCTTGCAGTAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAGATTATTTTCACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTGTGACAATTGATTTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTTTTGTGGTTTGTGGAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTTTTTTTTTTTTACCAGCATTTTGTCTTGTCTTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACCTATATCTGCTAACATACTC
GGCAACAACAAAGAAAGAGAATTTGAACCTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAAACAGAAGATTTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAGCCTTGAAAAACGTCGTTACAGTCACCACTGGAAG
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAAGCAAGAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTTCTTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAAATAGATTTTCAGTAAAGAAGGTTTGAGTTTCAATTGGATAAGTATACCTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCAGCAAGATACCTTGCCCAAC
TGCAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCTTAAATTTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACCTATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTGCT
TTGTGGTGCAGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCCTGTAGACTTGATGCTTTTTGATAAGGCTTTTCAGAAAAACGGGAAATCC
AACCGGGTGATTTATTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAAACCAATGTGTCAAGTATTTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTGGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAGTCTAGTACAA
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
ATAAAAATGGGTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG
GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAACTAGGTTCTGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTACATATTGGGTTTGATCCAACAGGTACATCTTTGAACC
AAAATAGTACCTTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTTCGGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)
MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHDKEDAHKIDFSKRRFEF
QLDKYTFTPKDVDDLEPISKLYLRRRYLAQSQIADI I AETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGCKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPOKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNQIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDL SVETSGHKSLSSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTRRLQNLVKGQTHATLVDKRKR VVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTGTAGTAGA
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT
TTATGCAAGTCGTGTACTGGTGATATCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTCAATGTAAACTGATGGTTAAGGGATTATAAATCAAACAGTAGTGCTT
TTGTTCCATAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCCTTGAACTTAACTTAATGAAAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAAACTTCCACAAAGCCTCCGTGCAGGGTGTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACCTGGCAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACCTGTGGTGTTGCCTGAAAGTTCGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTGTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA
AGCAATTACCCAACCTTGATAAAGTTAAGGGGGTCATTTGTTCCGGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAAATCATAAGGAGATACCAGTGTGGCAATTGAAACTAAACAAG
CGGCCACGTTTACGAGGCGGTCAAAGAAGGTAAAGTTGTTTCAATTTACAAAAAGTGCAAACTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACATATTTGAGCGTCTACAG
TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCGGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTTVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMHVLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSCTVLPESSKPTVIEKLKSLGADVIIHGKHWEADNYLTDFVIKNL
DKTVYPVYCHPFDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFHYMVEPACGASVASVMHRQDLLNKFGTLLSPDDIIIVVICGGSAINKYIIDEYRSLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)

TTTTTGAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGATATAATTTGCGACA
TTTGTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTATGGTTGTAACATTTCTAGTATATTCTACGTAATAGGTGAGGTCCCT
ATATGCAGTACACACAGGTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTCACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTTGATTTTTTGAATTCCTTTCT
TTTTTTTGTCAATTTATTTATTAACATTCCTTGTAATACTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAAATCTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCTTATACCATTTTGGTTTTCACCGAAGCACG
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCCTTATTCCTGTGTTGGTGTATGAAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
TTTCATCTATGGTTTTGGGTAAAATGAAGAGTATTCGCTGAAGATTACCTTGGCAAAAAGTTACTC
ATGCCGTTGTCACCTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
TAGACAAAGGCGACCAAGAAAAACAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGTATGTTT
CTTTATTGTCCATTGAAGGTGGTGTTCGAAGCTTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAAGCTT
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAAGACTTTGAAACCAGTTG
ACAAGTGTGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT
CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGGCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCATTGACTTTAGGTATTGAAACTTCTGGTG
GGGTTATGACCCTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTGTATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG
ACAACAACAGATTGGGCAAATTTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCACACAAA
TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAAGT
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAATCTATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAACAAAAACAAAATTAATTGACG
TTGCAACCCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCGGTGATGATGATTCAGATGATGAATTCGATCACGATGAATTTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAASVDDDESSTDNYGTVIGIDLGTITYSCVGV
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDDTVQKEL
KHLPYKIENKGNKPVVKVEYQGEKTFSP EISSMVLGKMKSI AEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKGDQEKQIIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDDFDKIVRYLAKQFKKKHNIDITANSKAI SKLKREAEKAKRTLS SQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKSDIDDIVLVGGSTRIPKVQELLE
FFDGKKASKGINPDEAVAYGAAGVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDDSDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCTGGTGACAGAAAAGTATTGATCCAGTTTCTTTGAAGGTTTGTAATACGTTTAAACTTG
TGACCTAACTCATTTTCATAAAATTCTTGTATAAAATTGGTTTCTTTGAATTGTTTGTAATCTCTT
AAGATTGTCTCGTCTTCAGTGTTCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCTATCTTCTACTAAGCCGGACAATCCCAAAGCCGCTCTTGTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCGTAAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACAG
TAGCTCCAAACCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTCGCGTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCTAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTTCGGAGGAAATGGTACCATT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACCTATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAATAATTGAATTTCACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFLVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQVPFLEDELGQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
AAACTTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTGTAGTATCAATTATTG
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAATTCTGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTTTGTAATGCTTCTTGATTCATGATTAAATGAGACGAGT
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
AAAAATATACAATCTATAATCAGTATGTTTTCAGTTTTGGAATGGAAGCCCCAAGAAGAACAACAGGG
AAATTAATAAATAAAGGTGTTGAGAGAAAAAATAATTGAACAGAAAGATTCATCCTTTTGA
TCAAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT
GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT
ATCAATTAATAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAACTGGTACTAGATTTTGGAAAAAAGGTGAAGTTAAATTCATAATG
AACTCAAAAATATGAAATTCAATTAGATGGGAAAACTCTACGCACACCACTTGGATTCCCATTAG
AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
TTAAAGTGAAATCAAGTACTTTACCATTAAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC
AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTTGGAAGATATTAATTTAC
AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTACAA
TTTATGCTCATAATAAAAAATTTAATCCCTCGACAAAAATCTATTGAATTGAAATTTTAGATTGTG
AACTGATGGATTAAAGAGGTAATAAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA
ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAAACAATCTTAATACTAAATCATTTTTTAT
GTGGAATTACTTTATTAAGATCAAATGTTAATGATATTGAACTTTAAAAGAATTATATCAATTTA
ATAAAAATTCATTGATGAAGATTATTATCATAAACTTTAGAAGAATTAGTTGAATTAGGAAAT
TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVFKFNNETQKYEIQLDGKTLRTPPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSLTPLTAL
ATRAIDLSSQQLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLKRQEEIYRPL
INEFNEFFTIIYAHNKNLIPRQKSIELKYLDCEITDGLRGNKQDETTQLVLDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

TATTTATATATAATCTAACAACAAGTACTATCCCTTAACCTATTAGCTCAATGTCATTCTTCATTA
AACAAGAGATATGGTAATTGTTGATTAGACAACAGTTGGGTATCCATTGTATTGGAACGCTTTTT

TTAAACTGCTGTTTTATTGTAAAAATTATTGTGCTCTTTCTTCATAACATTATTTGTAACAGTCTC
TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCAATTTTAGGAGTGATTATAATTCTCTGT
GAGAAACGCAAGCAACAAAAAAGAACAAGGAAACACAATCATGATTAATTATATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTTCTTTTTTTTTTCAATTTTACAACCAAAGATAAATAACTACACAACACCCAACATTA
CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCCTAATGACAGCACAAATCTCCTCTC
AGAACCA'TTCTAAAACTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC
AAATGCATTCTCATTACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT
TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACACCAACAATAGTTCAA
CAACAACC'TTAAATAAGAAAACCATTAACAAGTCACCACCATTCATATCAAGCAGGACTTATTAA
ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAACGATAGAAGATGGAGACGTCACAA
CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT
CGATGGCTACAATAAGGTTATCTAACAAC'TCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAATTCCCCTGATGAAATAGATGACA
TTAGTTTGAACGAAATAGATGTTGCAGTGGCACCTAACGATTTTTCATCACCCTATCAGCAAGAA
AGCCGGACATATTTGCTGCTATAACTGCAGCAACGGAATTCCTCAATAATCAATTTAAAAAGGCCAC
ACAAGTTGGTTAGTCAATCGCCTTCCCCGTGCTCAAAGAATAAGTTTTCGCATATCATCATCAACCA
CATCTTCGCCACAGTCTAACTTGCATTACCTTCCAAGTTGGGACTGAAAGGATTCAAATGTTTA
AAAATGCAAATAGAGACGCGATAATGTCGTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG
TATCTAAAAATATTTGGCAAGTCAGCAAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC
CAATGGCTGTCTCATCACTCAACCC'TCCTTCATCATCTACACTGAATTCAACAACGGCAGCAATAA
CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA
ATAGAAAAC'TGTCTAATATTTCTGCATCTTCAATTATTATTTATCAAGATGAAAATCATATCAAGT
CAAATCATGCTAGAAAATCTAGTAATCCAATACCATACCCTCCGACCGAACCCTACCGACAAATA
TTTCTGCTTCTGTGGCTGAAACAGGGAAAGGGTCAACTACAAC'TAAAAGCAACCTATCTAAGGGTT
GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGT'TAAACCATTGCAAACAGCTT
TCAATTCCTCGGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAAACTACCTCCAG
AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA
GTGGATTTGCTGAAGGAAAAGATGTAATGGGTGATCAACATGATATATATTTCCCATATTCCATGTC
AAAATCAACGTTTTCCTGGCAGCGTGAATCCCAACACTACTACGAACAACAACAACACTCAACAGC
ATCATGATAGTGATCTTTCTATTGAAGTTGGAAGGAATAATTCTTATGATGCCAGTAGTAGCACTA
TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCCGAATTGAAAAAGGAGCAGGTGCTTCAGC
GACCACAAGAAGATTTAGAATTAGTTTTCATTTCTGACATTGAACTAGATGATAACATAATACCAG
AAACACCAACAAAGAACTGCTACTACCGAATCAGCACCATCAACATCACTTACCCCTTACACGC
AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAA'TAGTCT
TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCACCTTCAACACCAATCAATATGTCAT
TTGCAAAGAATAGTTT'TAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA
AGATAGATGAACATTTAATTGAAAAGTTTGGAAATGAAGAATATCAAGTATATTGGATCGGGAGCAT
TTTCCATTGCTTTTGAATGT'TTATTTAATAACGAAAAGTTTGCTATCAAAAGAACTAAAAAACCAC
TTATTGGAAAATTGGAGAAAACAAACTATAAAAACGAGAAATTGAAGCATTGAGAGTGTTGACAAGCA
TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGAGGAAAGAGTATCTAGTTTATTTCA
TTGAGGCCCTGGGATTTTAAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT
TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG
AAATTC'TAAATGGGT'TAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACCAGCAA
ACATTTTATCACTTTTGAAGGGTCATTGAAAATTTGGTGATTTCCGATTGGCTACTAAATGGCTTA
TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATATTGCCCCGGAATTGATTAATGACA
AAATTTATACTCCGT'TTGCAGATATTTTCAGTCTTGGATTGATTATATTGGAGATCGCTGCTAATA
TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGGAGACTTGAGTGATGCTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG
GCACTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

132/161

MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSQSQQSPYIN
QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKTINKSPFFNIKQDLLNDSIDTFLDNSNT
ETIEDGDVTTTTDDDDHDFDEDEDIEDPEAVQYPTTLNILKSKKVD SFNIISSKHKRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSQIFGKS AKIRRAYTPTHTSTPMAVSSLNPPSSS
TSNSTTAAITSTSPAAD EHYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTLEPLTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMDQHDYSHIPCQNQRFPQSVNPNT
TTNNNTQQHHSDLSIEVGRNNSYDASSSTINNTSYIKIFPSELKKEQVLQRPQEDLELVFNSD
IELDDNIIPETPTKKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRLSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK
NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSIKEDEATNMQEQE
EGKEYLVYFIEAWDFNNYYIMTEFCEGGTLDFLEENKHYKIDEFRIWKILIEILNGLKFIHSKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLS DAGRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506; intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTACCAGTTTTTTC
AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTTCCTCCT
TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAACATGATGACCTGCATATTATAAATCTTTCTG
AAAAAATTTTTTCCCTGTATTTTGTAAATCTTTTCGCTCTTTCTCACTCACTCACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA
GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAATTTCAAGCAAAAATTTTTTCCATC
TAGATTTTCTTTCTCAGAAATATCAAGTAACTTTAAAGATGCCTGTATGTACAATAACAGTGTTAT
AATGATGTCTTTCACTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA
TAATAAACCTTGCAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT
TGCTGGAACAAAGACGAGAGAAGTACAGCACTCAGATATAATAGAACATCCATACTAACTTCACTC
ATTTCTTATAGTCTCAAAAATCATTCAGAACTAAACAAAAGTTAGCTAAGGCTCAAAAAGCAAAACA
GACCATTTGCCACAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
GATTTTCATTTGCAAGGTATTATATCCAATATATTTCTCATCTGCCATTTATTATAATAATCACCCA
ATAAAAGACTGAAAGACATCATTATAACACTGTTATTGTACATACAGGCATCTTTAAAGTTACTTG
ATATTCTGAAGAAAGAAAATCTAGATGGAAAAAATTTTTTGCTTGAAATTTTTTTTTTCTGTTTCTG
AGAGAAAGGTTTGCGTGTGGGTCTGTGTGTGTTAGGCACAGGAGTGAGATTTTGTAGTGAGGTT
TGTAGACACCAAACCTTTTCATTCAATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA
AAATACAGGGAAAAAATTTTTTCAGAAAGATTATAATATGCAGGTCATCAGTTGTAACCTAGTGT
GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAATATCAATCGATTTTTTCACAATACTTC
CTTTTCACGGTTTCTTTTATCAACAGACAATTCAACCATGACTAGAACCTCCGTCTTAGCTGATG
CTTTAAACGCCATCAACAATGCTGAAAAAAGTGTAAAGACAAGTCTTAATCAGACCATCTCTCA
AAGTCATCATAAAATCTTGACTGTCATGCAAAACACGGTTACATTGGTGAATTCGAATACATTG
ATGATCACAGATCCGGTAAAATTTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTCTATTC
AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACTTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGGTAAAATCTTAGGTTTCTGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGEFYIDHRSGKIVVQLN
GRLNKGVIQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA
GAAGCCTAAAAATTGCTTGAATTGATAGATTTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA
CTTATCCTTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCCTTTGTTTTCTCTTTCTGCC
TCCCTCTGCCACCCCAAGTTTATTTGTTTGCTTGTCGACGTGCTGCCAAAAAAAAAAATTGAGTTC
TCTCTCTCTTTTTTACAACAGAGAAGAGACAAAGAAAAAAAAAAACATCAAAATTAAGATTCAAGC
TTTTTTTTTTAGTTTTTTTAACAACAAAATTGAAATTACAATCCTTGAATTTACAACCTCATATTC
AGCTCTAAATACTAATAATTATAACAATAAATTAATTGAATTATTCTATAAACCACTGATATTTGAT
TTTATCTTTTTATTTTTGTTTGTCCCATAAATTGTGTCAATGCCTGACAATATAGAAGATCGATCCG
AGATACCTTCTGATGCAAAGGAAATTTGTGACTACAAATGAAATTGAAGCAACAGATTCAGAACATA
CAACAAATGTCGATAATGAACCTCCCTCAAGGTGAATCCAATGAACAAACAGGAGATGACTCAAAATG
ACAACCTTGCATCCAAACGTCAATTAATCAATGATTTATTACACAATGATCATTTTGAAGAAGGAA
CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTTGAATTTACCAATCGATAATTTTA
GTGATTTGAAAGATCAACTTGGTCCATTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT
ATCCCGAGAATGAAGAACCAGTCACTTTTTGTGTCATGTATCGCCAGAAGTATTTCAACATTTGGGTG
AATGGTTTGGGAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAGAAA
AACAGATTGAAAGATTCCCGCCATTATTTTGGGTTCATCAATTAGGTAAAAAGACGCAACCAACAT
ACTTGGCAGACCCGTCATAATGGAAGCAACCACAATCATCATCACCATGGTTCATCAGATTCCACCA
TACCAAGTATTGCTTTCCAAAACAAGCACTTTTCATAGATTAATGGATGTTATACGTTATAATGTTTC
TTAAAGCACCACGAAAATCGACGAAAGATTTTAGGATTTGGTTTATTGTCCCAAGATAAAGGCT
TACAGTATTTGATTTCAATACAAACTTTTATGTTTGATATCTCCAAAAAACTTTGGTTTCACCAA
ATATGCTTGAGGATGCTTTTGAAAGATCACGGTATTGTGGCCAGTTCTTATAATATAATGGTAGAAG
CAAAAGAAAAACATCAAACAGAATTTCCCTATTGATCAATTTATTTTATCTCATTCTAACGCATATG
AAGAAGTATCACAGGGTGGTGACACCTTGGATTATCAAACATGGGGAACACATGTTATATGAACCT
CGGCTTTACAATGTTTATTACACGTTCCCTGAAATCAACTATTATTTTTTTTACAACATTTATAAAAA
AAGAATTGAATTTTGACAACCCCTTGGGATATCATGGAGATGTTGCCAATGCATTTGGTTCACTTT
TAAAAACAAGCATTGTGATCACGTGAAAAATAGTTCTAGTATATCTCCTCGAGAATTCAAATCAACTA
TTGGGAGATATTCTCGATGTTTTCTGGGTATCTTCAACAAGATTCTCAAGAGTTGTTGAGTTGGC
TATTAGATGCTCTTCATGAGGATTTGAATAGAATTCACCAAAAACCATATTGTGAAAAGCCCGAAT
TGAAAGATGACGAAATGATGACCCCAAGCCATCACCAACTTGCCAATACCTTGCTGGAATCAAC
ATAAGGCAAGAAACGACTCGGTGATAATTGATTTATTTACTGGGTGTATCAATCTACATTAATCT
GTCTGATTGTGGTAAGAAATCCATAAATTTGATCCCTTTAATGATTTAACTTTACCTTTACCCA
TCAGTAAGAAATGGTATCACACATTTACAATTTGATTTGATTTGTCCAATCAAGGCGTTATACCGGAAA
GGATAATGAAGTTGGAAGTTGAGTTGAATAAAACATCCAATTTTCGATGATTTACTTAGCTATTTGA
GTAATTTCTTGAATGTTCCATCTACTGAGTTGTTTGCTTATGAGATTTTCAAATGCAATCTATA
GTGACTTCCAATTAGATTACACCAAGAACAAGTTTTTACCTATCAGTGATATTATCAGAGATACAG
ATGATGTTATAGTGATATTGTTCCACATAACCCTGCCGTTGACATCATTTGTGCCAGTGTTCAATG
CCGTTGAAGATGCTGATAGTTTCATATCAAATGGTTAATTTTTTTTGGAAATCCCATTATTTGTGGTGA
TGAATAAAGAAGTCGATGTCAATAGTTTTGGTTTTATTAGAAAAGAAATTATTAGAAAACAGTTTCTT
TATTGAGTAAAATTGATTTGGTTGATGAATATGAAAAAATAAAAAGGAGTAATGAAGATTACGTTG
AAAAAGTATTTTACAAAAAACTGGATTTCCTGCATTGTACAGCCATTAGAAACCTCCGATTGTG
AAAAAAACAACAATAATACCTAGCGACAACGACGACGATGAGGATGCTGACAACGATGAAGGCTATG
ATAGTGAAAGTGTCTTTGGCTAACCCATACCTTGGAGCTAATTTTGGGTTCAAATCATGTATGTTTC
ATGACTATAGCCCTAAATTGAATTTCAACCTTCGTAGCAGGTACAATCATGACCAAAACAACCAAT
TCAACAAACAGAGAGAGTTTAAATGTTTCTTACACACAAACCTACTTTTAGCGATTTCAAACCTT
TATCGGACCAATTATCAGAATCAAAACGCAACTATTATTTTTTATCCTGATTATAAAAAAGATGGATG
ATGAGATGGACCAATTGGTGGAGGAAGTGAACCAAAATTTGGCAGAGCAANGAGAAGCGAGATCAT
CGGGGTCAGAAAATAGTAGTAGAGCACTGGAAGAACAAGATGGATTTGTATTAATAAATAAAGAGG
ATACTCTCAAGCAACAATCAACTGTACCTGCTGCTGCTGAAAACGGTACCTCCACCATTACCTGTTA
GAAATAATACTGGAGTTACATCCCGCTCATCCGATGAAGAAACAGAAAGTGAAGCTAATTTGGGAA
GTTTGTGATTCAACATCAAACTTGCCGTTGCTTCCACCATCTACATATCCGAATCAACAAAC
CTTCGAATGTAACTCCCCATGGAAGTAACCTTGAAAGTTCATCAGCAGACTTGAATTCCTGGTA

10030019, 122601
134/161

CAACATTGATATCGAAGGACACAGTTTTTGTATTGTGATTGGGATAAGGAAATTTATCAAAAATGCT
TTGGTGATAAAGAATTACAAGCATGGGAAAACATATCGAATTTACCGAATCCAGAATTGGAGAAAA
ATAGAGCTCATTTTGAAAGACAAAGAAAAGCTAAAATTACATTATCTGATTGTCTTAAGAGTTTCA
GTACCCCTGAAATTTTAGGTGAACATGATTTATGGTATTGTCCACGTTGTACTGAACATAAACGTG
CCAAAGACAAATCCAATTTGGTCAACGGGTGATATCCTCACTATTTCATTTGAAAAGATTTCATA
GTGCTCGTGCATTTAGTGATAAGATTGATGTTTTGGTTGATTTCCTCAATTGAAGGTTTAGATATAA
GTTCTGATGTTGCCAATACTGATTTGACACCTGAAGATTGTTTATACGACTTGATTGCCGTTGATA
ATCATTATGGTGGGTAGGAGGTGGTCATTACACTGCCTCGGTAAAGAATTTTCAGAGATGATAAAT
GGTATPATTTTTAATGATAGTCGAGTCACTGAAATTAATAATCCTCAAGAAGTCGTAGCTAATTCTG
CGTACCTTTTATTTTACCGTCGAAGAAGTTCGAAAGGAGCTGGTATTTTGGGAGGAGAAAACCTTTA
TCGACTTGCTTCAAAAAGGTTCGAGAGGAATACTCTGAGAGTTTGCAAAAAGAAAAGATTGGTTCTTC
AAAATGTTGGCCAAATAGTCAATACGTATGCCAAAATGAACAAGATATAATTGATAAAGAAAACAG
AGAAACAGAAAGAGGAACAAGAACAGGAACAGGAACAGGAACAGGAACAGGAACAAGAGCAAGAGC
AAGAGCCAGTTCAAGAGCCAGATCAAGAACAAGAGCCAGATCAAGAGCCAGATCAAGATCAAGATC
AAGAGCCAGATCAAGAGCCAGATCAAGATCAAGAGCAGAATGAAACAATAAAAAAATCTAGACCAT
TCGATGAACTCAAACCATCAACTAGTGAAACAAAATAACCAACAACAACAACCTCAGTTCAACTTTG
ATGATGAAGATAATGATTACGATTATGAAGCAGAAGTAGAAGATTCCAATATTCGCAAAACAAGAT
TACTTTCAAAAGAAAAATAACAGCAATAAATTGGTGCATATTAAAAGCAATGGTCGCCAAGAAGTCA
CTTCATCACCAGTACCAATTGAAACTGATGGTGACACTGATGTAAGTATTCCAATTCAACATAG

YJL197W_homolog 1372aa (SEQ ID NO 390)

MPDNIEDRSEIPSDAKEIVTTNEIEATDSEHTTNVDNELPQGESNEQTGDDSDNDNLASKRQLINDL
LHNDHFEEGTERYIIPQNFLHEFLNLPIDNFSDLKDQLGPIDFHSLLNEQGNLYPENEPEVTFCHV
SPEVFQHLGEWFGILGQPIIRAIINPDTKKEQIERFPPLFWVHQLGKKTQPTYLRRHNGSNHNH
HHHGHHDSPPIVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLISIQTFMFD
ISKKTIVSPNMLEDALDHDGIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGGHLGLS
NMGNTCYMNSALQCLLHVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS
ISPREFKSTIGRYSSMFSGYLQQDSQELLSWLLDALHEDLNRIHQKPYCEKPELKDDEIDDPQAIT
KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPDCKKSITFDPFNDLTLPLPISKWKYHTFTIVD
LSNQGVIPERIMKLEVLNKTSNFDDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFQLDYTKNKF
PISDIIRDTDVVIVYIVPHNPAVDIIVPVFNAVEDASSYQMVNFFGIPLFVVMNKEVDVNSFGFI
RKKLLETVSLLSKIDLVDEYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDDD
EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLSNLSRNYNDQTTKFKQTERVINVPTH
KPTFSDFKPLSDQLSESKRNYFYFDPYKMDDEMDQLVEEVNQNLAEQXEARSSESSRASEEQ
DGFVLINKEDTLKQQSTVPAAAETVPPPLPVRNNTGVHIPSSDEETESANLGSFLDSTSNLPLPP
PSTYSESTKPSNVNPMESNFESSADLNSGTTLSKDTVLLCDWDKEIYQKCFGDKELQAWENIS
NLPNPELEKNRAHFERQKAKITLSDCLKSFSTPEILGEHDLWYCPRCTEHRATKTIQLWSTGDI
LTIHLKRFHSARAFSDKIDVLVDFPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA
SVKNFRDDKWYFYFNDSRVTEINNPPQEVVANSAYLLFYRRRSSKGAGILGGENFIDLLQKGREEYSE
SLQKKRLVLQNVGQIVNTYAKIEQDIIDKETEKQKEEQEQEQEQEQEQEQEQEQEPVQEPDQEQEP
DQEPDQDQDQEPDQEPDQDQEQNETIKSRPFDELKPSTSETNNQQQTTFQNFDDDEDNDYDYEAEV
EDSNIRKQRLLSKENNSNKLVIHKSNGRQEVTSPPVIETDGD TDVTDNSNT

YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)

TTCATTTCCCTAAATTCAAATGAATTATCATCACCAATGCCACCATCATTTTCTATTAACATATGGTA
GTGAATGGGATTTAGAAATCATTCAAACTAGTTTAGATAATGAAAAAGAATCAGAACTAAATCAT
TTACTGGTGAATTAGAAATATACTTCAACTTCTTCCAATGGTGAACATGACACCACCACCATGCCA
CTAAACATGAATTGATATTACAACAAATTTTGAATTCTAATGATGAATCATATATTAATCTTAAAT
CATTAACATTTGATCCATTAAAAATTTTCACTAAACAATTAATTGGTGAATTAATTTAAATTAATC
AATTTTACAATTCAAAAGAATCGGAAATTTTCAAAATTTATAATAATTTAATTCATGATTTACAAA
ATCAAAATATTAATATTGATGATGTATTTAAATTCCTCAAGCTTATAATTATTCGATCCAAATA
TAATAAATACTGATGATCATCATCAATATCATTTTAAATCAACTTTATCAAGAACAGTTACTAATG
CTAGTGTATTTGATACCATTAATCATATTGATAATGATTATGATAATAATAACAACCAAAAAGA
ATAATTATGATTTGGAGAAACAAATAATACACAGTTGCAATTCATGATGATGATGATTGAGAAG
ACGATGAAGAAGAAGAGGAAGAAGAAATCATAGTCATGATTGATTACTTAATCATACACATT

TTAATGTTAAACAACAATTA AAAATCACATTA AAAACGTAAGCCATTACATTATTTATAAATCTTT
CTGAATTAAAATCATTATTTGAATTGAATAGAATTGGATTACAGAAAATTTGTAAAAAATTTGATA
AAACTTGTGGTTATTTCAATTAACAAGATTTTATTAATGAATTTTACCTCAATATTTCTCGAGTAT
TTGAAAATGATACCATTGAAGAATTAGATTATAAATTGAATCAAATTATTA AAAATTTATGCCTTTT
TATCAAATAAATTAAC TACTCAATCAACAAC TAAAGAAGATTTTGGATAATATA AAAATTTGATAA
GATCTTATTTACGTGATCATATTTGTATTTGAAAGAAATACCGTTTGGAAAGATTTATTTATCATTAG
AAAAGAAATCTTATAATATTGATTTAGATAATTCTGTGGTTCAAAATAATA AAAATGGGTGATGAAG
GTCATATAATTAATTC AATGATGAATTTATCCATGAAAAGAATTAATTTACCACAATGCCTTAAAA
AATTGATTA AATATGATCATATTTGATATTCCACAATTTTATTAAC TACTCAAATGCTTAAAAATTA
TTATTATTGTCATTTGTTTTCATTATATTTAGCAGTGAAAAC TTTTAATGATCCAGTTCAAGGTC
GTTGTTTAGCAGTATTTAGTTGCTGCTGCCATGCTTTGGGCTTCAGAAAGCATTACCTTTTATACACTA
CAGCTTTATTAATCCCACTTTTGGTTGTTACTTTGTAAAGTTTGTAAAAC TCCGGGAACCGATGATC
CAATGGATGCCACCAAGGCATCACAATATA TTTTGGGACAATGTGGAATTCACAATTTATGATAT
TAATTGGTGGGTTTACATTAGCTGCTGCATTATCAA AATATAATCTTGCCAAAATATTATCATCAT
ATATTTTAGCATTAGCAGGTACAAATCCAAGAAATGTATTATTGGCAATCATGTGTGTATCATTAT
TTCTTTCCATGTGGATTTCTAATGTTGCTGCCCCGTTTATGTTTTCATTAATTC AACCAGTTT
TAAGAAGTATCCCCACAGATTCCCCCGTTGCTAAAGCATTAGTGTTAGGGATCGCTTTGGCGCTG
ATGTTGCTGGTATGGC TTTACCAATTGCATCTCCACAAAATGTTATTGCTCTTGAATCAATGAATC
CTAATCCAGGTTGGGGGAAATGGTTTGTGCTGTTGGCATTACCTGTGGCAATCATTAGTTTAATTTTAA
TTTGGGTGGAATTATTCATGACGTTTAAAATCAATAATGTTAAAATCAAACAATTCAAACCAATTA
AAGAAAAATTAACCATGAAACAATGGTTTGTATTTGCCGTCAC TATAACTACTATTCTTTTATGGT
GTGTTATGCAAAAAATTTGATGGAACATTTGGTGAATCAGGTATAATCACTTGTATCCCAATTTGTAT
TATTTTTCGGTACCGGTTTATTA AAAAGTTGATGATTTAAATAATTATCCTTGGTCAATTTGTTATGT
TAGCCATGGGTGGTATTG CATTAGGGAAAGCGTTACTTTCTTCAGGTTTATTGAAAAC TATTGCTT
TAGCATTACAAAAACGAATTATGCATTATGATGCCATTGTTGTATTAATCATTTT TGGAGCATTAA
TTTTGGTGGTAGCTACATTTGTAAGTCATACTGTATCAGCACTTATTATTATCCCCCTTGGTTAAAG
AAGTTGGAGATTCATTACCTAAACCTCATCCATTAATGCTTATTATGGGTGTAGCTTTAATTGCTT
CAGGGGCAATGGGATTAACCAACTTCAGGATTCCCTAATGTGACGGCAATTGGTATGAGAGATGAAG
TTGGTAAACCTTATTTGACGGTTAATTTATTTATTACTAGAGGGGTTCCGGGCAAGTATAATTGTTT
ATGTTTGTATTATCACCATTGGTTATGGTATTATGTCATCAATTGAAC TTTTAA

YJL198W_homolog 896aa (SEQ ID NO 392)

HFLNSNELSSPMPPSFSINYGSEWDLEIIQTSLDNEKESETKSFTGELEYTSTSSNGEHD TTTTAT
KHELILQQILNSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYNSKESEIFKIYNNLIHDLQN
QNINIDDVFKFTQAYNYSDPNIINTDDHHQYHLKSTLSRTVTNASVFD TINHIDNDYDNNNNNQKN
NYDLEKQNNTTVAIHDDDDSEDDDEEEEEETHSHDSVLLNHTHFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFKDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLLSLEKKSYNIDLDNSVVQNNKMGDEG
HIINSMMNLSMKRINLPQCLKKLIKDYDHIDIPOFLTTQMLKIIIIIVIVFIIILLAVKTFNDPVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCKVKCTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFSLMWISNVAAPVLCFSLIQPVL
RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMPNPNPGWGKWFVAVALPVAIIISLILI
WVELFMTFKINNVIKIQFKPIKEKLTMKQWVFVAVTITITILLWCVMQKIDGTFGESGIITCPIVL
FFGTGLLKVDDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
LVVATFVSHTVSALIIIPLVKEVGDSLPKPHPLMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV
GKPYLTVNLFITRGVPASIIIVYVCIITIGYGIMSSLNF

YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

TATAAAGTTTCAAGTATAAAAAGGCGTTTAAAATTAATTCTTGTGATTAAATAAGTTAAATTCTT
TTTTTTTTTTCTTTGTTAGTTTTTCGCTTTATCCGTTTTACCCAAGAAAGGAGCAATACTGTTTCAC
CCCTCCCCCTTCCAGTTCCATGGCCCGCCCCCCCCCTCTCAACAGTTGCTGTGCTTCCTGCCTC
ATTTTCCACGCCCATTACATTATATGACTAATATCCGTTGCCTTATTATTAAAGTCACAATACATT
GAAAGATAGAAAGCAAGCAAGGTGGA AAAATTTT TTTTATACATTCAATACTTATATCC
TAAATTGATAAACAATAGAGTAATTGATACTTTCTGAAGGACAATAAAACGATATATTTATATAT
TAGAGTGAACAATAGCGATTGCCAATCAGACAACAGATAATTTATCTTCTCTATTTCATTTGC

136/161

ACAATTAAATCCAAAAAAGAAATCGAATTCATATGTCGCATAAGACTCAGAGCCAATTAT
CTTCACAAATGAAAACTTGAATACTCCACCAATAGACTTCAACTCAACTTCAAGTAACAATACCA
TGCCCTTCTGAACCAAATCTGCAACCGCAACAACAATCACAACCAGAAAGCAAAACGGAGCCAC
AAACCATACGCCCTGCTACTTTTACAACCTAGTGGCAATTCATCATCTTCGTCGATATCTACCTTAT
CAGCAGATATCATTCAACCACCTCATCAACTACTGTATAAATAACAACAATTCAACTGTGACGCAAC
CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA
ATGTATACACTGACTTCAATAGTACTACTTTCATCTGCTTCAAGCATTAGTAGTTCACCAAAAGATT
TCTTCACCAGAGAGCCACCACGGATCCATAGTAAATTGATATGTGAAGAGATTGCCCTCTGCCAATA
ATCGAGCTGCTAAAGAGGTTTTATCACGTTTATCTACTGATGAATTGCGTTCAGTTAAATCACATA
CTGAATTAGCTGAACTGCTAATGGAGTGAGAATGTTAGCCAAAAATTTATCCCGAGCAACCATTTC
AATTAGACGTTAGAGCTATTATGATTATCACTAAAGCTAGAGATAATGGACTTATTTATTTAACAA
AAGAAGTTGTTGAATGGATTTTGGATCAACATCCTCATATAACAATTTATGCTGATGAGAAATTAG
CAAAGTCGAAAAGATTCAATCCGGAAGTATTATTGCCAAATTTATCCAAATGGTTGTAAGAAATTAA
AATATTGGAATAAAAAATTAACCTACGAAAAATCCAGAAATTTTCGATTTAGTACTTACATTAGGTG
GTGATGGTACTGTATTATTTGCTTCAAACCTTATTTCAAAAAATTTGTTCCACCTATACTTTTCAATTTT
CATTGGGCTCATTAGGTTTTTTAACCAATTTTGAATTCAGTGCATTTAGAACAGTATTGAGCAAAT
GTTTTGATTCTGGAGTTAAAGCAAATTTGCGTATGCGATTCACTTGTGAGTACACACTGATGAAG
GGAAGTTGATTTGTGAACAACAAGTGTGTAATGAATTGGTAGTTGATAGAGGACCTAGCCCATATG
TTACTCATTTGGAATTTATACGGCGATGGATCATTTGTTAACGGTTGCCCAAGCTGATGGGTTGATTA
TTGCAACTCCAACCTGGTTTCGACTGCTTATTCATTATCTGCTGGTGGGCTTTTAGTTTACCCTGGTG
TGAGTGCCATTAGTGTTACTCCAATTTGTCCTCACACCTTATCGTTTCAGACCTATACTATTACCTG
ATGGGATGTTTTTGAAGGTTAAAGTCCCCTGAGCAGTAGAGCCACTGCGTGGTGTTCATTTCGATG
GTAAAGTGCGTACTGAATTGAAGAAAGGTTATTATGTCACCTATTCAAGCTTACCATTCCCCTTAC
CTACAGTAATGTCTTCCAAAACAGAAATATATTGATTCTGTGTCAGTAGAAATTTACATTGGAACATCA
GAGAGCAACAAAAACCATTTAGTTTCATATTTGAAACCAGAAACGCGACAAAGTATTGCTGAAAGTG
AAAGATTGGATAATTTACATATTTCAAGTGAACAAGATGAATCGAATCATGAGGAACCTGAAATAA
CTGAAGATTTTGTATATTAATTATACTGACAATGAACGTGATTCTTCTAGTTCCACTCCTAGTGAAG
AAAGCAACGAAGAATGTGCTAATACCACGACATAA

YJR049C_homolog 592aa (SEQ ID NO 394)

MSHKTQSQLSSQMKNLNTPPIDFNSTSSNNTMPSEPNSQPQQQSQPEAKTEPQTIRPATFTTSGN
SSSSSISTLSADIIQPLHQLSINNNSTVTQPAQSSSFQRRNNPQRFNRNQLNVYTDNFSTTSSA
SSISSSPKDFFTREPPRIHSLKICEEIASANNRAAKEVL SRLSTDELRSVKSHTELAETANGVRML
AKNLSRATIQLDVRAIMIITKARDNGLIYLTKEVVEWILDQHPHITIYADEKLAKSKRFNPESIIA
NYPNGCKKLKYWNKKLTTKNPEIFDLVLTGGDGTVLFSANL FQKIVPPILSFLSGLSLGFLTNFEF
SAFRTVL SKCFDSGVKANLRMRFTCRVHTDEGKLICEQVNLNELVVDGRGSPYVTHLELYGDGSL
TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVKVPSSS
RATAWCSFDGKVRTELKKGYYVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
ETRQSI AESERLDNLHISSEQDESNEEPEITEDFDINYTDNERDSSSSTPSEESNEECANTTT

YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

ATAGCGGCCGCGCATATAATAGAGAATATGTCATTACCAGCTTCATTTGACTTAACTCCAGAAGAT
GCTAAATTGTTATTAGCTGCCAACGTCATTTGGGTGCTAAGAACGTTCAAGTTCACAACAAACCA
TATGTTTACAAAACCAGACCAGATGGTATGAACATCATCAACATTGGTAAACTTTGGGAAAAAATT
GTTTTGGCTGCCAGAATTTATTGCTGCTGTTCCAAACGCTTCTGATGTTGCTGTTTGTCTTCAAGA
ACTTTTCGGTCAAAGAGCTGTTTTGAAATTTGCTGCTCACACTGGTGTCTACTGCCATTGCTGGTAGA
TTCATCCAGGTAACCTTACCAATTATCACTCGTTCAATTCAAAGAACCAAGATTAGTTGTTGTT
ACTGACCCAAGAACCGATGCTCAAGCCATCAAGAATCATCTTATGTTAACATTCCAGTTATTGCC
TTGACTGACATGCAGTCTCCATCTGAATACGTTGATGTTGCCATTCCATGTAACAACAAAGGTAAA
CACTGTATTGGTTTAACTCTGGTGGTTGCTTGCTAGAGAAGTCTTGAGATTAAAGAGGTATTATCCCA
GACAGAACTACCGAATGGTCAGTTATGCCAGATTTGTACTTCTACAGAGACCCAGAAGAAATTGAA
CAAAATGCCGTCGAAGAAGCTAAACTGAAGGAGTTGAAGGAGCTCCAGTTGCTGAAGCTGAAACC
GAATGGACTGGTGAAACTGAAGATGTTGATTGGGCTGATTCTGGTGTCTACCCCACTGCTGAAGA
TGCTGCTGCTTCTATCTGGTAAACACTGAAATCTACCAATAAGAAGTAGAAGTAGAAGTAGAAGAA
GAAACAATAACAACAATAACAACCAAAATAAAAAAAGGTTTAAATGATGTATATTATCGATAAGGA

GAAAGAAGAGATTTTCTTTTTTAATAATGAGGATGCCATTTTATACAAATCCAAAATTGTAATTAA
GAAAGATTAATAAATATAAAATATATATATATAAGTAAAAAAAAAAAAAAAAA

YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
MSLPASFDLTPEDAKLLLAANVHLGAKNVQVHNKPYVYKTRPDGMNIINIGKTWEKIVLAARIIAA
VPNASDVAVCSSRTFGQRAVLKFAAHTGATAIAGRFTPGNFTNYITRSFKEPRLVVVTDPRTDQA
IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNGKHCIGLIWWLLAREVLRLRGIIPDRTTESWSVM
PDLYFYRDPEEIEQNAVEEAKTEGVEGAPVAEAEETEWGTGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
TCGGGGCTACAAATTTTCGTCCATGAAAATTGGGTTCGCCACCAATACTTTGTATGCGATTATGCAT
GCTCCACGAGGTGAAAATACCGAGGCAATGGCGTTGGTTGTGCCATGGACTAATTCTGACAACGAG
TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG
TCGAAAAACATTATTTTGTATTTCTCTGAGACGGGCCACAGACCGTTGAGGTCGTGGGTGAGGCA
TACCATACGGTGTGAGCAGATACTGCGGGGTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG
AACGGTGATTATTTTGTAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG
GACTTGTGAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCGTGTCATGCAAGGGATG
TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGTATCCTCAAATTGACG
CTTGTCTGGGTGACTGATGAAGTTCATGGGTGTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT
ACGATCAAGGTAAGGGGGACTGAAGGGAAAGATGTTACGCAGTTTGGCCGGATTGTGATTCTACG
TTTAGGTCGGTTAACAAATTTGCTTGAAAAGTTTCACCAATCGTTTTTCTTTTACTTGATGTTGTGCG
CCAAAACACTTTGTGTCTATTGGGACGTACTTGCCTGCGCGATTTTGTTGGCAGTATCGTATGCG
TTGAGCTCTGTCAAGTGGGTGGTGGTTCGGGGTTGATTTCGAAAGCTATATTGTGGTGGTG
GTTGAAATTGCGTGTGCTATTTTGGCGTTTGTGCGGTGAACCAGGTGATGCTTGTAGCGATTCTG
GCGGTGGTGTGTTGCCGCGCCAAGCCATCTTTTCCAAGCAGCGCGGCTTTTCGCTAATTTCTATT
GCGTTGTTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT
ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCGACATTAATGAAGAACAAGTCTAGGCTAACA
GCTTTTTGTTTGGCGGTGTGCAATCCGTTTTTTGTGATTTTCGTTGCTGGGAAAGTGCTTGGCCAC
CCCGAGCTATTTGACCGGTTGGTCACTGCCTGGTCCGACATACAGTGTGACATGCTTATCGTT
GTTTTGGGGTGGTTCACGCGTGGTGATTATCACACTAAGCTACTGTGGCTACAAGCCAGTTAAG
GAAAAAAGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398)
SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW
SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAALIMEYGKNGDYFEYYDMFYEGNLGQLPNL
DLNLTANVTYHEQIPCAMQGMSDRVINYSTRLQTLFRGILKLTGLVGLTDEVHGCFAFSGWQIQAF
TIKVRGTEGKDVTFGRIVDSTFRSVNNLLEKFHQSFFFYLMLSPKHFVSIGTYLPSAILLAVSYA
LSSVSAVVVAGFDFRKLIFVVVVEIACAILAFVPVNQVMLVAISAVVLLPRQAIFSKQAASFSLISI
ALLAVALLLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
PELFDRLVTAWSDIQCWTWFIVVLGWFPWVIITLSYCGYKPVKEKSE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
TAGGTCATTTCATAACAATTGATAGATGCAAGCTAATTGGAATGAAAAATCCATCTTGTATCAAAAC
CCTTTGTTCCCTCATAGTTAATCCGACTAAAGAAGTGTTTTTTTTTCTTTTCTTTTGTCTATATC
CTAGTTGCCTTAACGACAGTAATAGTTAAAGCGTTGGGAAGTAATGGTGAACCTCGAACCATTGGT
TGACGCTGACGATTAATAATGTGAATTTCTTTTTCTTTTGGTTGTAGTAATTGCTTTGTTTTGT
TGCTTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACACATACCACTGTCGTGACTGACC
AACACAATGCGGTGTTAATCGATAACCAAAAAGATTATAAATAGGGGGTGAAGGTGCGCACTGTT
TGAAATGAATCAACACAGTTTTTTTTCTTCTTGTCTTTTCTTTCTATTTTACATTACAAATCTGA
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAATTTTCGTTAAAACTTTGACTG
GTAAAACCATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG
ACAAAGAAGGTATTCCACCAGACCAACAAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA
GAACCTTGTCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTTTAAGATTGAGAGGTG
GTATGCAAATCTTTGTTAAAACTTTAACTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA

138/161

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
CTTTACATTTGGT'TTTAAGATTGAGAGGTGGTATGCAAATCTTTGT'TAAAAC'TTAACTGGTAAGA
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGATTGATTTTTGCTGGTAAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACATCCAAAAAGAATCTACCTTGCAC'TTGGTCTTGAGATTGAGAGGTGGT'TTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKLTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRRLRGGMQIFVKLTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRRLRGGMQIFVKLTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
GATACATCTTATTATATTTCTTATTCATGGGAAAGCACCAGTATATGGAAATGCTGCCAAGGTAGT
GCACACAACAACTAGTTTACAAAGTAAAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGCTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTTCTCATCAAACTT
GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
ACAAAAAATAAAGGAAC'TTAAACAAGAAGTAATCCCCATTAAACTTGATCAACACTTTT
AGGGT'TCCGATTTCCCATT'TTCTTGACTAAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC
CATCGATTTCAAAAGAGGTGGCAAACATTTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG
AAAAATTCATCAAAAGCTACGATTTACCTTCACTTTCAACTCTGAAGATGGGCCATGTCAAGTAA
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTTCGTGGGGAAATT
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA
ATATTGCAGAAGAGCCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG
AATACAT'TGGATTTGAAAT'TATGAATGCTGCAAGAAAAATACAATAGGAACCTTGGGTTAAACAATA
TTTGGCGAGCTAGGTTTTCACATCT'TGAACGAAATCACTATTATTCGAGCAGCAAAAAATCCCGTGA
ATTTGGATATGAGTGAGTTTCTGCGATTTCTTGTCTGATGGAATCGATCTTCGAGTGGGTACCA
GTTTTACACGTTTGTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAATGAAGTAGCTT
CTTATGGTACATGTCAATTCCCGACATTGGGGTTTGTGTTGATCGATACAAACGAGTCAAGAGTT
TTACACCGGAACCATCTCTGGTATATTGAGATTGAAACTAGGAAAGAGAATAAAAAAGACAATTTTCA
ATTGGGTTCGAGGTCA'TTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA
GTGGAGAATTTGGAACCATATCAAAAAATAGAATCAAAACCGGAAACCAAAATTTCCGTCCATTCCCAT
TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAAGATGTCTGCTAAGACGGCGTTGG
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCTGATCCTAGAACTGAACTGACAGGTTTG
CCAAAGAAACCGATTTCAAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA
CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGT'TCTCATGATGATAAGGCGCATC
CTCCAATCCATCCTATCAAATATGTTTCTTTGGACACCCTAAACACCCTCGATGAAAAGAAAGTGT
ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAAACCGTGG
TGACTTTAAATGGGGAGATGAATTCTTACCAGCAAGTGGAT'TAATGGTGCATGAAAAAATTATT
TGGAAGTGTATACTTACAAAAATGGGAAAGCTCTAAACAAC'TACCGAAATTTACAGAGGGGAGAAC
AGGTCAAGTTGTGAGTGGAAATATTGAAAGACGGTAAACAAGTCCACCCAATCATATGACCGAGC
CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA
ACAAAATAGAGACTAGGCATATATTAATAAATGAAAAAGGGGAAAAATGAATATATTTCTTCTTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTGGTGGGAAGTCGTTGGAACGATCACTTGGAGGACATAGCAACCGGGTCCCGGCCAAAAG
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGT'TTGTCTCATCAGATAC
TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAAATAGCAGTAACAACAACAACAATA
ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVMTMTSVAGHITGLD
FGSAFSWGNVCVPGRLEADIKTIITKKSIIYENIAEEARNADKLMIWTDREGEYIGFEIMNAARK
YNRNLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEIDLRVGTSTFRLITDQLRQK
GIIKKNELASYGTCQFPTLGFVVDYRKRKVSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS
YPRTESTRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVYEVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK
QLPKFTEGEQVKLSSGILKDGKTSPPNHMTPELIALMDANGIGTDATIAEHINKIETRHYINKLK
KGKNEYILPTPLGMGLIEGLEKMEFEDVLSKPFRLKSLERSLEDIATGSRPKVDVLTNTTIGVYVD
AYSVCSSHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACCTTAAC
AAACAAGGAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT
ATTGCCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACCTACAACAAAAAACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTTATCAGTTTCCTTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTAT
TTTTTTTTGTTTTTGACCACACCCACTTTTTTAATATCACAAAGATATTTAACTGATTATAGAAAAACA
CAACAATAACCCAAATACGTTAACCACTTTTTATTACATATGATAGACAATATAATCAATAATTGTC
AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
TATTTTCTATCTTACGATTAAAATATCCCAAAATATATGTGGCAAACCTTAAATCATTGTAATTTCA
GTCTACATTTCGACCTCAAGAAGGAATTTACCTGAATTCCTTCAAATTCATTATTTGGTTGGATTTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAAACATGCTGGATTAGATGCAGTTGTGTTTT
TGGAATTTTTTAAAAATGTGCATTCTGAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGAGCTGGAATTC
TGGTGGCAAGTAAAAATAACGATGGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG
GATCATTACGAGATGAAGTGGCCTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAACTATTCAAAGAAGGAGAAGAATAGTTC
GAAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAGAAATGGGATAACCAATAAGAGCGATTGTA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACCTCGCACAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATTCGCTTGTGAATGATGAACCTGAGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAAGTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA
AAGTCAATCATCTTATCACCAACTTGGCCCCCTGCTCCTCATGATATCCGATGGGATAATTTGTTCAT
TAACTAGACAAGACAGAAATACAAAGATCCTTGCTGTACAGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTTATCCAGTCAGATTTATGGCTAGTTTTTTTAAACACTAAAAGCATTCTTAAAAATATGGC
CATCATTGGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCCGTTTTTTTATGTATGGATTTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAAGCTTTTCTATATATTTGTGA
ACTTATTTTTGGTTTTTCAAACTTTTGGTACCGCCTCTTTTGTGATACGACCAAAATTCGATTTG
ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG
GTATATTTCCCATCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTGTAGTGAATTCATTATTTA
GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCGAAGATATTAA
CTGCAGGGTTACTATATTTTATTATTGGTTATTTTGTGAGCAATACCAATTGCTTTATGCTTGTG
TTCATCCTCCACACTCAACGGGCAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTTGCCGTTTTTGGACACTTTACTTTTGGTGGGATTTCATATAACAATATATCCCTTGT

CAACATTTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACCTGTACGGAAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLQIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLTYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRINIGEVDVSLIVKEWQNLNKLFRRRRIRVRKLEESWVEYFEKNGITNKSDLISLHPQVGESYRF
SNRYTDDAEESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLNDESRTSPSLRKGWFLGFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPSPGKAIESHKWA
ETLITGLPTYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFTGTAS
FVDTTKIAFDLARSRLDLSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGQLQPQPIILFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKVWPI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTGAAGGAAATTTCTTTCTTAAAGCATCTAGTGACACATGATCTCTAATCT
CCAGTCTTTTGGATTAAATATTCTTTTGTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGCTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGATATATT
TTCTTTTGTCAATTCATCTTTTCTTTTCTCTTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTTCATTCCTTCTTGTGTTTGTCTGTT
ATACCCCAAAAGTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGCAACTAGTTTCCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
TTAATGTTGCACTCAACTGGTTCGACAAGCCAAAAGACATATTCACAGATTAATTACTCCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTCCTATCTTCGACACCCGGTACTAGAAGCTTAAATGAAA
ATAAAGCTCAAAATAGAAGCACAAAGATATTCCTTTCGCAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTATCTGAGTTGGTTGAAAAACCAGTGGTGTCTTATTCCTATCAAAATAATGA
TTGAGAATTTGAACACAAACCAAAAGTTGATTGATTCTTTATGTGGAACCTGAATGAAAGCTTGA
TTACACCAACTGAGTTTTCGGAATTTGTCAGTGATTTAGATTTACCATTCAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTATCAGTAAACTTAAATAAACAATTATACCAAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTTCGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACCTGCATCTAGTAAAAGGTA
TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAATGACCGTTGGG
AACCTTTGGTCGAAGTATTGACTTCTAGTGAAAATCGAAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSSEFGDDLDLDFDEFPSS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSDLDFPSMAAQIADSIQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNHLHLVKGIMFEQGIRIFTENSVQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRD
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGCTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTGGCAGTTAGGGCTATAGCCCTAAGACATTCACACAATAACAAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAATTTTCCTTTGAAAAAATTCACA
TCACGCTTTAACCACCTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAATTCAGGTCAAGAGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTTGTA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNKVNANGKKFKQTKFKVRGSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCCTCATT
TTTGAACCCACCAAATTTTCTTTTCACATTTATAATGAAATAAGAGTATTCCTTGGCTTCTTTTTTTT
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTTTCTATT
CGTTTTTATATTTTTTTAAGAAATTTGATGTTGATTGGTAAATGCCAAATTTTAAATGTGTGTAG
GGCTATAGCCCTAATGTACTGTATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTTTGTAGTAGAGGAGCTACACTAGACCACAGTGGC
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAAAGAAAGAAATAA
AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTAAGTTTAAATAC
AGTTTCAATAAAGAGGGTTTTTTTTTCTCAGAACAAACCATTTGACTGAAGTACTACACCAAGAAGGTA
TAATGATTTACAGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAATAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTTCAAACCTTGTGTAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCCTTCAATATATTCCTTCTCTTACTTTTCCT
ATTAAACAAAGACTAAGAAACATTCAGTAAAATACTAACAAAAATTCATTTATATAGACGTTTTT
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
ATCTGCTCCATTATCCAAAGAATTAAGACAACATACAATGTCAAATCTTTGCCAATTAGACAAAA
TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT
CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLEPIRQNDVLLVVRGSKKGS
EGKVNVSRYRLKFAIQVDKLQKEKSNNGASVPINIHPSKVIVITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTTCATCTTTTCAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTTCGGTGCCCTTGACTAGCAC
AACTTTGTTTCAAATCTTTATTTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAATCTT
TGTACTGAACGTCTTCATCTTCATGCTTTGCAAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATTTGTGCTTCCCTCAATCTGAAACATTATTCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAAATCTAACTAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCAT
CGGTAATTGGATTCGACATATCTTGTATTTTCTATGATTAATCTTTCTTTTTTCTTTTCTTTTTCAC

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAAACAAC TTGT
GTGAGATCATTC AATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACTTTTTTCTT CATACT
TTTTTTTTTCTCTCTCTCTCTTTTCTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAA TTTTGA
AAAACCGTGGT TTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGTATTCATCCGGA
CTTTTGCTACCTCAAGAATAGAGT TCCAGCGGTACCAGCCGCGTTTTGTTAATACCATTAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACAGTTT
TGTTAAATCATAAATTGTCAGACACATACTCATTTGTCCAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAGAAAGAAGACAGAAACAAC TAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAAGCATAGTCAAATTTGTTTCTTCTGTTGCTGGTGAGCAGTGTAACCGTTCTG
ACTTTAAGGTTGAAAACAAAGATTACTATTCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTATCTTGCCTGGCC
ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRFTFFPSYFFFSLSLFFQSHCSSVKGWLFC AEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMQSVFIRTFATSRIEFQRYQPRFVNTIKETVKS AQEKSYSIT
RPLGLSKPVLLNHNKLSDTYSLSNIYEELFGQSKERRQKQLDYDLKHSP IYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQRSLSYDLSLNRSLIVKLFSSVAGEQCTR SYFKVENKDYYSD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMS AEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKL MWKVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

CCAGTGC GTTTTGT TTTGTTTCCACATCATACTTCACTGAAACTAAATAAGTTTGT TTTACATTTT
GAGACTTCAGGTACGACCCAGGTTGCGACAAAGTTTAGGTAGTTTGTCGTC TGAATGTCGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAG AATTGCTGGTGCGCAA
AAAGATTATGTGTATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGTACACACACA
CATATTTGGGCTGTATTTTATTCTTGT TTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCCATA
CTACTGAAAATTTCTTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGT T
TTTCACTTGTTTCATATAATCACCAACTCAAGTACAACATGGCTGTCGGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTCGTTGACCCATTCAACCAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAAAC TTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGT TTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAAC TTTGTTGA
CCAAC TTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTTGGTCAGAAAATGGCAATCAT
TAGTTGAAGCTAATGTC ACTGTTAAAAC TCCGACGATTACGTTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAAGACAACCAACCAAATCAAGAAAAC TACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAAT TATGCAAAGAGAAGTTTCCAAC TGTACTTTAGCTCAATTAAC TT
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCA TTTTCCCATTTAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCA TTTATTGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHGLDFTSDKLRSLVRKWQSLVEANVTVKTSDD
YVLRVFIAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNC TLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVLLKQPKFDLGSLLALHGE GSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTCAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
TAATTCATGACCTCGAGTCATATTTCCACGTTTTAAGTATGAGTGTGTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTTGTTTCTTTCTTTCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTTCACAACGATTGCTATATGACCCCCCCCCCTAAGCATTTCATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAAATTTTACATTTCTTCT
TCTTCTTCTTCTTCTATTTCAACATTAAAGAACAATTTAATATGTATTTCCCAATCATTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATTATGTTTTGATCAATGGACAAATGATGATTTAAAA
AATTTTAAAAGAACGTAAAGTTGCATTCAATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAATAACAATTT
TGAATCCTCCAGATGATTCATTAAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTTATTCAATTAAAGAATGGATTTTTGAAAGTTGGCCAGTAACCAGTTTGCAAACTTTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGCTAGTTTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTCATTGGATTATTTGATAAAACCATTTTGTATAAAAAAGGTCAAA
TTGAAGATGAATTTTCCAAACTTGGTCATATCTCAATTACGTGAATGGCTTTATTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAAGGGAGAACAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTATGATA
CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKQFVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNLNNPDDSLNDYLNFDYLFGRKENYSIKWIFESWVPVTSLOTFLTQNNIQYSKDKT
DDLINKVKDQFDSISKKNHGSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKFS
YQATHSIRDSKESLFDLFDKTIFFDKKGQIEDEFFQWTSYSQLREWLHLHGFFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAATTCTGCATAAAGATTAAAGTGAAA
AACAAATTTCCGAAAAAAGAAGAAAATCGAACACATTAGAAAAAGAAACGAACAAAAAGAAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACCTCAGAAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATCTTGCCTTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTTGATTCACCAGAATTTTGTTCACAGATCATAACTCCCACTTGTAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGGAAATGCTCAACATTTT
GTGCTAGTGAAAACTGTGCTGTTGAAATATTGGAAGATTTCAAATTGGAGTCAAGTCACCAATGAAA
GTTTGAAACCTTCAGGATTAGGTAAGATTTTATTACCTGACAAATCATCAATTGATAATTCCATTG
AAACCGAAGAAGTTCAAACCTGTGAAGATTTAGATTATAGTGAATAGATGATGACCATCATTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTTGATG
TTTGGAAGGCTATTTACCTGGAAAATTTGTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTCTGAAACTGGTGAATTTTATCTCAATT
TAAAGGTGTTTATGGAAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCAATCAACTGG
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTGCAATCAGTCG
AAGTTTATGATCGTTTGTGTTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTTGTTTGTATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACATATGATAATCACAAATTTGAAATTTAGAAGAA
TTGAAATTTGTTGCCTTGATTAATAC'TTTT'GATCGT'TTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTTACG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTGTTAGTCCATTACCTCAGA
AAAAACCTGACCAAACCAACACCCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATTGCCCACACAAAACCTGAAGATCGAACTTTTATTGAAGACTTCA
GATTACCTTTTATGAAGTTTGGCAAGCATTAAAGATTTGTTTAACTAGTTATCAAAGATTCCCAG
CCGTATTGAGTAGATTACATTTGGTTCAATTGAATGAATGGTGAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO. 418)

MKIFRLFSLILVQFIINTTAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKTSYFRYFKVNLQCRFWNAQHFCASENCAVEILEDNFWSQVTNLSLKPGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGGNQSFVDVWKAIYSENCFPN
TNPMSVTNDADNGGEQCIKLNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIYFNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRRFRNISAIMDCVGCDCRMWGIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQNTNPKNQKKQKPQETDKRLTLEBIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLRSRFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419):

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAAACAAGT
AACAAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTTCCCGCTCTGTGTGGCACGAGACAATTG
AGTCGACCAGTACGTTTTTAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTTCCACTT
ATTCTATATCAATGTAAAGTCATTTTTTTGATAATATCGTAATTTACACATTTCTGATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCCAACAACCTAGATTTTCCGAATGCGAAACGACGAGGACGACACAACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT
TTTGATAATACTACCACCACACAGCTCATTACCACCTCATGCCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAATG
GAGTATCCCACGAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGCATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLETEYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAULTFPKDY
PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTTCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTAAACAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTTTAATTTTTTTGATCAAAAGTACACTCATCAG
TCTATTGTCTGATGTTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTGTA

145/161

TTGTAAATTACAATTTTTCTATTGGTTAAAATGATAATTTGTTAACAAGTCTTTTTTTTTCCCCGGGA
TTGAATCCGGAACTACCATTAATTCCTACTCTACTCTACTCACCTTACACCTCCTACTCACTCAA
ACAATTATATCAACCCAAAAAATCTTCTACTACACCAATAACAAAGAACCAATAGTTCAAT
C'TAATAAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTGGATCATGTCATCATTTCCATAGAA
TCACTGGTGTTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT
TAAATATTCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTATATAGAAGTGGGATGCTGTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKATCAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTTAATAAT
TATTTAATCAAACCTGGTTGTAACCTTATGATTATGGTAGTGATCTAAGAACACAACCTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCCCTGTTTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTTCTACACTACTAGTAAAAAAATTTTCTTTCCGCTCACTATTACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTTCTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAAGAGATTCAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG
CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTGCTGTTGCTAAGAAAGACTTCAACCAACCAAAGCACGATGAAATT
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTTCTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGEVFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAGCAATAGGTCAT
TTATTGCTGTAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTTCTAAATATTTTTTTTTTTTGTGTTGTTGTTA
TTAAACAATATTATTTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCTTTGCATATT
TTTTTTTTTTTCTTTTCTGCCAAGTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG
ATATGTCTAGCACTGGAAACATGAATGAAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTGTGCTGCACGATTGGCTAGTGGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTAAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACCTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAACCTAGTAGTGTGGCCACTCAATCA
ATGAAGGATACAATGATGATACATTTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTGCA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACCGCTCTAAAA
GAAATTACAAAACCTCATCCACTTCCTCAAAATTAAGATCAACTACATCAAAAACCTTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTGTATGATATTGACATTGAAGATTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAAGAATCCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGTATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAAACAACAGTGATCACAATATTAATTCTCCTTTGACTGCTAATAATAATAATAAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACATTGCTAATAATAGAG
CATTTCCATTTTCCTTATCAAGATCAACAACATCATTAATTACTACGACTACGATGATTTTGACCAAG
AATCACAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAACAACAACAATAACCCCCAAAAGATTTGGCGACAGTCATTTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTTGGGGTTTGTTTTGGCCACAACAAAAGATTTAAGTATGATAGGTA
TCACATCCATTGAGAACCCCATTTGTTAGTAAGATGAGTTAGTTTTCATGTTTGTATTGAAGCAT
TTAATCCAGGGTGGTTTTCCTGTTGACATCAATGAAGTAGAGTTGGATTTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAAATTCAAAAGGGAGGAATCCGATTATTATATCTCGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAATAAGCTGCCTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAAACTGGGTATATTGATCCTTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNANINNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISNSISSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDDKKSQPRRYSTIPDDIDIEDFDDLIYYDNTARFPANESTSLLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNNGNSDHNINSPLTANNNNNNVNHNHDHGDNKKSN
NNNNIANNRAPFPYQDQHHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFLVLTATKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDNDNSKISNMGGSQKVETVKLGITILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMDIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTYIDPTLFVIPQGENNISI

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;
CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTTACCAACCAAAAACCTCTGATATCAATGATTGCAAAAAGATTTCATTCA
ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAAATAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAACTTGTTGTGTTAGATGAGCTCAAATATCTGGTGGAACAATTGTGTAGTAGCTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAAATACCATCGCAAAAATCCTAACAAAAAATAAAT

TAATAAAGAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTTAACAGAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTACGATGAAAGTGAACAAATAGAAATTTGATGACGAATACAGTCGGTTGTCTGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTCAGATTT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTGCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCTCATGGCCCAACTCGCGATTTTCACGTTACATAATGTCA
AACTAAGACACGATTTGCCAAACTTTGGGAAACGTCTCAGAGTCCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAAATATTGCAACATTTGTTTCTCCAGGTGTCA
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATG
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTCGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTA

YNL075W_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQDFIYDESEQIEI
DDEYSRLSGISDPKVVITTSRDPVSKLLQESKEIKLMFPNSLKLNRGNYYISDLVSTCNRVQVSDM
ILLHEHRGVPSSLTVSHFPHGPTAIFTLHNVKLRHDLPLNGVSESYPHLIFENFQSDLGKRVVKI
LQHLFP PGVKKSSRVITFVNDDYISVRHHVYVKT KDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058;
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCCTAGGAACAGGA
AAAATAAAAACGAATAAACAAAAACCCCCCAATCGGCATGCATCGGAATTCCTTTCAGCCCAATTAC
TTTATTTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
TGCAGTCTATTTTTATTTTTCTTTTTTTTTTGGCTGTTGGTAAACTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGAATAGTCAACC
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAAATCATGTCTCTAAGATCTTATCAGAAAACC
CAACTGAATTAGAATTAAAAGTTGCTCAAGCTTTCTGTTGATTTTGAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAGCTT
TAGCTGTTTTCTGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACCTAGATTAACTAGAG
AATTAGAAAAAAAATTTCCAGATAGACATTTGTGCTTTTTTTAGCTGAAAGAAGAATCTTACCAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAAGCTTTGACTGCTGTTTCATGATA
AAATTTTGAAGATTTAGTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAAAATTGACTGGTAAACAAGTTGTTTTTGAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELKVAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQQRPRSRTLTAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVLDSKDSSTAVDYKLDSFQQLYSKLTGKQVVF EIPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
501..1253 (SEQ ID NO 431)

TGTTTTGTTTTTGAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTTTTTGTACTCTCC
CGTAGTTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTTGTTAAGGATAATACTTCTTCTTCTTCTTCTTGTTTAATCAAATTTGCAATAAATA
AAAAAAAAAAAAAAAAACAAAGCCGCACAAGTTTTCCTAAAATGACTTATTTTGTGTAACGCATTAC
GTGATCATAATTTTTTTAAATTCAAAAACCTGAACCAAATTCCTGCATATTGAGGTTGAAAAA
AGAAAAAGAAAATTTTTTCAATCTTGTTTGGAGAGAGAGAGGTGAAAAATTTTTCTCTCTCTCTTT

CTTTCTTTCATTCTCATATACCATAAACTTAAACAACTTCTTTTACTTTTTCTTTCTTTTCTTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
AACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCA'TTATGCTGAAAGAGTTGAAGAAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAAATATGCTGATGGTTTTATGATTCATTCTGGTCAAC
CAACTAGAGATTTTATTGATATTTGCCATTAGACATGTTTTAATGAGACAAGGTGTTTTGGGTATCA
AAGTTAAAATTATGAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTTCCAGCTCCAAGCTGTTAAATCTTATAAACAAA
CTGCTGAAGATGAAACTGAAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEQGR
IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLGKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCTTCGGCATATATCAAACCATTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTTGGTGGCACCATTGGAAATAACTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATCACTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCAAAATTTGGTTGCCTTTTTATTCT
TCTTGTCTTTTTTTTTTTTTCAGTGCTAACATAAATTTGGGATGTATGTATTGAAAAAATTTTGT
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCAGGAGAAAGAATTTTCACTGCTGTTTCTTAACAAGGCATTAATCA
ATGTATATTCTAGGGGAAAGAAAGTGTGTGATCAACGTATACCGATACCCAGATACCAAGCTTGTA
TCACGTTGATAAACCATTCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAAGTTATACA
AATTACCAAAATTACCGAGTTCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTTGTACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTGTCAGAGACGCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATTAAGTGGAGGAGAGGATGCCAGATGTCTTGTATGGAATT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTACAAAAGAGTTTGTGTAACCAT
TTATTTTACCCAGTTCCGCTGAATGTATCACCAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTGAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTGTTGTGCTGACATTGTAACGA
AACAAGTTGTGAAAATCATTACACCTTGTGAACCTCTCCAATAGCTTATATTGCTGTTGAACTATCC
CTGATGACTTTGTCAATAAATAGTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTCTGAAGAACATCAGATATTCTTGGACA
TTCCTGGTAAAACACCGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAATCTATTTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGKSSCGTFLITGG
EDARCLVWNLAELISIDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSSEDSVRIYD
IVTKSLLTFFILPSSAECITKDPANRALYVGLNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFFVAHQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVFSVDIVTKQVVKSFPPCNSP
IAYIAVETIPDDFVNNLATSTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTELNRKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCAATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTTTAGGAAATTGCGGTATTTTCTTGTCT
GTTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATTTGACTTTTTTTTTTACTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCCTACTGTTGCCACTGTTT
TTGCTATTTCTCTATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTTCGTTTTGACAAAACCAGTAGATCTAAAAAGC
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCAGTTACCACACTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACCTCTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTGAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTGGTGTGCTGCTTTGGTTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFATSSLAAGGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN
KTPRPVTTTVLVKESDLPKKRDAVVARDSKNASSNSTTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTTGGGTGGTGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTGTGTAACAAATTAAT
TATAGGGAGTTGGAAAAATTAAAAAGCTTGAAAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAAATTGCATAGAAATTTAGGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTTATTTTTCGTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTT
TCTCTCTCTAACTCAATTTCAATTTTCCCAAACCAAAATTTCCCTTTCTTTCTTTCTTTATT
TTTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTTATTATCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCATCAAAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCGCCGGTGGTGTGCTGGTGGTTATGGTGGTTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC
CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGLTGLTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRDRDRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCCAGATAGCTAACGGTTTTGCGATTACGAATTTGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTTATTTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA
AAACGAGAAATTAATGAACACGACTTCACCTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCAGATC
CAGAAAACCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAACCATTAAC
CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCAGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC
TGGAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAGGTTGCATTGCGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTTCA
GTTTTGTCAACATTGCCAATGGTGTCTCTGATCCAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTCCCAAACCTGGTCCCAAACCTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTTCAAAATTTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAAATTTAATCAGAATTCCTTTGTTGGAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNSSIVDTSEELICPDENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR
NIDTLEKEAKLMSADEKDEPVQEVVGGELQDHSREAITENLQKLHESKHPEVKQEHHRTKVSQ
DLSNFDAACSEIESFKPHESDVERLHLALDLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNLTNFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRRSLEDQDPESQVSKFISFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADDEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCTCTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAACTATTCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATACCATTAAATTTCAATAATCAAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTACCAACATAACACG
ACAGAAAGGGGTGTACTATTTGTAAACATATCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCCTTACACTAGTCACTTACCTGATTATGTTTTTCATTGTTCTTCCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCGTGGTATAGTTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTACAAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAAATGATGTGGTACTAATGGGAAAACCTTAGGAGGTATA
GAAAACCTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTTCGGTATTACTTCATACCCCTTTGTAGGTCCAATCA

151/161

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
 GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
 TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTCCACCAATACTTTGG
 GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGCGAG
 CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
 AACCAGCAACTAATATACCTGAGGCTACCCCCAAAACTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIVYTLLMGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQVRVAYDAILSRECANDV
 VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
 AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPPFINMFFMFTNTLGAALWAVDIEQQE
 KAVTENVAATTTATDTNSVNQQLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:
 948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTTGATTTTGTTTAACAGTGAA
 AGTTTTTATTTTGTTTTAAAGTTTATTTTGTTTTAAAGTTTGTATTATACAA
 TATTTAAATTATAGTAATCATCCTATAAAATTTCAAAGTCAAAGACAGATCTTAAGGTCTAATTA
 TAACTCTCTATGGCCTTCTGTGTCAAATTTGTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT
 GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAA
 AAAGAAAGAATTTTCTTCCATTTTCAAATTTGAGAGATCGAAATAATTTCTTGAATTTA
 TTAAGGGAACCCCTTCCGAAAAATCCAAAACCAAACTTCCACCCAAATATCAAATAACTAAC
 TTATCATTTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
 AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAGGCGATTGAAGCATTCACTAAAGCAATTG
 AAGCATCACCTGAACCAAAACCATGTTCTTTATTTCAAATCGTTCTGGATCTTATGCCTCTTTAAAG
 ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
 ATAATAGAATTGCTGGGGCTGAATTTGGTTTAAAGTAATTTTGATCAAGCCAAATCCAATTATGAAA
 AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAATCAGTTGAATCTGCTT
 TATCATCTGGTGGTGGTGATGACAAGGATTTAGGATTTGGTAAAAATTTTAAATGATCCTAATCTTT
 ATACTAAATTTGAAAAATAATCCTAAAACAAGTGAATTTATGAATGATCCTCAATTTGTGTGCTAAAC
 TTGAACGCTTAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAAGATTATTGA
 CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCACTGCTCCAAACG
 AATCACAATCCAATGCATCAGAACCAAAACCTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC
 CAAAAGCAGAACAAAAGGAAGAAGATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
 CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG
 CCTTATACAAGAAACGTCATTTGATGAAGCAATGCGCGCTATAATAAGGCTTGGGAATTACATA
 AGGATATCACTTATTAAACAATCGTGTGCTGCGCAATATGAAAAAGGTGATTATGCTGCTA
 TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
 AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
 TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTAAATAAATTAAGATCAACTCAACGTG
 AAATTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
 GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
 GAGCACCAGAAGATGCTAGAGGATATTTCTAATCGTGTGCTGCATTTGGCAAAATTTGTTATCATTTT
 CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTTATTAGAGCTTATATTA
 GAAAAGCTAATGCTCAATTTGGCAATGAAAGAATATAGTCATGTGATGATACTTTAACCGAGGCAA
 GAACTAAAGATGTTGAATTTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
 CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAAATATGGAAAAGAGTTTCTAAAG
 ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
 ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
 CTGCTGGTGTTATTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSYSYASLKDFNNALKDAQECV
 KINPSWAKGYNRIAGAEFLGNFDQAKSNYEKCLELDPNNMAKEGLKSVESALSSGGGDDKDLGF
 GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
 PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPTMTDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIKSFARLGNIIYLKKDELPEAVKNFEKSLTEHRTDPVLNKLKLRSTQREIKTRELNAYIDP
EKAEEARLQGKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIETGETP
EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGACTATACACCCTGAAAAAAAAAAAAATTTTTGTAAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAAGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCTACCCCTTGTCAACTTGTCAATAATTTTATTGCTCGTCTTTAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAAGATGAGAATTTTTGTCTC
CAACACCCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATGCATAAAGTTAAAAAAG
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAAGTTGTTGAATTAGAAAAAACTGATGATGTTAAAAGACAATACGTTAAAC
AATTTTGGACTAAAGATTTGAAATTCCTATTACCACACAGAGTCCAAAAATCTAAGAAATTTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHNMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVVKQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS: 501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA
TTAACATACCTTTGTCACAAGCAATTATATTGAAGTTTTTTTGATACAAGTGTGTTGTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCTTAGGGCTATAGCCCTATTTAGTTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGAAAAATTTCCACTAGTCTTCCCATACCCACCTAGGTTCTTTC'TTTTGGAACCACT
GAGCAGTAAATCAATTTACTTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCTCCCCCCC
CTTTTTTTTTTAACTAACTAAGAAGAAAAAATTAAAAAAATGTCTGACGTTGAACAAGAACAATTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAAGTTGTTT
TAAGAAGTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTGGTTG
AAGCTTTATGTAATGAACCAGAAGAAAAAATCCCATTGATTAAAGTTTCCGATGCTAAATTATTGG
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCCTCTT
GTGTTGTTGTTCAAAAACCTGGGGTGCTGATTCTGATGAAAGAAACATCTTGTGGAACACTTTTCTC
ACAATAA

YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEQIVEEVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS: 501..878 (SEQ ID NO 449)

YPL047W_homolog 126aa (SEQ ID NO 450)
MLFCFII TKICFFFFSKADSIFNDLINNI IKQHTLTSLTNIKDHSLLNSSNSNTNSNTNGTIAN
GGNGTTS DENNEIENSTIODKSKLKOLETSRYFRCLNCGRN IAGGRFASHISKLERKRK

CTCTAGAAGTAGGACATCGTATAGTGTATAAACACTCAATAAGTAATGAAGAAACACGTTTTTGTGTG
TGCAATGTTAGCTGGCGAGCTCAATATTGGGTCTCTCCGCCGTCTGTCTGCCTTGCATTCTACTTTT
TTTTTCTCCTTATGGAACACATTAGTACTAGTAGTGGTGGTAGTAGT'TTGCTGTTGTTTGCACCTTTGC
ACGTAGTTGTTTTTCCCC'FCATTTCTTTTCATCTGATTATTTCTGTCTTTTGTTAACTGCATACAAAGGGA
GGGGAAGAAGAAACAACAAAGGGGAATTTGAATATACGTCAATCTTTTAATCCTACTACCACGGG
GGGGGGGGGGTGCATACTTCTTGGTGTAATAATGTATGGAGATTGAGGTTTATTAGACTTTTAGAA
AGAGGTCTTGGTTGAGTAAGGCGGGATAGCACAAATAATGCGTGTCTAATTGGTCAGAGAATAAT
TGCTTTTGGGGAACAATAGAAAGATGTAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAAC
TTTTTTTTTTTTTAATGCTTGGAGTACTTTGTTGTTGGAAAGAGTA'TTGCAGAAGTAATAGTTTAAT
AAAAGAAAAGTATATAAC'T'ITAGTAATCCGAGAACAAT'GAAATCAATATTTTGAAATAATAGTTT
TATAGTAGTAACCTGGGTGCAGGTGAACCGGAATTCATATTTGGTTTTCGGTTGTTATATGCTACAT
AACCATCCTCATCTTGAATGAAACAAGGATAATAGAAATGAGTATATTAACAAACAACATTATGT
TGTTACTGTTGTATTCT'G'I'TTTTTTGGTCATTGCCATGGTAATTTTCATATTTAGTAACAATTTAGT
TTCATCGTAAGTCTCTCCTTCTCT'GGGAGATGTTCTCTCTCTCTTCTCTCTCTTGTGTGTGTGT
TGTTAATTTGTTAATTTGTGATTATTGATTGTT'CCCCAATTAATAATCCCGATAAACTTGAACAATAA
ATTGTCATCATAAATTTTTTTTTTGAAGAAATCACTCCATAAATTAATTTATTTATATTAATAATTT
TAAATCGGAAC'TTCCGTCAATTTGGATTTCGGTTTTTTTTTTTTTTTATTTGTTTCATTTATTTCTTGT
TTTTATTTTCTTTTTTGCTTCCTACTTCTCT'ITTTATTTTCTTTAGTTTCATAATTTTTTGACAGATAATA
CTTGAAACTGGTTAATTTTAAATCAACTTCGTGAT'ITTTTTTCCGGAATCTAATAATATCAATGAC
CAGTAATCTGCCACCACCTTGGTTCTACAACATAACGATCAGAGACTACCCCAAAGCGGAGTTTCATC
CATACCCACAATAAAAT'GGCT'ITACC'TAATGCCAATGAAGATTTTGCCACGGGTGTGTGCAATGG
AGATGTTGACTGGCTATTTTCGAGGTAAATCAAAGAAATTTGGGGAAAAGATGGCTAACACAATGC
CAATAAGGATGAACGAAAGAATAGTTCATGGTAACATCAAAAACCTCGGAAAAAACTACCGCAAAACC
CAATGAAACTAAACATGAGTCTAATGGTGAGAAGTTAGAATTCAATGTTCCAAAATCTGTAATGC
AACAAAGCATACATCGTCTGGGAACCCAAAAGCACCTACCAATGGACAAATCTCAAATGTAACACC
AAGTCAACCAAGTCCGAAACAGACCAC'TTCTGGGTCAACAAATGCAATGATATACCTCCAATTTCT
TCCTAAACAACCCAGAAAAGGCATCAAAAGTTGAATAAACTAAAAAT'GGGCGT'TCAAGATCGTCTTC
TGCATCAACAGTCGTACCTTCATCTACAACAGCTTCAACTACTACTATCTCGAGATCTCTAAAG
TCAACCAAAAAGACGGAGCAGTAGTTTTTAAC'TTTGTTACTCCTTCC'TTGACGAGTGATTTGGCATA
TGACGATCCTGCATTGGTATCTCAATTATCAAAACAATTCAAATTTCTCTGAACCTATCCTCGCC'TAA
TGTTTCTCGTTCAAATAGCAAAAAAGGTGGGTTATTTCAGTTCACTTTTCATCAAAATTTAGATCAAG
CTCGGCTTCATCTAAACAACCACAACCTGCATTTCATCGTCTACACCATCAACCACAACGACAAAATGG
TGGCGGTAACCTCGTCCGCTGCTCCAAAATCATCCCATCACTCCCCAAATTTAATCTTCACTTGT
TGGTCCAGTATCAAAGCACAAATCGAGAAGCTGAAGATTTGGTGCTCTTACCAATACTTTGCC'TGC
TGGGAGTGGAATACCAATTTAAACGTAAACCATCAATATCGGGAAATTTCAATTTTCAAAGATTCAT

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTCAG
GAGACGTTCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA
AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTCCGGTTACCTT
TTCTGTTGATAAACTCGAGCACGATCCGCAACAGCAGATTCCCTTCAAGAAGACCTAAACGAGGTAA
TGTTTTAATTTCCACAGGACATCAATGCACCACCTCCAAGACTATGTC'TTGGGATTTCAAGTTAATGA
ACCAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT
AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATT'CATATCCATTAAAGAAGG
TGGTAGTGTGGTAATTCTAACACCAACGGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA
AGCAGTTGATAAGAAATTGGCAAATGATGTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA
TTTTGAAGAAGAAATTGAAAGCAAAACAGGT'GAAAAGACCATTTCATTGGAAACAATCTATACAAG
ATGTTGTCTATTACGAGAAATTTTACCAATCCCAGCAACATTGAAACAATTGAAAAATAAGACAGC
ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCT'TTTTCAGA
TTTTATTGCCATTACACCTATTAACACGGTCATTTTTTGATAACGTGACTATGACAACAGAGATGTT
GAAAAACTTTCTTGGATCGTTGACATATAATAACAAT'TGGAAAAGTTATCGTTGAGAAATGTTTC
CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTTGGCAACAAAATAAACAGTTAAGAAATT
GGATATATCACAACAACGTATCAAGCCAGATACCCAGACACAAGCATTCGTGGTAATATGAAGT
GGACTTATTTATTCGATCA'TTAATTTTGGCTGGTGGAATAGAAGATTGGTTATCAATGGATGTAA
ACTATCCGATGCAATATTTGAAAAGTTTCATCAATCAAGCGGT'TAAGAAGTCAACCTATCGATTAGG
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
TTCTCAATGTGTTGGTGTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTATCAT
TAATGCGTTTAAACACTGGCAAAGTCAACAATTTAGTGT'TTTTTTCATTGAATTC AACCAATTTACT
GAACATTGAAGAAACTTCTGACTTGATCAAGTCA'TTAATTAATGTTAAAAACATTACGATTTTTAGA
TTTAAGTTCCATACCTAATATCTTCCCGAAAATAAATTACCCATT'TGGACAAATACTTGGCCAGATA
TCTTAATCTTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAAGCTATTGGGTCAATGGC
GGGGTGTTTACTGAAAATGCCCAAT'TAGTT'CATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC
TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTG'TTTGCTCTTGATTTGGA
CTACGATTTAATACCTGATCAAT'TATCACAACGTATTGCCTTTTATTGATGAGAACTTGGAAATA
CACTTTGAAGCCATCTCATGGCGGCAATAT'TGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
GGATATCAAAATGCAAAGAATTATATCCGATT'CAAGTATTGGAAAGAACAGATCGATTTCGTAAGGA
TATTCACAAAACCATTGATACATTATTTCGAACAAAGAAAATTTAGGTAAATTATCATTTGAAGGTAA
AGAGAATTTAGTTTCGATTTTGT'TATTAGATTCGTCTTTAGAAAAATTTGGTTGTTATGGTTGAGGA
ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAAAATGAGTTGATTACTGCTGGACCAATTTT
ATCACCATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGGCAATAATGATAA
TTTGACCCTCATCTAAGTTGTCTGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT
GACAGGACGACCAGT'TTTGATTCGATCAATTAGTCAAACCTTCTGTGCATGCAAAAGAGCAAGAAAT
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA
ACAACAACAACAACAAGAACTCACACCACCAGCACCAACCGGCCAGCTGATCCAACAAGAAAA
CCAGC'TGCCGCTGCCACAACAAGGAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG
ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAAATGTTACTGAATTAATTGATCG
AATTAATAATCATCGTGTTAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC
AAATTCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDVDWLFGRGSKKLKGKMMANN
NANKDERKNSHGNIKNSEKTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSASTVVPSSSTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSNSSSPNVSRNSKKGGLFSSLSKFR
SSSASSKQPQSHSSSTPSTTTTNGGGNSSAAPKSSHSPKFNPSLVGPVSKHNREEDLVSLTNTL
PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIDEEISEVRLRRVTFVVDKLEHDPQQQIPSRPRKRGNVLI PQDINAPPPRLCLGISV

NEPNKDDGKSHNHSKYSDEHIALAEDAQRRAIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK
EGGSVGNSTNGNDNDEDDDEVEEAVDKKLANDVSVGDGPLHVHEQHFEIEIESKTGEKTISLETIY
TRCCHLREILPIPATLKLKNTAPLEVLKMLNPKPTLIDVLSFSDFIATPINTVIFDNVTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQQRIKPDPDTSIRGNM
NWDLFIIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLTD
GNSQCVGVDFIANDLSKGQLRPFINAFNTGKVNNLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF
LDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLLGNRNL
STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL
MYDGSLLMETAEKLLVEIEKGKKEDIKMQRIIISDSVLERTRSIRKDIHKTIDTLFEQRNLGKLSFE
GKENLVRFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGP
ILSPHVNRKAEQSSYFPVFANNDNLTPHQVVVESNDEGRDVPIDKMTGRPVLIIRSISQTSVHAKEQ
EIEEGELHKFGFFIQOKERQKQQQQQQQNSHHQHPAQSIQQENQSPSPQQGKYEDLPILNTLP
SGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS
TNGDDLHQLGDGKHNGNGTVDPMVSEVYDKLLNDAERVRSNRDI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:
394;CDS: 501..1856 (SEQ ID NO 453)

ACGGAATAATGTTATGCGAACAGAGTAAGTGGGATTATCAACAAGCATCAGTCAATTTCAAAAACCT
CGGCTGCTTCTTTGCCCTAGTGATGCATTTGTACAATAGAATTATAATTAAAAGAAAGGTAGAATAG
AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAAA
TTATAATGAAGTAAAAACATGTAAGTGTGTAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG
TAGAGTGTGAGCATTTAAATATGAAGGAAGACCGATAACCTAAAGTTTTCTCAGGGTGTCGAA
GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCTGTTTATATCAGTTTTTTGCAAGAAAAAAGG
AAAACAAAACAAAATAACACCAACAAAGCAATTAACACAGCACATCCTAAACACCACTCTGTTGGAG
CACCAATCAACCTGAGAAATGCAAACTTGTAAATAAAATATGGGATACAATATAGCAATCGTAACAG
ATTTTTTTTACCCTCAACCTGGAGGAGTAGAGTTTCATGTGTATCATTTATCACAAAACTCATTG
AACTAGGACACTCAGTGGTTATCATAACTCATAATTATTCATCAAGAAATGGTGTACGAGTATTAA
CGAATGGTTTGAAAGTGTATTATGTACCCTTTGGGTGATCTATAGAAGCTCAGTTTTCCCAACTG
TATTTCTGTGCTTCCCAATATTGAGGAATATCTTCATACGAGAAAACATTGAGATTATTCACGGAC
ATGGTTCCCTTCAGCACATTATGCCACGAAGCTATTACATGGCCGAACAATGGGATTAAAAACAG
TCTTCACTGATCATTCACTTTTTTGGATTGTGCCGAGATTGGATCAATTATGGGGAATAAAGCATTAA
AGTTCACTTTTCAGTGATGTTGGCCATGTTATCTGTGTCTAGTCACACCTGTAAAGAAAACACGGTTT
TAAGAGGATCAATAGACCCCATAAAAGTGAGTGTGATACCGAATGCAGTTATTCTGAAAGATTTC
AGCCCAAAATCGCATTGTGTTAACAAGAACTATACTAAAGAGATCACCATTGTGGTGATCACGAGAT
TGTTTTCAAATAAAGGAGCCGATCTATTAAACGGCTGTTATCCCCAAAATTTGCCAGTTGAAACCAA
AAGTGAAATTTCTAATTGCTGGTGACGGCCCCAAGTTTTAGATTTAGACAAATGAGAGAAAAGT
ACTTTCTTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAGTAAGAGATGTAATGG
TCCAAGGTGACATATACTTACATCCTTCATTAACAGAGGCGTTTGGTACAGTTATTGTGGAAGCTG
CATCATGTGGGTTATATGTTGTCCTACAAAAGTTGGAGGCATACCCGAAGCTTTACCAAACGAAA
TGACAAGCTTTGCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA
TTGAAAGTAATGAAATCGATACCTCAAATTTACCGATGCGGTTGCAAAGATGTACAGTTGGAATG
ATATTGCAAGAAGAACAGAAAATGTTTATAAATTCACTTGATTAGACAAACTAAACGAGTCTTTAC
TTCACCGATTACAAAGATACCTATTGTTGTGGTATAATAGCAGGCAAACCTTTATGCTTTATGTGTAA
TAGTGATATTTTTATTTTCGTGATACCTAGAATGGTTGTATCCCGCTGATCATATCGATAAAGCAA
CAAATGGCCACTGGCTATCAAGGAAGAAGACGAGCTGGAAGAAGAAACATTTATTTTTCCGAACA
AAGTAAATTAG

YPL175W_homolog 452aa (SEQ ID NO 454)

MGYNIAMVTDFFYPQPGVEFHVYHLSQKLIELGHSVVIITHNYSSRNQVRVLTNGLKVVYVPLWV
IYRSSVFPTVFSFPILRNIFIRENIEIIHGHGSFSTLCHEAILHGRMTGLKTVFTDHSLFGFAEI
GSIMGNKALKFTFSDVGHVICVSHTCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPFLDLEQMREKYFLQERVTLVGAI
KHEEVRDVMVQGDIIYLHPSLTEAFGTVIVEAASCGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTENVYNSLDLKLNESLLHRLQRYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETFIKPNKVN

10/030019

156/161

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTCCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA
AATAATTGAATAATGATATAAAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC
TCAAGTGTGTTACACTCTTGTTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA
ACAGCAAATACTGTTCGTTAATAGGAATCAGAGGCAGAAAAGAGAGAGAGAAAAAAGGACA
CATTTACACGTACACCTTAACTTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA
GAAATACTTTCAACAACGAAAGATTGAGATATTGGTGATTTTCACAAACCAAAAAAAGAATAC
ACAACCTGTAGATTAAACAGAAATTTGAACATTTCTAGAGTTTCTTATATTCCCCCAAGGTGGACAA
TTAATAATAACATTTGATTATACAAGAACATTTCAATCATGTGGATTTTGGACTGGTGTATGTAAT
GATTTATCTTTACCGAATCAATACTTTATTTATGAGTGATTTGGTTGGTTGGTTATAATACCACCAC
TTTATTCTATTAAACCAAGTTTGATCTAATTACTGATCTGTATATACTAACCAAATATTTACCTTAT
CACTTAATTATTTACAGTTCAAGATATATTATCATCATTAGGATTTATGGAATAAACATGCCAAATT
ATTATTTTATAGGGTTAGATAATGCTGGTAAACTACTCTTTTACATATGTTAAAGAATGATAGATT
GGCCACTTTTACAACCAACATTACATCCAACCTTCAGAAGAATTGGCCATTGGATCAGTTAGATTTAC
TACTTTTGA'TTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA
TGGTATTGCTTTTTTAGTTCGATGCTGCTGATACCGAAAGATTTGCTGAATCCAAAGCTGAATTGGA
AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTCCATTTGTTATTTTGGGTAATAAGATTGATGT
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAATACTACTGGTAAAGA
TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTTTATGGTTTCCGTTGTTATGAGATC
TGGATATGGTGAAGCCTTCAAATGGTTATCACAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
TTFDLGGHQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESFRIEELSQVPFVILGNKID
VPTAVGEMELKNALGLYNTTGKDTGKLPETRPVIEFVMSVVMRSGYGEAFKWLSQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)
CTTAGCAACTACTAAAGCTTCAGCTGCTAAAAAAGCTGCTTTGAAAGGTGTTAACGGTAAAAAG
GCTTTAAAAGTTAGAACTAGTACTACTTTTACAGATTACCAAAAACCTTAAAATTAACCAGATCTCCA
AAATACCAAGAAAAATCAGTCCCACACTACAACAGATTGGATGCCACAAAATCATTGTTGCTCCA
ATTGCCACTGAACTGCTATGAAAAAAGTCGAAGATGGTAACACTTTGGTTTTTCCAAGTTGACATC
AAATCCAACAAACACCAAAATCAAATCTGCTGTTAAAGAATTATACGATGTTGATGCCTTATACGTT
AACACTTTTATGATCAGACCTAACGGTACCAAGAAAGCTTACATCAGATTAACCTCTGACTACGATGCT
TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKKIIVAP
IATETAMKKVEDGNLTVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACTTAGTTCTTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAAGAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGTCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT
AAATTATGAAAAACGTCAAAGGAAATTCCTTGAAGGTGAAGGTGAAGAAGAAGATGACGAATAA

YGR183C_homolog 65 aa (SEQ ID NO 480)
MLTVLGRLLERNISIYVATIFGGAFQGFDDVAVNKKWEEHNKAKLWKNVKGKFLEGEGEEDDE*

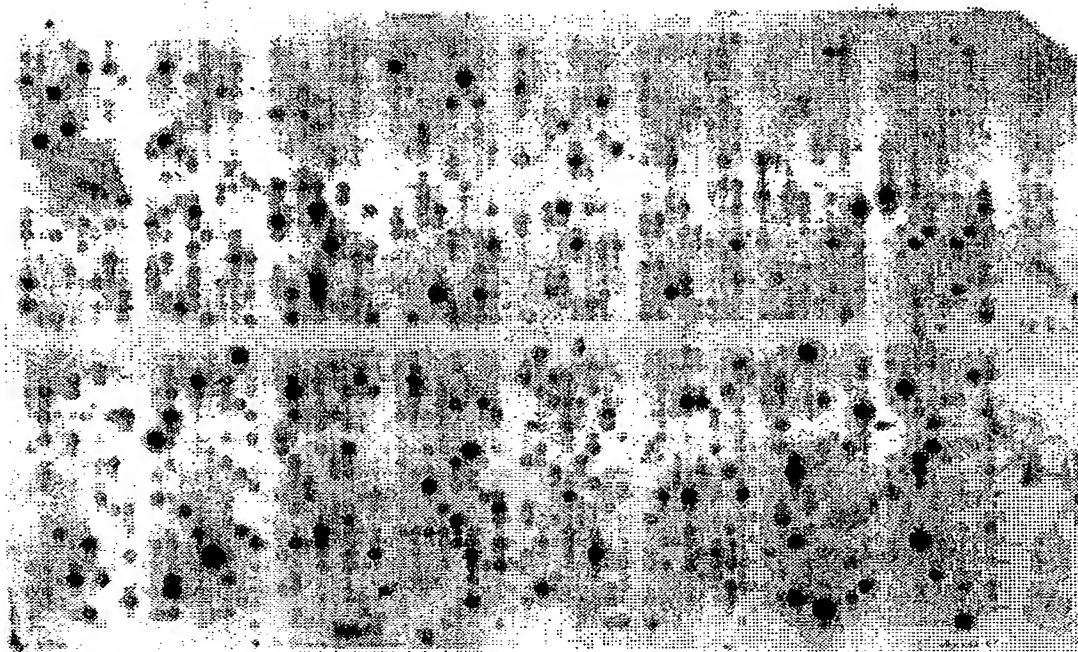
YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)
ATGGTTCAATCTATGACATCTGTCGTTAAGGCAGCTAATTTTCATTTTAGCAAGACCAACATTATCA
AAAATCATTACACCACTTGCTCAAAAATTCAGTCTTATGCAGGGTATAGAGAAATGGGATTAAAA
TTCAATGATTTACTTCTTGAAGAAACCCCAATTATGCAAACTGCTATTTAAAGATTACCTTCAGAA
TTAAATTATTCAAGAAATTTTAGAATTCTTACTGCTCATCAATTAGCTTTATCTCATCAATTATTA
CCAGCTGAAAAAGCTGTAAACCTGAAGAAGATGATAATTATTTGATTCTTATATTTTAGAAGCT
GAAAAGGAAGCTTTTGAAAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
ACGAATAAGAAACGGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)
MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
LNYSRNFRILTAHQALALSHQLLPAEKAVKPEEDDNLYLIPYILEAEKEAFEKAVLGNIDASIVINT
TNKKRTRKRKKMRRSNIEI

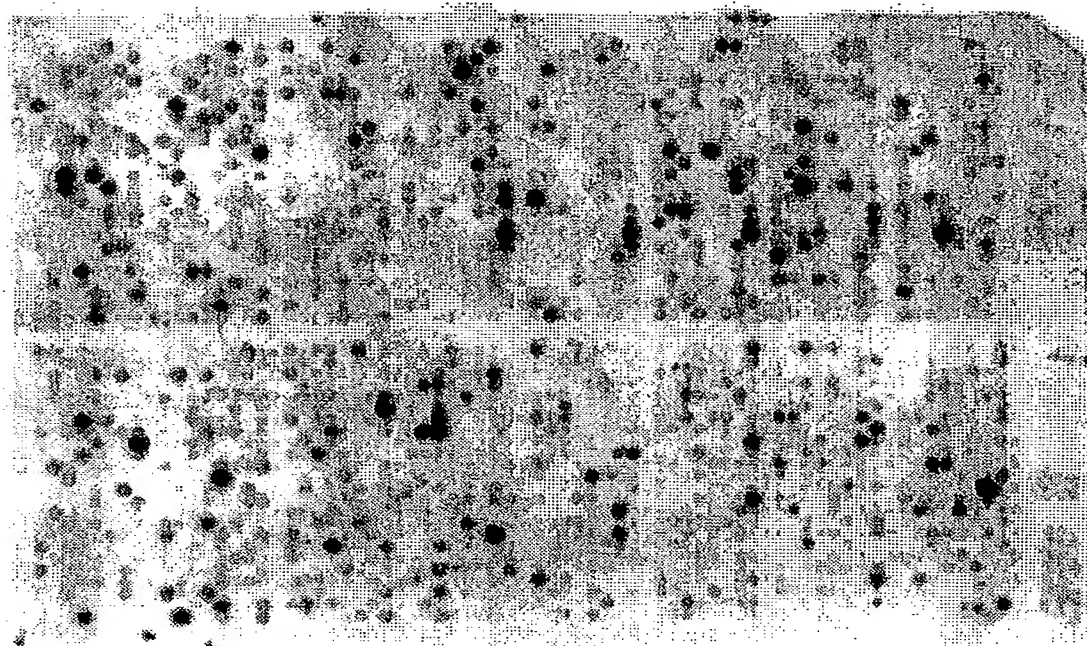
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)
CTACAATTCTTGAGAAGCCTTAACACCACCTTTACCTGATTTCTTTGGCAACAAGTTTTGATGGAT
GTTTGGTAACACACCACCTTGGGCGATGGTGACATCACCCAACAATTTGTTTAATTCTTCATCATT
TCTGATGGCCAATTGTAAGTGTCTTGGGATTATTCTGGATTTCTTGTGTCTCTGGCAGCGTTACC
AGCTAATTCCTAAAATTTTCAGCAGCTAAATATTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
ACCGATTCTCTGAGCGTAGTTACCTTTTCTTAACAATCTGTGGACTCTACCGACTGGGAAAGTCAA
ACCAGCTTTGGCTGATCTTGAAGTTGAAGCTTTTTCGGAAGTTCCTGCTTTACCTTTACCACCTGA
CAT

YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)
MSGGKGKAGTSEKASTSRSAKAGLTFPVGRVHRLLRKGNYAQRIGSGAPVYLTSVLEYLAAEILEL
AGNAARDNKKSRIPRHLQLAIRNDEELNKL LGDVTIAQGGVLPNIHQNLLPKKSGKGGVKASQEL

158/161



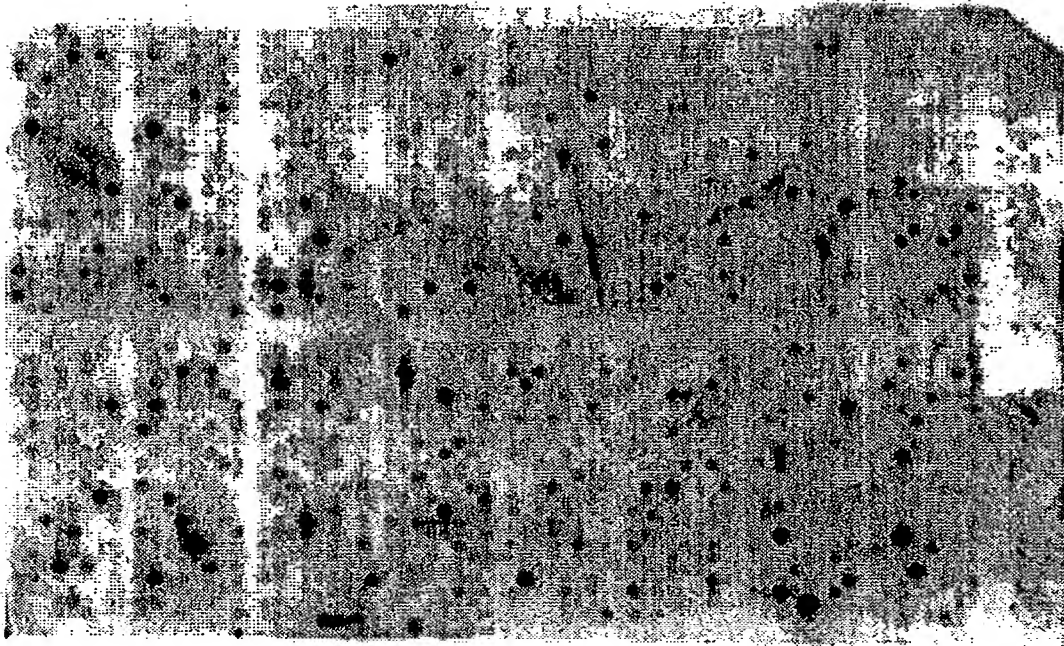
Filter I



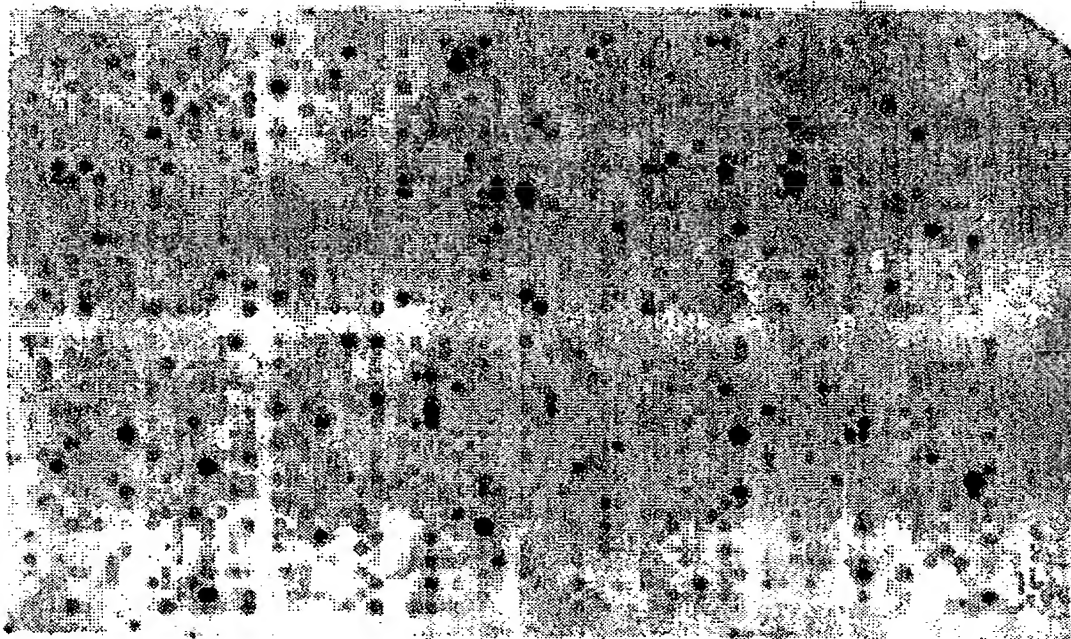
Filter II

FIG. 3A

159/161



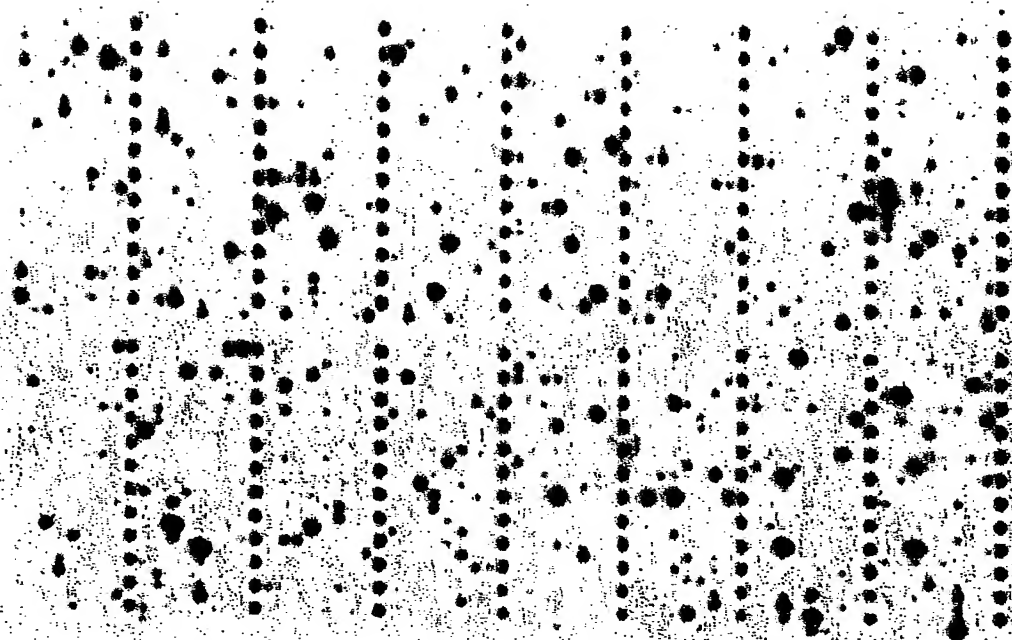
Filter I



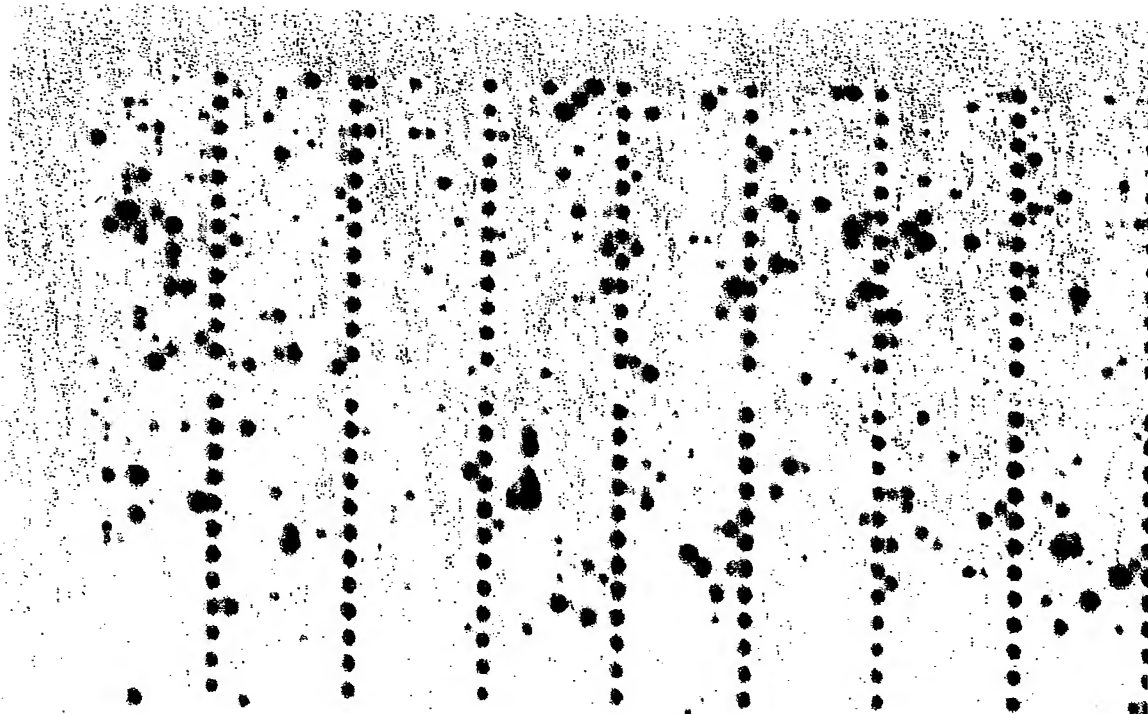
Filter II

FIG. 3B

160/161

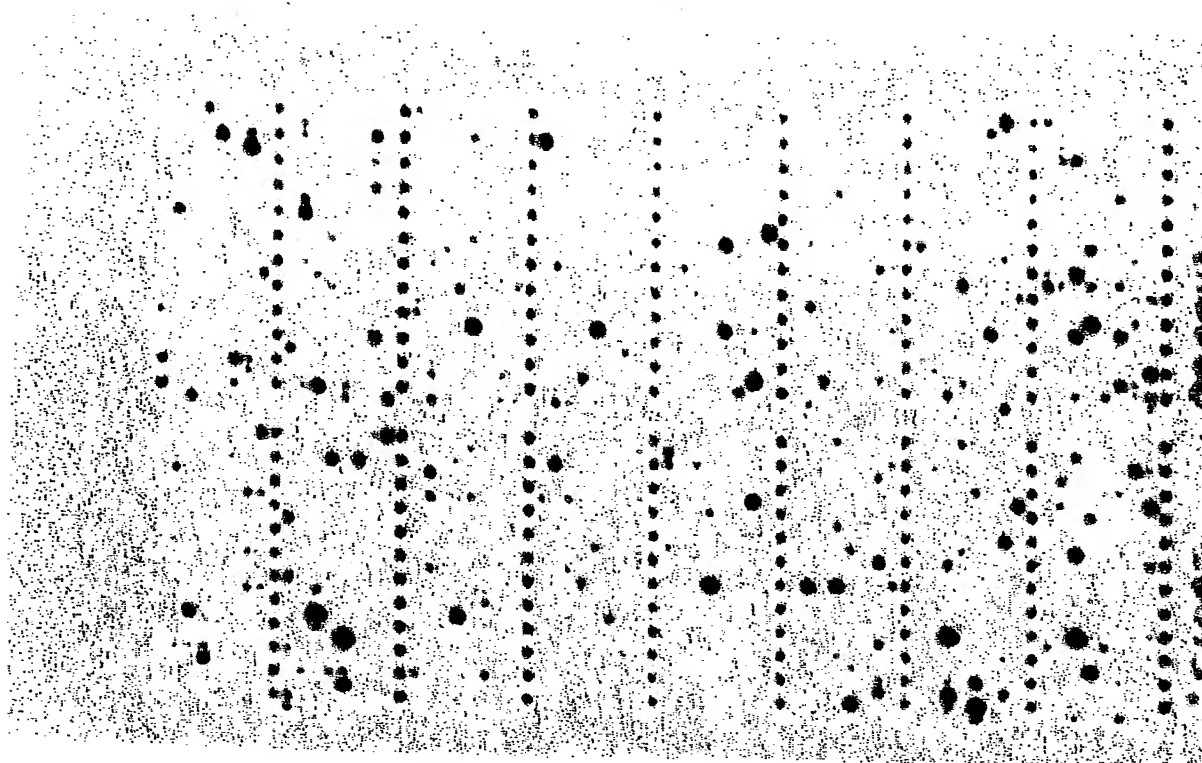


Filter I

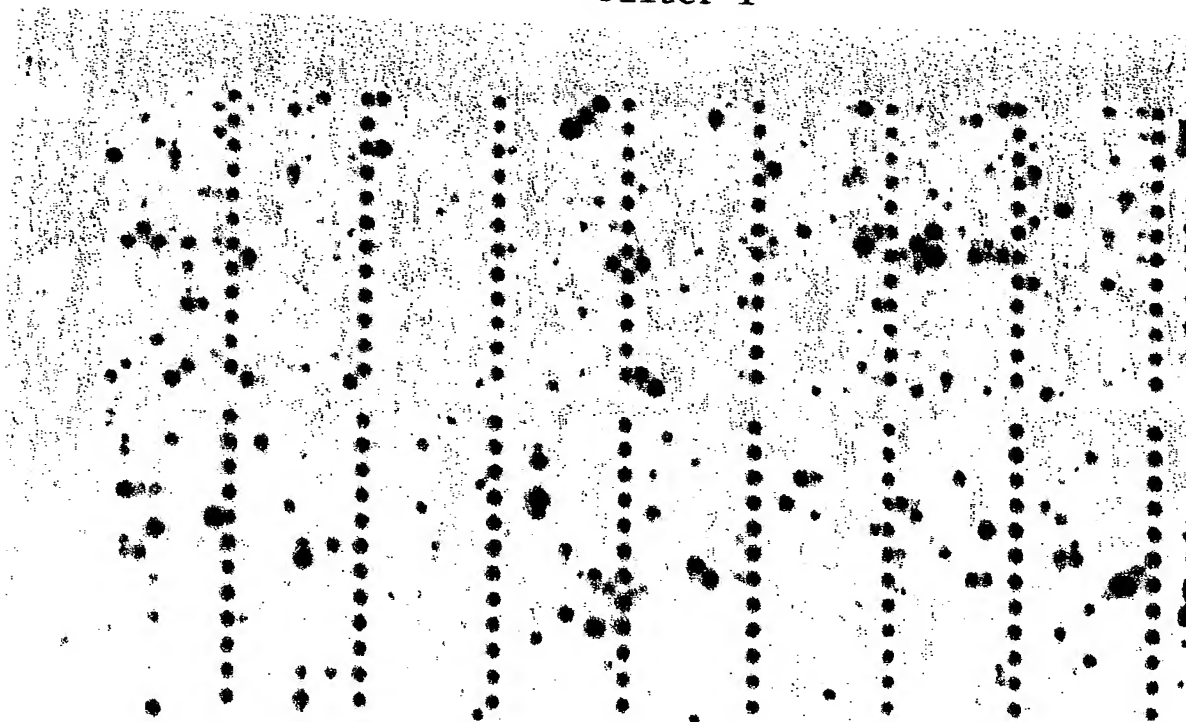


Filter II

161/161



Filter I



Filter II

Please type a plus sign (+) inside this box → ☐

PTO/SB/01 (12-97)

Approved for use through 9/30/00. OMB 0651-0032

Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no person is required to respond to a collection of information unless it contains a valid OMB control number.

DECLARATION FOR UTILITY OR DESIGN PATENT APPLICATION (37 CFR 1.63) <input checked="" type="checkbox"/> Declaration Submitted with Initial Filing OR <input type="checkbox"/> Declaration Submitted after Initial Filing (surcharge (37 CFR 1.16 (e)) required)	Attorney Docket Number	JAB 1521-PCT-USA
	First Named Inventor	Contreras, Roland Henri
	COMPLETE IF KNOWN	
	Application Number	/
	Filing Date	
	Group Art Unit	
	Examiner Name	

As a below named inventor, I hereby declare that:

My residence, post office address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

the specification of which

☐ is attached hereto

OR

☒ was filed on (MM/DD/YYYY) **07/03/2000** as United States Application Number or PCT International Application Number **PCT/BE00/00077** and was amended on (MM/DD/YYYY) (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment specifically referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or of any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application Number(s)	Country	Foreign Filing Date (MM/DD/YYYY)	Priority Not Claimed	Certified Copy Attached?	
				YES	NO
99870141.1	EPO	07/01/1999	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
			<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
			<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
			<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

☐ Additional foreign application numbers are listed on a supplemental priority data sheet PTO/SB/02B attached hereto:

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States provisional application(s) listed below.

Application Number(s)	Filing Date (MM/DD/YYYY)	
		<input type="checkbox"/> Additional provisional application numbers are listed on a supplemental priority data sheet PTO/SB/02B attached hereto.

[Page 1 of 4]

Burden Hour Statement: This form is estimated to take 0.4 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

Please type a plus sign (+) inside this box → ☐

PTO/SB/01 (12-97)
 Approved for use through 9/30/00. OMB 0651-0032
 Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
 Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it contains
 a valid OMB control number.

DECLARATION — Utility or Design Patent Application

I hereby claim the benefit under 35 U.S.C. 120 of any United States application(s), or 365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application or PCT Parent Number	Parent Filing Date (MM/DD/YYYY)	Parent Patent Number (if applicable)

☐ Additional U.S. or PCT international application numbers are listed on a supplemental priority data sheet PTO/SB/02B attached hereto.

As a named inventor, I hereby appoint the following registered practitioner(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

☐ Customer Number

OR

☒ Registered practitioner(s) name/registration number listed below

Place Customer
Number Bar Code
Label here

Name	Registration Number	Name	Registration Number
Michael Stark	32,495	Myra McCormack	36,602
Steven P. Berman	24,772	Ellen C. Coletti	34,140
Andrea L. Colby	30,194	Mary A. Appollina	34,087

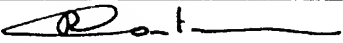
☐ Additional registered practitioner(s) named on supplemental Registered Practitioner Information sheet PTO/SB/02C attached hereto.

Direct all correspondence to: ☐ Customer Number OR ☒ Correspondence address below

Name	<u>Philip S. Johnson</u>				
Address	<u>Johnson & Johnson</u>				
Address	<u>One Johnson & Johnson Plaza</u>				
City	<u>New Brunswick</u>	State	<u>NJ</u>	ZIP	<u>08933-7003</u>
Country	<u>USA</u>	Telephone	<u>(732) 524-2359</u>	Fax	<u>(732) 524-2808</u>

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Name of Sole or First Inventor: ☐ A petition has been filed for this unsigned inventor

Given Name (first and middle [if any])		Family Name or Surname	
<u>Roland Henri</u>		<u>Contreras</u>	
Inventor's Signature			Date
Residence: City	<u>Gent</u>	State	<u>Belgium</u>
Post Office Address	<u>c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium</u>		
Post Office Address			
City	<u>Schelderode/Merelbeke</u>	ZIP	<u>9820</u>
Country	<u>Belgium</u>		

☒ Additional inventors are being named on the 1 supplemental Additional Inventor(s) sheet(s) PTO/SB/02A attached hereto

Please type a plus sign (+) inside this box → ☐

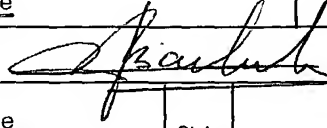
PTO/SB/02A (3-97)
Approved for use through 9/30/98. OMB 0651-0032
Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it contains a valid OMB control number.

+

DECLARATION

ADDITIONAL INVENTOR(S)
Supplemental Sheet
Page 3 of 4

Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Marianne Denise		De Backer	
Inventor's Signature			Date 10/16/2001
Residence: City	Beerse	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium		
Post Office Address			
City	San Diego	State CA	ZIP 92122 Country USA
Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Walter Herman Maria Louis		Luyten	
Inventor's Signature			Date
Residence: City	Beerse	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium		
Post Office Address			
City	Turnhout	State	ZIP 2300 Country Belgium
Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Isabelle Karin Pieter		Lenaerts	
Inventor's Signature			Date
Residence: City	Gent	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium		
Post Office Address			
City	Zoersel	State	ZIP 2980 Country Belgium

Burden Hour Statement: This form is estimated to take 0.4 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

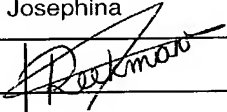
+

Burden Hour Statement: This form is estimated to take 0.4 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

Burden Hour Statement: This form is estimated to take 0.4 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

PTO/SB/02A (3-97)
Approved for use through 9/30/98. OMB 0651-0032
Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
e required to respond to a collection of information unless it contains a

DECLARATION	ADDITIONAL INVENTOR(S) Supplemental Sheet Page <u>4</u> of <u>4</u>
--------------------	---

Name of Additional Joint Inventor, if any:				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
Bart Jozef Maria				Nelissen			
Inventor's Signature					Date		
Residence: City		Beerse	State		Country	Belgium	Citizenship BE
Post Office Address		c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium					
Post Office Address							
City		Meerhout	State		ZIP	2450	Country Belgium
Name of Additional Joint Inventor, if any:				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
Rieka Josephina				Reekmans			
Inventor's Signature					Date		10/03/0
Residence: City		Gent	State		Country	Belgium	Citizenship BE
Post Office Address		c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium					
Post Office Address							
City		Wevelgem	State		ZIP	8560	Country Belgium
Name of Additional Joint Inventor, if any:				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
Inventor's Signature					Date		
Residence: City			State		Country		Citizenship
Post Office Address							
Post Office Address							
City			State		ZIP		Country

Burden Hour Statement: This form is estimated to take 0.4 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

SEQUENCE LISTING

<110> Contreras, Roland
DeBacker, Marianne
Luyten, Walter
Lanaerts, Isabelle
Nelissen, Bart
Reekmans, Rieka

<120> Cell death related drug targets in yeast and fungi

<130> JAN-002-PCT

<140> PCT/BE00/00077

<141> 2000-07-03

<150> 99870141.1

<151> 1999-07-01

<160> 484

<170> PatentIn Ver. 2.1

<210> 1

<211> 704

<212> DNA

<213> Candida albicans

<400> 1

```

aaaatttggc acttcagagc ttatcgtatc ttctcccgga gttcctcaag acttatactt 60
cagcccgttt aggaatgcat aaaagcaaat aggattcggt acaactgctg caggactctt 120
taggactgca tcaaggtaag cctcgtcgca cctaaacgca aaatgtgggt gtaacctttt 180
taattttttt cttgaacttg ttgagtcgta ataaatcggt tctgggaagt ggaaggtaat 240
aatgtaatgg aatcggcggt actcgcgtgt gcagatatca gcgacaaaaa gtgttgtagg 300
gacgtttcga taccaaaaatt tcctaaatac agcgcaggaa catcactacg ctaaacaaat 360
cgtagcgcac acatctgatc gaaaaaagac agttcccaaa acaatgacat atgaagagac 420
cagcatcaaa attttcatca ttaacagcat ggctaaaagt tattgtttta tatacccata 480
cctgattgac gaaccaagaa atgccttacc actatttatt tttggcactc ttcacctacc 540
tggccacgtc caatgttggt tcaggaagta cacaagcatg cctgccagtg ggcccaggga 600
aaaatgggat gaatgtcaac ttttataaat actcattact ggattcaaca acgtattcct 660
acccgcaata tatgacttct ggatatgcct cgaattggaa ttag 704

```

<210> 2

<211> 67

<212> PRT

<213> Candida albicans

<400> 2

Met Pro Tyr His Tyr Leu Phe Leu Ala Leu Phe Thr Tyr Leu Ala Thr
1 5 10 15

Ser Asn Val Val Ser Gly Ser Thr Gln Ala Cys Leu Pro Val Gly Pro
20 25 30

Arg Lys Asn Gly Met Asn Val Asn Phe Tyr Lys Tyr Ser Leu Leu Asp
35 40 45

Thr Gln Lys Val Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr
 340 345 350

Asn Val Cys Glu Phe Ala Asn Gln Phe Gly Val Pro Cys Met Ala Asp
 355 360 365

Gly Gly Val Gln Lys His Trp Ser Tyr Tyr Tyr Gln Ser Phe Gly Ser
 370 375 380

Trp Phe Phe Tyr Cys Tyr Asp Gly Trp Tyr Val Gly Arg Tyr Tyr Arg
 385 390 395 400

Ile Thr Arg

<210> 5
 <211> 812
 <212> DNA
 <213> Candida albicans

<400> 5
 gggagaagct tatcttactg tagaagaaaa tgggattgcg ttactccata tatattgaaa 60
 atccgttatc ttcccatca tcacgtata aatcaataaa cgaccggtta ttccactctc 120
 agcatcgatc gcaaaaaaac gtgagcttca tcacctacgg ttgtagacat tgcaagacac 180
 atctttccag ttccctccag attatttcta gagattatag gggtaggacc ggaactgctt 240
 atttaatgaa caaagttgtt aatgtcggtt aaggaaaggc cgagcaacga agaattgtga 300
 ctggcgacta cttagtctgt gatattcttt gtcattggtg caagaggaac gtaggttgga 360
 aatacttgca gagcagcaat gatgatcagc agtataagga aggaaagttt atcttagagc 420
 tgaaaaacat ttgtaaatgt acttgatgtc ttcccttggtc tgctatctag cacctctcgt 480
 ctttttagtgc ttttttagcgt atgattcttt ttaagaatct ggtctttctt ccttctattt 540
 tgattgggta tattttctatt cgtgtttcat tactgggtctg ggtaattgg gttttgggtt 600
 ggtccagttg ttttcaagta gcctttattt ttccattgtg gtattttatc ttatcgattt 660
 atactttttt ttattcaaag aaaattaaac agataatctc ttatgagcct agctactttg 720
 tttttttcta cagggccatt gacttatgcc ctgaacgagt cttactttac tttttttgta 780
 ttttcaataa tgtcgtggtt cccatgttgt aa 812

<210> 6
 <211> 103
 <212> PRT
 <213> Candida albicans

<400> 6
 Met Ile Leu Phe Lys Asn Leu Val Phe Leu Pro Ser Ile Leu Ile Gly
 1 5 10 15

Tyr Ile Ser Ile Arg Val Ser Leu Leu Val Trp Val Asn Trp Val Leu
 20 25 30

Val Trp Ser Ser Cys Phe Gln Val Ala Phe Ile Phe Ser Leu Trp Tyr
 35 40 45

Phe Ile Leu Ser Ile Tyr Thr Phe Phe Tyr Ser Lys Lys Ile Lys Gln
 50 55 60

Ile Ile Ser Tyr Glu Pro Ser Tyr Phe Val Phe Ser Tyr Arg Ala Ile
 65 70 75 80

Asp Leu Cys Pro Glu Arg Val Leu Leu Tyr Phe Phe Cys Ile Phe Asn
 85 90 95

Asn Val Val Phe Pro Met Leu
 100

<210> 7

<211> 2507

<212> DNA

<213> Candida albicans

<400> 7

```

gggaaatatc aattcccgtt tttcaatggt agtaatttgc cttcgtaaata tacggaatca 60
catagctttc attttggtcc tttgatatat ttccctacta catactcttt tcaataactc 120
tacagggtct gacattttta acttttcagggt taatgatggg gttcttacta tattctcgag 180
tcgtacagaa gttagttcag ataaaactgct tcgggtgctgc ccacttctta tcattacttc 240
aactttacct tccctatacc tgtgtgtcct tattaattca agttaatccg aggtaataga 300
ttagggtaac cttcaatgat gtcacgaaac acggatgctg caactttgcy attttttcct 360
ggaaaagaat aacaattaaa ggcagccttt cagctgagat taccagcagg tctttggaga 420
ttagcgcaag aagaagtgtg atatagtact catagaggca ggctacagac tagggaaagc 480
gtgttcaaca acaataagaa atggagacca gttcttttga gaatgctcct cctgcagcca 540
tcaatgatgc tcaggataat aatataaata cggagactaa tgaccaggaa acaaatcagc 600
aatctatcga aactagagat gcaattgaca aagaaaacgg tgtgcaaacy gaaactgggtg 660
agaactctgc aaaaaatgcc gaacaaaacy tttcttctac aaatttgaat aatgccccca 720
ccaactgtgc ttggacgat gatgttatcc caaatgctat tgttattaaa aacattccgt 780
ttgctattaa aaaagagcaa ttgttagaca ttattgaaga aatggatctt ccccttcctt 840
atgccttcaa ttaccacttt gataacggta ttttcagagg actagccttt gcgaatttca 900
ccactcctga agaaactact caagtataaa cttcttttga tggaaaggaa atcagcgagg 960
ggaaattgaa agtggaatat aaaaaaatgc ttccccaaagc tgaaagagaa agaatcgaga 1020
gggagaagag agagaaaaga ggacaattag aagaacaaca cagatcgta tctaattctt 1080
ctttggattc tttatctaaa atgagtggaa gcggaaacaa taatacttct aacaatcaat 1140
tattctcgag tctaataaac ggcattaatg ctaatagcat gatgaacagt ccaatgaata 1200
ataccattaa caataacagt tctaataaca acaatagtg taacatcatt ctgaaccaac 1260
cttcaacttc tgccccacat acttcttcat cgttgtacca aacaaacgtt aataatcaag 1320
cccagatgtc cactgagaga ttttatgcgc ctttaccatc aacttccact ttgcctctcc 1380
caccccaaca actggacttc aatgacctg acactttgga aatttatcc caattattgt 1440
tatttaagga tagagaaaag tattattacg agttggctta tcccatgggt atatccgctt 1500
cccacaagag aattatcaat gttttgtgct cgtacttagg gctagtagaa gtatatgatc 1560
caagatttat tattatcaga agaaagattc tggatcatgc taatttacia tctcatttgc 1620
aacaacaagg tcaaatgaca tctgctcatc ctttgcagcc aaactccact ggcggtcca 1680
tgaataggtc acaatcttat acaagtttgt tacaggccca tgcagcagct gcagcgaata 1740
gtattagcaa tcaggccgtt aacaattctt ccaacagcaa tactattaac agtaataacy 1800
gtaacggtaa caatgtcatc attaataaca atagcgccag ctcaacacca aaaatttctt 1860
cacagggaca attctccatg caaccaacac taacctcacc taaaatgaac atacaccata 1920
gtttctcaata caattccgca gaccaaccgc aacaacctca accacaaaca cagcaaaatg 1980
ttcagtcagc tgcgcaacaa caacaatctt ttttaagaca acaagctact ttaacaccat 2040
cctcaagaat tccatccggt tattctgcca accattatca aatcaattcc gttaatccct 2100
tactgagaaa ttctcaaatt tcacctccaa attcacaat cccaatcaac agccaaaccc 2160
tatcccaagc gcaaccacca gcacagtcac aaactcaaca acgggtacca gtggcatacc 2220
aaaatgcttc attgtcttcc cagcagttgt acaaccttaa cggcccatct tcagcaaaact 2280
cacagtccca actgcttcca cagcacacaa atgggtcagc acattctaata ttctcatatc 2340

```

<400>	8																		
Met	Glu	Thr	Ser	Ser	Phe	Glu	Asn	Ala	Pro	Pro	Ala	Ala	Ile	Asn	Asp				
1				5					10					15					
Ala	Gln	Asp	Asn	Asn	Ile	Asn	Thr	Glu	Thr	Asn	Asp	Gln	Glu	Thr	Asn				
			20					25					30						
Gln	Gln	Ser	Ile	Glu	Thr	Arg	Asp	Ala	Ile	Asp	Lys	Glu	Asn	Gly	Val				
		35					40					45							
Gln	Thr	Glu	Thr	Gly	Glu	Asn	Ser	Ala	Lys	Asn	Ala	Glu	Gln	Asn	Val				
	50					55					60								
Ser	Ser	Thr	Asn	Leu	Asn	Asn	Ala	Pro	Thr	Asn	Gly	Ala	Leu	Asp	Asp				
	65				70					75					80				
Asp	Val	Ile	Pro	Asn	Ala	Ile	Val	Ile	Lys	Asn	Ile	Pro	Phe	Ala	Ile				
				85					90						95				
Lys	Lys	Glu	Gln	Leu	Leu	Asp	Ile	Ile	Glu	Glu	Met	Asp	Leu	Pro	Leu				
			100					105					110						
Pro	Tyr	Ala	Phe	Asn	Tyr	His	Phe	Asp	Asn	Gly	Ile	Phe	Arg	Gly	Leu				
		115					120					125							
Ala	Phe	Ala	Asn	Phe	Thr	Thr	Pro	Glu	Glu	Thr	Thr	Gln	Val	Ile	Thr				
	130					135						140							
Ser	Leu	Asn	Gly	Lys	Glu	Ile	Ser	Gly	Arg	Lys	Leu	Lys	Val	Glu	Tyr				
	145				150					155					160				
Lys	Lys	Met	Leu	Pro	Gln	Ala	Glu	Arg	Glu	Arg	Ile	Glu	Arg	Glu	Lys				
				165					170					175					
Arg	Glu	Lys	Arg	Gly	Gln	Leu	Glu	Glu	Gln	His	Arg	Ser	Ser	Ser	Asn				
			180					185					190						
Leu	Ser	Leu	Asp	Ser	Leu	Ser	Lys	Met	Ser	Gly	Ser	Gly	Asn	Asn	Asn				
		195					200					205							
Thr	Ser	Asn	Asn	Gln	Leu	Phe	Ser	Thr	Leu	Met	Asn	Gly	Ile	Asn	Ala				
	210					215						220							
Asn	Ser	Met	Met	Asn	Ser	Pro	Met	Asn	Asn	Thr	Ile	Asn	Asn	Asn	Ser				
	225				230					235					240				
Ser	Asn	Asn	Asn	Asn	Ser	Gly	Asn	Ile	Ile	Leu	Asn	Gln	Pro	Ser	Leu				

	245		250		255										
Ser	Ala	Gln	His	Thr	Ser	Ser	Ser	Leu	Tyr	Gln	Thr	Asn	Val	Asn	Asn
	260							265					270		
Gln	Ala	Gln	Met	Ser	Thr	Glu	Arg	Phe	Tyr	Ala	Pro	Leu	Pro	Ser	Thr
	275						280					285			
Ser	Thr	Leu	Pro	Leu	Pro	Pro	Gln	Gln	Leu	Asp	Phe	Asn	Asp	Pro	Asp
	290					295					300				
Thr	Leu	Glu	Ile	Tyr	Ser	Gln	Leu	Leu	Leu	Phe	Lys	Asp	Arg	Glu	Lys
305					310					315					320
Tyr	Tyr	Tyr	Glu	Leu	Ala	Tyr	Pro	Met	Gly	Ile	Ser	Ala	Ser	His	Lys
			325						330					335	
Arg	Ile	Ile	Asn	Val	Leu	Cys	Ser	Tyr	Leu	Gly	Leu	Val	Glu	Val	Tyr
			340					345					350		
Asp	Pro	Arg	Phe	Ile	Ile	Ile	Arg	Arg	Lys	Ile	Leu	Asp	His	Ala	Asn
		355					360					365			
Leu	Gln	Ser	His	Leu	Gln	Gln	Gln	Gly	Gln	Met	Thr	Ser	Ala	His	Pro
	370					375					380				
Leu	Gln	Pro	Asn	Ser	Thr	Gly	Gly	Ser	Met	Asn	Arg	Ser	Gln	Ser	Tyr
385					390					395					400
Thr	Ser	Leu	Leu	Gln	Ala	His	Ala	Ala	Ala	Ala	Ala	Asn	Ser	Ile	Ser
				405				410						415	
Asn	Gln	Ala	Val	Asn	Asn	Ser	Ser	Asn	Ser	Asn	Thr	Ile	Asn	Ser	Asn
			420					425					430		
Asn	Gly	Asn	Gly	Asn	Asn	Val	Ile	Ile	Asn	Asn	Asn	Ser	Ala	Ser	Ser
	435						440					445			
Thr	Pro	Lys	Ile	Ser	Ser	Gln	Gly	Gln	Phe	Ser	Met	Gln	Pro	Thr	Leu
	450					455					460				
Thr	Ser	Pro	Lys	Met	Asn	Ile	His	His	Ser	Ser	Gln	Tyr	Asn	Ser	Ala
465					470					475					480
Asp	Gln	Pro	Gln	Gln	Pro	Gln	Pro	Gln	Thr	Gln	Gln	Asn	Val	Gln	Ser
					485				490					495	
Ala	Ala	Gln	Gln	Gln	Gln	Ser	Phe	Leu	Arg	Gln	Gln	Ala	Thr	Leu	Thr
			500					505					510		
Pro	Ser	Ser	Arg	Ile	Pro	Ser	Gly	Tyr	Ser	Ala	Asn	His	Tyr	Gln	Ile
		515					520					525			
Asn	Ser	Val	Asn	Pro	Leu	Leu	Arg	Asn	Ser	Gln	Ile	Ser	Pro	Pro	Asn
	530					535					540				
Ser	Gln	Ile	Pro	Ile	Asn	Ser	Gln	Thr	Leu	Ser	Gln	Ala	Gln	Pro	Pro

<400>	9							
atcccaagaa	gaagattaga	ctgattttta	cctacccttc	caccgtcgga	agaaacactt	60		
ctgaagtgtt	aagggtaatc	gacgccttgc	aattgactga	caaggagggc	gtagtaactc	120		
caattaattg	gcagccagct	gacgatgtca	ttattcctcc	ctctgtctcc	aatgatgagg	180		
cgaaggctaa	atttgggtcaa	tttaatgaaa	ttaaacccta	tttaagattc	accaagtcca	240		
aataagcttt	gaaataaacg	acttttactat	atacagggtat	atgaagtatc	tctaactcaa	300		
acttttatct	atcttttcatt	cttatttatat	ctcatctcgt	acgaagggcc	gtcattgga	360		
tcatttttct	ttacataaccg	taaaggaaatg	gcgttaaaaa	tatatatatg	aaaatgcattg	420		
taataaaactc	tctgcagaaa	ccttaaatgtc	aaagggtccg	tatacagatt	atattggctc	480		
tgcgtatacg	cattctctgtc	atgggtgaagg	ataatcgaga	ttctgaccaa	gaccaagatt	540		
ttagtctctgc	tcacatgaaa	agacaaccgg	agcagcaaca	gttgcaacag	caccagttcc	600		
caagtaagaa	acaacgaata	tctcaccatg	atgacagtca	tcaaatcaac	catagaccag	660		
ttacctcatg	tacacattgt	agacagcaca	aaatcaaatg	cgatgctagt	caaaatttcc	720		
ctcatccttg	ctccagatgc	gaaaaaattg	gtctccactg	tgaaatcaat	cctcaattca	780		
ggcctaagaa	gggctcacag	ttgcaactac	tgagacaaga	tgtggatgaa	atcaaatcta	840		
aactgcatac	tcttctggcc	aatgacagcg	ttttcgttca	tcttttaca	cagattccca	900		
tggcgcaatg	ctcttttgaat	aagctcaatc	tgcattccaac	tccaactccg	ggtactatta	960		
tccctaacc	agattcttct	ccttcctcag	gtttctccaac	ttcttccg	gctcaacgag	1020		
attctaagg	ttcagttcaa	acttattttgt	ccagggaacc	ccaactctta	caagcaaata	1080		
agggcagcaa	tacgaataaa	tttaaagcaa	ataatgaagc	atcttctcac	atgacgttgc	1140		
gcgcattcttc	tttagcgcaa	gattcgaaag	gcttggttgc	aacagagcca	aataagctgc	1200		
ccccgctgct	aaatgactca	gcattgcta	ataattcaaa	agaatcttta	cctcctgctt	1260		
tgcaaattggc	tttttataag	aacaactctg	caggtaacc	tccgaacggc	cccttctctc	1320		
caattcaaaa	aacataattcc	cctcatacta	cgctgacac	cgttacaacg	acaacaaata	1380		
agccaccatt	tgcagacaaca	agccacgtag	caacaataaa	caatgcagat	aggacgaaga	1440		
cgcggtagt	agccaccacc	acgactatgc	cattattggc	ttcgccgcat	gcaaatgtag	1500		
atgaqtttqt	actggggcat	attagtattt	ccattgaaaa	agcgaataga	ttacaccata	1560		

```

<400> 10
Met Val Lys Asp Asn Arg Asp Ser Asp Gln Asp Gln Asp Phe Ser Ser
  1          5          10          15
Ala His Met Lys Arg Gln Pro Glu Gln Gln Gln Leu Gln Gln His Gln
  20          25          30
Phe Pro Ser Lys Lys Gln Arg Ile Ser His His Asp Asp Ser His Gln
  35          40          45
Ile Asn His Arg Pro Val Thr Ser Cys Thr His Cys Arg Gln His Lys
  50          55          60
Ile Lys Cys Asp Ala Ser Gln Asn Phe Pro His Pro Cys Ser Arg Cys

```


370					375					380					
Val 385	Met	Leu	Thr	Ala	Cys 390	Leu	Ser	Asp	Pro	Glu 395	Pro	Thr	Met	Tyr	Cys 400
Lys	Leu	Ser	Ser	Leu 405	Ile	Lys	Gln	Leu	Ala 410	Ile	Glu	Thr	Cys	Trp 415	Ile
Arg	Thr	Pro	Arg	Ser 420	Thr	His	Ile	Ser	Gln 425	Ala	Leu	Leu	Ile	Leu	Cys
Ile	Trp	Pro	Leu	Pro	Asn	Gln	Lys 440	Val	Leu	Asp	Asp	Cys 445	Ser	Tyr	Arg
Phe	Val 450	Gly	Leu	Ala	Lys	Ser 455	Leu	Ser	Tyr	Gln	Leu 460	Gly	Leu	His	Arg
Gly 465	Glu	Phe	Ile	Ser	Glu 470	Phe	Thr	Arg	Thr	Gln 475	Thr	Ser	Met	Pro	Asn 480
Ala	Glu	Lys	Trp	Arg 485	Thr	Arg	Thr	Trp	Leu 490	Gly	Ile	Phe	Phe	Ala 495	Glu
Leu	Cys	Trp	Ala 500	Ser	Ile	Leu	Gly	Leu 505	Pro	Pro	Thr	Ser	Gln 510	Thr	Asp
Tyr	Leu 515	Leu	Glu	Lys	Ala	Leu	Ser 520	Cys	Gly	Asp	Glu 525	Glu	Ser	Glu	Glu
Asp	Asn 530	Asn	Asp	Ser	Ile	Asp 535	Asn	Asn	Asn	Asn 540	Asp	Lys	Arg	Asn	Lys
Lys 545	Asp	Glu	Pro	His	Val 550	Glu	Ser	Lys	Tyr	Lys 555	Leu	Pro	Gly	Ser	Phe 560
Arg	Arg	Leu	Leu	Ser 565	Leu	Ala	Asn	Phe	Gln 570	Ala	Lys	Leu	Ser	His 575	Ile
Ile	Gly	Ser	Ser 580	Thr	Ser	Ser	Pro	Asp 585	Gly	Leu	Leu	Glu	Pro 590	Lys	Tyr
Arg	Ala 595	Glu	Thr	Leu	Ser	Ile	Leu 600	Gly	Lys	Glu	Leu	Asp 605	Leu	Leu	Ala
Lys	Thr 610	Leu	Asn	Phe	Gln	Ser 615	Asp	Asp	Thr	Val	Asn 620	Ile	Tyr	Phe	Leu
Tyr 625	Val	Lys	Leu	Thr	Val 630	Cys	Cys	Phe	Ala	Phe 635	Leu	Pro	Glu	Thr	Pro 640
Pro	Thr	Asp	Gln	Ile 645	Pro	Tyr	Val	Thr	Glu 650	Ala	Tyr	Leu	Thr	Ala 655	Thr
Lys	Ile	Val	Thr 660	Leu	Leu	Asn	Asn 665	Leu	Leu	Glu	Thr	His 670	Gln	Leu	Ile
Glu	Leu	Pro	Ile	Tyr	Ile	Arg	Gln	Ala	Ala	Thr	Phe	Ser	Ala	Leu	Ile

675	680	685
Leu Phe Lys Leu Gln Leu Thr Pro Leu Leu Pro Asp Lys Tyr Phe Asp 690 695 700		
Ser Ala Arg Gln Ser Val Val Thr Ile His Arg Leu Tyr Arg Asn Gln 705 710 715 720		
Leu Thr Ala Trp Ala Thr Ser Val Glu Asn Asp Ile Ser Arg Thr Ala 725 730 735		
Ser Met Leu Glu Lys Leu Asn Phe Val Leu Ile Met His Pro Glu Val 740 745 750		
Phe Val Glu Glu Asp Gly Ile Ile Ser Arg Met Arg Ser His Leu Thr 755 760 765		
Gly Ser Leu Phe Tyr Asp Leu Val Trp Cys Val His Glu Ala Arg Arg 770 775 780		
Arg Glu Met Asp Pro Glu Tyr Asn Lys Gln Ala Leu Glu Lys Ala Ala 785 790 795 800		
Lys Lys Arg Lys Phe Ser Ser Asn Gly Ile Tyr Asn Gly Thr Ser Ser 805 810 815		
Thr Gly Gly Ile Thr Asp Arg Lys Leu Tyr Pro Leu Pro Leu Tyr Asn 820 825 830		
His Ile Ser Arg Asp Asp Phe Glu Thr Val Thr Lys Thr Thr Pro Ser 835 840 845		
Gly Thr Thr Val Thr Thr Leu Val Pro Thr Lys Asn Ala Leu Lys Gln 850 855 860		
Ala Glu Lys Leu Ala Lys Thr Asn Asn Gly Asp Ser Asp Gly Ser Ile 865 870 875 880		
Met Glu Ile Asn Gly Ile Pro Leu Ser Met Leu Gly Glu Thr Gly Ser 885 890 895		
Val Lys Phe Gln Ser Leu Phe Ala Asn Thr Ser Asn Ser Asn Asp Tyr 900 905 910		
Asn Asn Asn Arg Thr Leu Leu Asp Ala Ser Asn Asp Ile Ser Ile Pro 915 920 925		
Ser Asn Ser Ile Tyr Pro Val Ala Ser Val Pro Ala Ser Asn Asn Asn 930 935 940		
Pro Gln Ser Thr Lys Val Asp Tyr Tyr Ser Asn Gly Pro Ser Val Ile 945 950 955 960		
Pro Asp Leu Ser Met Lys Arg Ser Val Ser Thr Pro Val Asn His Phe 965 970 975		
Pro Ala Ser Val Pro Gly Leu Arg Asn His Pro Val Gly Asn Leu Ser		


```

<400> 12
Met Lys Ser Thr Phe Lys Ser Glu Tyr Pro Phe Glu Lys Arg Lys Ala
  1             5             10             15
Glu Ser Glu Arg Ile Ala Asp Arg Phe Lys Asn Arg Ile Pro Val Ile
          20             25             30
Cys Glu Lys Ala Glu Lys Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys
      35             40             45

```

14

Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile
50 55 60

Arg Lys Arg Ile Met Leu Pro Pro Glu Lys Ala Ile Phe Ile Phe Val
65 70 75 80

Asn Asp Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr Gln
85 90 95

Glu His Lys Asp Lys Asp Gly Phe Leu Tyr Val Thr Tyr Ser Gly Glu
100 105 110

Asn Thr Phe Gly Arg
115

<210> 13

<211> 1145

<212> DNA

<213> Candida albicans

<400> 13

```
gcagcagcaa ctccgtgtgt acccctaact ccgtgtgtac ccctaaagaa ccttgectgt 60
caagggtgcat tgttggatcg gaatagtaac cgtctttaca tgaacatcca caaccaacga 120
aagtgcctttt tcaagcattg cttgatttct agaaagatcg atgggtattc cctccccctt 180
atgCGTCCaa aaatataggg tgctcgtaac agtaaggat tgcgacttag cgtgctcgca 240
acacaaaatt aagtaatatg cgagtttttag atgtccttgc ggatctatgc acgttcttga 300
gtgggtatttc ataacaacgg ttctttttca cccttattcc taaacatata aataggacct 360
ccattagtta gagatctgtt tttaatccat tcacctttca ttctactctc ttataactaat 420
aaaaccaccg ataaagatat atcagatctc tattaataca ggtatccaaa aaagcaaaca 480
aacaactaa acaaattaac atgtcattta acagtccatt ttttgatttc tttgacaaca 540
tcaacaacga agttgatgcc tttaacagat tgctgggtga aggcggctta agaggctacg 600
caccaagacg tcagtttagca aacacaccgg caaaggattc tactggcaag gaagttgcta 660
gaccaaataa ctatgctggc gctctttatg atcccagaga tgaaacctta gatgattggt 720
tcgacaatga cttgtccctg ttcccatctg gtttcgggtt ccctagaagt gtcgcagttc 780
cagttgatat tttggaccat gacaacaact acgagttgaa agtcgtgggt cctgggtgtca 840
aaagcaagaa ggacattgat attgagtacc atcaaaacaa gaaccaaatt ttgggtttctg 900
gtgaaattcc atctaccttg aatgaagaga gtaaagacaa ggtcaaggtc aaggagagca 960
gctctggtaa gttcaagaga gtcatcactt tgccagacta cccagggtgtg gatgcagaca 1020
acattaaagc agactacgca aatgggtgtt tgacattaac agttccaaa ttgaagcctc 1080
agaaggatgg taagaaccac gtcaagaaga ttgaggtttc ttctcaagaa tcgtggggta 1140
actaa 1145
```

<210> 14

<211> 214

<212> PRT

<213> Candida albicans

<400> 14

Met Ser Phe Asn Ser Pro Phe Phe Asp Phe Phe Asp Asn Ile Asn Asn
1 5 10 15

Glu Val Asp Ala Phe Asn Arg Leu Leu Gly Glu Gly Gly Leu Arg Gly
20 25 30

<400> 15						
agaaggatgg	taagaaccac	gtcaagaaga	ttgaggtttc	ttctcaagaa	tcgtggggta	60
actaaagtga	cctggctcta	tagtgttgtc	cctctcgcga	ggaccattgt	tgcttgcata	120
tggcttgaaa	catatgtcat	cacatctgag	cgattttacc	tcttagaatt	agtttagata	180
tatatgagtt	gatgaataaa	tagttataaa	aacttgcttt	ggcttcgata	tataacggtt	240
atttttgcac	aagttttaac	gaaggaaatc	aacctcgttc	ttgtaattac	caaaactctc	300
aacaacgcgc	tgttggagg	atctctatgg	atgtggcgctg	aaatatggat	gtcttgcccta	360
cttctacttc	tgggaaaggc	atttttactc	gatcgcggtta	atatatgcat	caagaaaata	420
aaaaataaaa	cgcgaagagc	taaaaaaaaa	aaagaaaacc	tactataaat	aaccgattag	480
aatcgagttt	ttgtattgaa	atggcggttaa	taagcggttaa	acctcgacga	agagagaaga	540
tcctacagga	ggtaaaaaaac	agctcggtat	atcaaaccgt	atttgattcc	ggtactactc	600
aaatgcagat	accgaaatat	gagaacaagc	cattcaagcc	tccaagaagg	gttggatcaa	660
ataagtacac	acaactcaaaa	ccaaccgcc	ctgcagtcac	aacagcccct	atatctaagg	720
ccaaagttag	tctcaactttg	aaaagaagca	tttcggcggg	acctacttta	aatcttgcca	780

```

agaagccgaa taatctgtcc tcaaatagaaa acactagata ttttactatc atgtacagga 840
agcctactac caaaaaagcac aagacttgga gtggtgatgg ctacgctacc ttaaaagcca 900
gtagcgataa gttatgcttt tataacgaag cagggaaatt tcttggttca agtatgctac 960
caagtgattc agatttctctc ttcgaaactc ttttcaaagc aggctccaat gaagtacaat 1020
tggtattacga attgaaggaa aatgcagaaa tacgtagcgc caaagaagcc ttatcacaaa 1080
acatgggaaa tcccagccca ccgaccacaa gcacaacaga aacagtgcct tctacgaaga 1140
atgacggtgg caaataccaa atgcctctgt ctcagctgtt ttcactaaac actgtgaaaa 1200
gattcaaatac agtaacaaag caaacaatg aacacatgac cacagtacct aaaaccagtc 1260
aaaattccaa agccaaaaaa tattatccag tatttgatgt caacaaaatc gataatccta 1320
tagtaatgaa caaaaatgca gccgctgaag ttgacgtaat tgttgatcca ttactgggca 1380
aattcttgcg ccctcatcag agggaagggg tgaagttcat gtatgattgc ttaatgggct 1440
tggaagacc aactattgaa aatccggata tcgattgtac tactaaaagt ttagtggttag 1500
aaaatgactc agatattagt ggatgccttt tggtgatga tatgggttta ggtaaaacac 1560
taatgagtat aactttgatt tggacattaa ttaggcaaac tccttttgca tcaaaagttt 1620
catgttcgca atcaggcata ccattaactg gactttgtaa gaagatttta gtcgtttgtc 1680
ccgttacttt aatgaaaaaa tggaaaagag aatttggaat atggttaaat ttgtcaagaa 1740
taggtgtttt gacattaagc tcaaggaatt ctctgatata ggataaaatg gctgtcagaa 1800
atttttttaa agtgcaacga acttatcaag tcttgattat tggctacgaa aaactcctga 1860
gtgtttctga agaattagag aaaaataaac atttgattga catgctgggtg tgtgacgaag 1920
gccatcgact aaaaaacggg gcttctaaaa ttttaataac gctgaagagt ttagacataa 1980
gaagggaagt tttgcttacg ggaactccta taaaaaatga tcttaatgag tttttcacta 2040
ttatagattt cataaaccca ggaatccttg gaagcttcgc ttctttcaa agaagattca 2100
ttatccctat aactagagcc agagacactg caaacagata caacgaagaa ttgttgaaa 2160
agggggaaga aaggtcaaaa gagatgatag aaattacgaa aagatttatt ttgagacgaa 2220
caaatgcatg tttagaaaag taccttctctc caaagacgga tataatttta ttctgtaaac 2280
catacagcca acagatattg gcattcaaag atattttgca gggcgcacgt ttagattttg 2340
gacaattgac gttcagttct tcgctaggac taataacatt actgaaaaag gtttgtaact 2400
ctcctggatt ggttggtcca gatccctatt acaaatcaca tataaaggat acccaatctc 2460
aggacagcta tagtcgttct ttgaactctg gtaagttaaa ggtattaatg acattactag 2520
aaggtattag gaagggtacc aaggagaagg tcgtcgtagt gtctaactac actcaaacat 2580
tggatataat tgaaaatttg atgaatatgg ctgggatgtc acattgcaga ctgcacggtt 2640
ccatacctgc taaacaaagg gactctatcg tcacatcttt caatcggaat ccagccatat 2700
ttggattctt gttgagtcca aaatcgagg gtagtaggatt gaatctagtc ggtcgttcgc 2760
gacttatttt atttgataat gattggaatc cttcagtaga tttgcaagcg atgtcacgaa 2820
ttcatagaga tgggtcaaaaa aagccgtgct tcatatatag acttgtcaca actgggtgta 2880
tcgatgagaa aatattgcaa aggcaattaa tgaagaacag tttgagccaa aaatttctag 2940
gtgactcgga gatgagaat aaagaatctt ctaatgatga tcttttcaat aaagaggact 3000
tgaaggacct gttttctgtc catacagata ccaagagtaa cacacatgac ttaatttggt 3060
cttgcatgag ttttaggtgag gaaattgaa atcctgaaac aaatcaacag cagaacaccg 3120
tagagctgag aaagcgtagc actacgacat ggacaagtgc gctggattta caaaagaaaa 3180
tgaatgaagc agccaccaac gatgatgcca aaaagtcaca atacattagg caatgtctcg 3240
ttcattataa gcatatcgat ccagcaagac aagatgaatt atttgatgag gttatcacag 3300
attcgttcac cgaattgaaa gatagtatta cttttgcgtt tgtaaagccc ggcgagatat 3360
gtctcagaga acaatga 3377

```

<210> 16

<211> 958

<212> PRT

<213> Candida albicans

<400> 16

Met Ala Val Ile Ser Val Lys Pro Arg Arg Arg Glu Lys Ile Leu Gln
1 5 10 15

Glu Val Lys Asn Ser Ser Val Tyr Gln Thr Val Phe Asp Ser Gly Thr
20 25 30

Thr Gln Met Gln Ile Pro Lys Tyr Glu Asn Lys Pro Phe Lys Pro Pro
 35 40 45
 Arg Arg Val Gly Ser Asn Lys Tyr Thr Gln Leu Lys Pro Thr Ala Thr
 50 55 60
 Ala Val Thr Thr Ala Pro Ile Ser Lys Ala Lys Val Thr Val Asn Leu
 65 70 75 80
 Lys Arg Ser Ile Ser Ala Gly Pro Thr Leu Asn Leu Ala Lys Lys Pro
 85 90 95
 Asn Asn Leu Ser Ser Asn Glu Asn Thr Arg Tyr Phe Thr Ile Met Tyr
 100 105 110
 Arg Lys Pro Thr Thr Lys Lys His Lys Thr Trp Ser Gly Asp Gly Tyr
 115 120 125
 Ala Thr Leu Lys Ala Ser Ser Asp Lys Leu Cys Phe Tyr Asn Glu Ala
 130 135 140
 Gly Lys Phe Leu Gly Ser Ser Met Leu Pro Ser Asp Ser Asp Ser Leu
 145 150 155 160
 Phe Glu Thr Leu Phe Lys Ala Gly Ser Asn Glu Val Gln Leu Asp Tyr
 165 170 175
 Glu Leu Lys Glu Asn Ala Glu Ile Arg Ser Ala Lys Glu Ala Leu Ser
 180 185 190
 Gln Asn Met Gly Asn Pro Ser Pro Pro Thr Thr Ser Thr Thr Glu Thr
 195 200 205
 Val Pro Ser Thr Lys Asn Asp Gly Gly Lys Tyr Gln Met Pro Leu Ser
 210 215 220
 Gln Leu Phe Ser Leu Asn Thr Val Lys Arg Phe Lys Ser Val Thr Lys
 225 230 235 240
 Gln Thr Asn Glu His Met Thr Thr Val Pro Lys Thr Ser Gln Asn Ser
 245 250 255
 Lys Ala Lys Lys Tyr Tyr Pro Val Phe Asp Val Asn Lys Ile Asp Asn
 260 265 270
 Pro Ile Val Met Asn Lys Asn Ala Ala Ala Glu Val Asp Val Ile Val
 275 280 285
 Asp Pro Leu Leu Gly Lys Phe Leu Arg Pro His Gln Arg Glu Gly Val
 290 295 300
 Lys Phe Met Tyr Asp Cys Leu Met Gly Leu Ala Arg Pro Thr Ile Glu
 305 310 315 320
 Asn Pro Asp Ile Asp Cys Thr Thr Lys Ser Leu Val Leu Glu Asn Asp
 325 330 335

Asp Pro Tyr Tyr Lys Ser His Ile Lys Asp Thr Gln Ser Gln Asp Ser
 645 650 655
 Tyr Ser Arg Ser Leu Asn Ser Gly Lys Leu Lys Val Leu Met Thr Leu
 660 665 670
 Leu Glu Gly Ile Arg Lys Gly Thr Lys Glu Lys Val Val Val Val Ser
 675 680 685
 Asn Tyr Thr Gln Thr Leu Asp Ile Ile Glu Asn Leu Met Asn Met Ala
 690 695 700
 Gly Met Ser His Cys Arg Leu Asp Gly Ser Ile Pro Ala Lys Gln Arg
 705 710 715 720
 Asp Ser Ile Val Thr Ser Phe Asn Arg Asn Pro Ala Ile Phe Gly Phe
 725 730 735
 Leu Leu Ser Ala Lys Ser Gly Gly Val Gly Leu Asn Leu Val Gly Arg
 740 745 750
 Ser Arg Leu Ile Leu Phe Asp Asn Asp Trp Asn Pro Ser Val Asp Leu
 755 760 765
 Gln Ala Met Ser Arg Ile His Arg Asp Gly Gln Lys Lys Pro Cys Phe
 770 775 780
 Ile Tyr Arg Leu Val Thr Thr Gly Cys Ile Asp Glu Lys Ile Leu Gln
 785 790 795 800
 Arg Gln Leu Met Lys Asn Ser Leu Ser Gln Lys Phe Leu Gly Asp Ser
 805 810 815
 Glu Met Arg Asn Lys Glu Ser Ser Asn Asp Asp Leu Phe Asn Lys Glu
 820 825 830
 Asp Leu Lys Asp Leu Phe Ser Val His Thr Asp Thr Lys Ser Asn Thr
 835 840 845
 His Asp Leu Ile Cys Ser Cys Asp Gly Leu Gly Glu Glu Ile Glu Tyr
 850 855 860
 Pro Glu Thr Asn Gln Gln Gln Asn Thr Val Glu Leu Arg Lys Arg Ser
 865 870 875 880
 Thr Thr Thr Trp Thr Ser Ala Leu Asp Leu Gln Lys Lys Met Asn Glu
 885 890 895
 Ala Ala Thr Asn Asp Asp Ala Lys Lys Ser Gln Tyr Ile Arg Gln Cys
 900 905 910
 Leu Val His Tyr Lys His Ile Asp Pro Ala Arg Gln Asp Glu Leu Phe
 915 920 925
 Asp Glu Val Ile Thr Asp Ser Phe Thr Glu Leu Lys Asp Ser Ile Thr
 930 935 940

<400>	17						
agatcctaaa	acagcacgaa	gcatattatt	gcgcataatt	tgttcttgta	ggatcttttc	60	
ttgacatttt	ttttcactct	gcgagaaact	tctctttttt	tttccctcta	gggacgaaaat	120	
caaacaaggg	cacttttttt	tatctttttt	ttttctctgt	tgttttcaaa	acaaaaagat	180	
tccaccacta	catcagtggt	aaagactgtg	aaagctttct	gataaataag	cactttccat	240	
atttttcaac	tgaaaaatag	ttttcttttt	gcagctatta	ttgacttcat	taagaaatat	300	
cccttttttc	cccgttgcaa	ttattttctat	aagggaagct	ggaaataggg	ggctggaaaa	360	
gatat ttgaa	cagtcgctcc	aataaccggt	ctcaccatca	ttaacatttt	tgaagggtgaa	420	
tactgtttcg	gtcgatttat	ggctaatttg	tcaaatacat	ttgaaaaaga	ttaaaacaag	480	
cacaagcgg	tgagcatact	atgtcgcaga	caattacatc	tctagatccg	aattgtgtta	540	
ttgtattcaa	taaaacttcg	agtgcgaaag	agaagagttt	gaatgtcgaa	tccaacggtt	600	
tgaatataca	ttctattatc	gaacctggcc	atgatctgca	aacaagctat	gcggtttatta	660	
gaatccatca	ggataatgcg	aaaccgcttt	tttcattttt	gcagaatctg	gacttcattg	720	
aatccatcat	accatattcat	gatactgaat	tgtccgatga	tttgcataaa	ctgattttcta	780	
tcagcaaadc	aaaaataactg	gagggtccaa	aacagtatga	gttggtacaac	ctatcgaatt	840	
tgaccaataa	tcccaaacaa	tccttatatt	ttgcattctt	acagaactat	ataaaatgggt	900	
tgattccctt	ctcctttttt	ggattatcaa	ttagattttt	atctaatttt	acgtatgaat	960	
tcaattccac	atactcgctg	tctgccactc	tatggacatt	gtcattttaca	gcctttttggc	1020	
tttataaata	tgaaccattt	tggctctgata	gactgagtaa	atactcatca	ttttctacca	1080	
ttgagtttct	tcaagataaa	cagaaaagccc	aaaaaaaaagc	tagttcgggt	atcatgtttga	1140	
agaaatgttg	ttttattcct	gtggctttgt	tgtttggcgc	aatattacta	tcattccagc	1200	
tatattgttt	tgcgttgga	attttctaca	agcaaattta	taacggccca	atgatttcca	1260	
tcttgtcttt	tttgctact	atacttattt	gcacgtttac	tccggtttta	actgtgattt	1320	
acaacaaata	tttcgtagaa	ccaatgacaa	agtgggaaaa	tcatagcagt	tgtgtgaatg	1380	
caaagaatac	taagaagct	agaacttttg	ttattatttt	tctatccagt	tactgtcccc	1440	
tattaattac	actattttct	tatctgccaa	tggggcattt	gttgaccgca	gaaataagaa	1500	
ctaagggttt	caatgccttt	tcaatatttg	cccgtttacc	tacccatgat	tcagatttta	1560	
ttattgatac	aaagcgctat	gaagatcaat	ttttctactt	tattgttatc	aaccaactga	1620	
ttcaatttag	catggaaaac	tttgttccaa	gccttggttag	cattgtctcag	cagaaaatta	1680	
atggaccaaa	tcctaacttt	gtcaaagctg	agagtgaat	cggtaaagct	caactcagct	1740	
catcagatat	gaaaaatttg	tcaaaggtta	agtcgtacca	aacagacccc	tggggagcaa	1800	
cat ttgattt	ggacgccaac	ttcaaaaagc	tcttctaca	attcgggtat	ctgtgtatgt	1860	
tttctacaat	ttggccacta	gtctcattta	tctgtttgat	agtcaatttg	attgtttacc	1920	
aagtgcgatt	gaggaaagct	gtgctttata	gtaaacctga	gtattttcca	tttccaatct	1980	
acgataagcc	atcctctgtg	tctaataccc	aaaaactgac	ggttgggtcta	tggaaactctg	2040	
tcttagttat	gttctccatc	ttaggttgtg	ttatcactgc	tactttgacc	tatatgtacc	2100	
agagctgtaa	tataccaggt	gtcggcgctc	atacttccat	ccatacgaat	aaagcttgggt	2160	
acctagcaaa	tccaataaac	cactcgttga	taaatattgt	actatatgct	gtttttattg	2220	
agcatgtttg	ttgtgctatt	ttcttctctt	tctctagtat	tttgaaatct	tcccatgatg	2280	
acgttgcaaa	tggcattgtg	ccaaagcatg	tagttaacgt	gcaaaaacca	ccaaaacaag	2340	
aagtctttga	aaaaattccc	tccctgaat	ttaattcgaa	taacgaaaaa	gaactagtct	2400	
aaagaaaagg	gtctgcgaat	gagaagttgc	accaagaact	cggtgagaaa	cagcctgcct	2460	
cttctgccaa	tggatatgag	gcacatgctg	ccactctctc	caacaatgat	ccgtcttctt	2520	
tatcctcagc	ctcctcgctt	tcattattct	cttctctctt	tagcagcaaa	accggctgtag	2580	
tcaaagctgt	tgataacgat	acagcgggat	ctgtctggtaa	aaagccattg	gccacagaaa	2640	
gtactgaaaa	aagaaattct	ttgggtgaagg	tgcctaccgt	tggctcatat	gggtgttgcg	2700	

Thr Ile Glu Phe Leu Gln Asp Lys Gln Lys Ala Gln Lys Lys Ala Ser
195 200 205

Ser Val Leu Val Met Phe Ser Ile Leu Gly Cys Val Ile Thr Ala Thr
 515 520 525
 Leu Thr Tyr Met Tyr Gln Ser Cys Asn Ile Pro Gly Val Gly Ala His
 530 535 540
 Thr Ser Ile His Thr Asn Lys Ala Trp Tyr Leu Ala Asn Pro Ile Asn
 545 550 555 560
 His Ser Trp Ile Asn Ile Val Leu Tyr Ala Val Phe Ile Glu His Val
 565 570 575
 Ser Val Ala Ile Phe Phe Leu Phe Ser Ser Ile Leu Lys Ser Ser His
 580 585 590
 Asp Asp Val Ala Asn Gly Ile Val Pro Lys His Val Val Asn Val Gln
 595 600 605
 Asn Pro Pro Lys Gln Glu Val Phe Glu Lys Ile Pro Ser Pro Glu Phe
 610 615 620
 Asn Ser Asn Asn Glu Lys Glu Leu Val Gln Arg Lys Gly Ser Ala Asn
 625 630 635 640
 Glu Lys Leu His Gln Glu Leu Gly Glu Lys Gln Pro Ala Ser Ser Ala
 645 650 655
 Asn Gly Tyr Glu Ala His Ala Ala Thr His Ala Asn Asn Asp Pro Ser
 660 665 670
 Ser Leu Ser Ser Ala Ser Ser Pro Ser Leu Ser Ser Ser Ser Ser Ser
 675 680 685
 Ser Lys Thr Gly Val Val Lys Ala Val Asp Asn Asp Thr Ala Gly Ser
 690 695 700
 Ala Gly Lys Lys Pro Leu Ala Thr Glu Ser Thr Glu Lys Arg Asn Ser
 705 710 715 720
 Leu Val Lys Val Pro Thr Val Gly Ser Tyr Gly Val Ala Gly Ala Thr
 725 730 735
 Leu Pro Glu Thr Ile Pro Thr Ser Lys Asn Tyr Tyr Leu Arg Phe Asp
 740 745 750
 Glu Asp Gly Lys Ser Ile Arg Asp Ala Lys Ser Ser Ala Glu Ser Ser
 755 760 765
 Asn Ala Thr Asn Asn Asn Thr Leu Gly Thr Glu Ser Lys Leu Leu Pro
 770 775 780
 Asp Gly Asp Ala Val Asp Ala Leu Ser Arg Lys Ile Asp Gln Ile Pro
 785 790 795 800
 Lys Ile Ala Val Thr Gly Gly Glu Asn Asn Glu Asn Thr Gln Ala Lys
 805 810 815

Leu Ser Ala Cys Asn Ser Cys Pro Ala Trp Asp Tyr Asp Ala Asn Asp
 210 215 220
 Asp Ile Val Asn Glu Tyr Asp Thr Thr Tyr Leu Asp Asp Ile Ala Lys
 225 230 235 240
 Arg Leu Asn Lys Glu Asn Lys Gly Leu Asn Leu Thr Ser Thr Asp Ala
 245 250 255
 Ser Thr Leu Phe Ser Trp Cys Ala Phe Glu Val Asn Ala Lys Gly Tyr
 260 265 270
 Ser Asp Val Cys Asp Ile Phe Thr Lys Asp Glu Leu Val His Tyr Ser
 275 280 285
 Tyr Tyr Gln Asp Leu His Thr Tyr Tyr His Glu Gly Pro Gly Tyr Asp
 290 295 300
 Ile Ile Lys Ser Val Gly Ser Asn Leu Phe Asn Ala Ser Val Lys Leu
 305 310 315 320
 Leu Lys Gln Ser Glu Ile Gln Asp Gln Lys Val Trp Leu Ser Phe Thr
 325 330 335
 His Asp Thr Asp Ile Leu Asn Phe Leu Thr Thr Ala Gly Ile Ile Asp
 340 345 350
 Asp Lys Asn Asn Leu Thr Ala Glu Tyr Val Pro Phe Met Gly Asn Thr
 355 360 365
 Phe His Arg Ser Trp Tyr Val Pro Gln Gly Ala Arg Val Tyr Thr Glu
 370 375 380
 Lys Phe Gln Cys Ser Asn Asp Thr Tyr Val Arg Tyr Val Ile Asn Asp
 385 390 395 400
 Ala Val Val Pro Ile Glu Thr Cys Ser Thr Gly Pro Gly Phe Ser Cys
 405 410 415
 Glu Ile Asn Asp Phe Tyr Asp Tyr Ala Glu Lys Arg Val Ala Gly Thr
 420 425 430
 Asp Phe Leu Lys Val Cys Asn Val Ser Ser Val Ser Asn Ser Thr Glu
 435 440 445
 Leu Thr Phe Tyr Trp Asp Trp Asn Thr Thr His Tyr Asn Ala Ser Leu
 450 455 460
 Leu Arg Gln
 465

<210> 21

<211> 1563

<212> DNA

<213> *Candida albicans*

<400> 21

```

taactttctca acataattat gtaaaaaaatt atctcattaa gccagatagc aaatatatca 60
catattgcat tgattaatatt gagaaaaata tacatgtatc ttttcagtta attttattaa 120
aaataaatta tttccttact tttttttcta cagtttgcac cattaacctc ttttcttgca 180
tccatacatc tttgaactcc atacatctta tttttttgct gttttttttc agtgtctcgg 240
gcatacaggc cgcttatctt catgccggcc catcatccta ggaaactcct tcggtatggg 300
ccaagggcag gcgaaaatcc tatgtgcgtg gagctgatac aatctcggct ggcttggttt 360
gtagggcacg gtcaatgaat gcctgatggg agaaaaattc atctttatga aaagtgatct 420
taatttgaat agtgtgcctt tcaaaacatt tggaagtcac taattgaaac tatccagtgt 480
gaatagacga ctgagccatc atgaaggtat gtaatatcac ccaaactcct agaattctaa 540
tgaatcagca cgcgctaacc ggctgtttct gactgtttga taaacgtata cccacaaaatt 600
agtgcactat aataaaaaatt ctcaagaaca acgttgttta aacgagataa ttccctctaa 660
tatacacgta ccgacactta ggaaaatatc tcgctaagtt caaattaagg aatgaaaaag 720
gaatttacga aaagggttta gaaatatcaa tgaaaataag aaaaacctgt aacggaagaa 780
aggacagcag ggattcggtg gaatttgcgt atattggctt cggacaactt tactaacaaa 840
tggtattatt tataacagtt gaacatttct taccagtcac acgggtctca aaagaccttc 900
gaaattgatg atgaacaccg tattcgtgtt ttcttcgaca agagaatcgg tcaagaagtc 960
gatggtgaag ccgttggtga tgaattcaag ggctacgtct tcaagatctc tgggtggtaac 1020
gacaaacaag gtttcccaat gaagcaaggt gttttgttgc caactagaat caagttgttg 1080
ttgaccaaga acgtttcttg ttacagacca agacgtgatg gtgaaagaaa gagaaagtcc 1140
gtcagaggtg ccattggttg tccagatttg gctgtcttgg ctttggtcat tgtcaagaag 1200
ggtgaacaag aattggaagg tctaactgac actactgttc caaagagatt ggggtccaaa 1260
agagctaaca acatcagaaa gttcttcggg ttgtccaagg aagatgacgt tcgtgatttc 1320
gtcatcagaa gagaagtcac caagggtgaa aagacttaca ccaaggctcc aaagatccaa 1380
agattggtta ctccctcaaag attgcaaaga aagagacacc aaagagcttt gaaggtcaga 1440
aacgctcaag ctcaaagaga agctgctgcc gaatacgtc aattgttggc taagagattg 1500
tctgaaagaa aggctgaaaa ggccgaaatc agaaagagaa gagcttcttc tttgaaggct 1560
taa

```

<210> 22

<211> 236

<212> PRT

<213> *Candida albicans*

<400> 22

```

Met Lys Leu Asn Ile Ser Tyr Pro Val Asn Gly Ser Gln Lys Thr Phe
 1             5             10             15

Glu Ile Asp Asp Glu His Arg Ile Arg Val Phe Phe Asp Lys Arg Ile
      20             25             30

Gly Gln Glu Val Asp Gly Glu Ala Val Gly Asp Glu Phe Lys Gly Tyr
      35             40             45

Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
      50             55             60

Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn
      65             70             75             80

Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser
      85             90             95

Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val

```

<400> 24

<400>	25						
acatgacctta	attttagct	taggggttctt	ttttgtcaat	tctatgcgta	tgacaaagag	60	
caccacgatg	gtgatcgaaa	tctctaggag	tagcatacca	cagcgatatt	atttagtagt	120	
aggcggttta	ttatctttgt	ccctttatac	tgttgtgttt	cttgcttatt	gcttcagtag	180	
gcagcgtata	gtataaccag	aaaaaagtga	aaaaataact	aaaaaagcac	tatgagatga	240	
acggtaaaaa	tcacaccagag	atttgtctac	taataactct	gtaccatgtc	catcaaccta	300	
cattccgcac	ccgagtatga	tccatcttat	aagctgatcc	agttgacacc	agagttactg	360	
gatataatac	aggatccggt	tcaaaatcac	cagttaaggt	ttaagtcatt	ggacaaagac	420	
aagtctgaag	ttgtactgtg	ttcgcacgac	aagactttggg	tgctgcaagc	agcgcaaaca	480	
ttcaaacaca	gttctactaa	tgaagagaatt	tgttctgtga	caacctatta	ctttcgacga	540	
aacgctcttg	tttgactgtg	ccaagccgta	catggacgct	gtgggattcg	ccaagactga	600	
atcagaattt	gagaccagag	agacacatgg	cgaattgaac	ttgaattcag	taccaatata	660	
caacggagaa	ctggattttct	ccgacaaaat	catgaagagg	tcattctacaa	aggttatcgg	720	
gaccctggaa	gaactacttg	agaactcacc	atgttctgcg	ctagaaggta	tatcaaaatg	780	
gcataagatt	ggtggacttg	tgaagaacgg	tgtgttgtgt	attctttcac	aagacttctt	840	
tttcaaagca	ctgcattgtac	tactgatgag	cggaattggca	gaatcacctg	atctacagca	900	
tctgaatggt	gaggatacac	atcacgctgt	ggggaaggac	attgaggacg	agttcaatcc	960	
atacacaaga	gaaatcattg	aaacagtgct	gaataaattt	gctgttcaag	agcaagaggc	1020	
tgaaaacaat	acgtggcgct	tgagaatacc	gtttatagct	cagtggtacg	ggattcaagc	1080	
gctaaggaaa	tatgtttctg	gaataagcat	gccaatlgat	gagttcctca	tcaagtggaa	1140	
gttcccttttc	ccacctttct	tcccatgtga	cattgacatt	gacatgctgc	gaggctatca	1200	
tttcaagcct	accgataaga	ctgtccagta	tatagcgaaa	agcacactac	caatggaccc	1260	
caaaqaacgg	tttaaagtc	tqtttaagct	acagtcacag	tqqqacttqq	aqqatatcaa	1320	

gcctctaatt gaagaactaa attcaagagg tatgaaaata gacagtttca tcatgaagta 1380
 tgcccgccgt aaaagactgg gcaaaaagac cgtggtcacg agcaggtag 1429

<210> 26

<211> 309

<212> PRT

<213> Candida albicans

<400> 26

Met Arg Glu Phe Val Pro Glu Gln Pro Ile Thr Phe Asp Glu Thr Leu
 1 5 10 15

Leu Phe Gly Leu Ser Lys Pro Tyr Met Asp Val Val Gly Phe Ala Lys
 20 25 30

Thr Glu Ser Glu Phe Glu Thr Arg Glu Thr His Gly Glu Leu Asn Leu
 35 40 45

Asn Ser Val Pro Ile Tyr Asn Gly Glu Leu Asp Phe Ser Asp Lys Ile
 50 55 60

Met Lys Arg Ser Ser Thr Lys Val Ile Gly Thr Leu Glu Glu Leu Leu
 65 70 75 80

Glu Asn Ser Pro Cys Ser Ala Leu Glu Gly Ile Ser Lys Trp His Lys
 85 90 95

Ile Gly Gly Ser Val Lys Asp Gly Val Leu Cys Ile Leu Ser Gln Asp
 100 105 110

Phe Leu Phe Lys Ala Leu His Val Leu Leu Met Ser Ala Met Ala Glu
 115 120 125

Ser Leu Asp Leu Gln His Leu Asn Val Glu Asp Thr His His Ala Val
 130 135 140

Gly Lys Asp Ile Glu Asp Glu Phe Asn Pro Tyr Thr Arg Glu Ile Ile
 145 150 155 160

Glu Thr Val Leu Asn Lys Phe Ala Val Gln Glu Gln Glu Ala Glu Asn
 165 170 175

Asn Thr Trp Arg Leu Arg Ile Pro Phe Ile Ala Gln Trp Tyr Gly Ile
 180 185 190

Gln Ala Leu Arg Lys Tyr Val Ser Gly Ile Ser Met Pro Ile Asp Glu
 195 200 205

Phe Leu Ile Lys Trp Lys Ser Leu Phe Pro Pro Phe Phe Pro Cys Asp
 210 215 220

Ile Asp Ile Asp Met Leu Arg Gly Tyr His Phe Lys Pro Thr Asp Lys
 225 230 235 240

Thr Val Gln Tyr Ile Ala Lys Ser Thr Leu Pro Met Asp Pro Lys Glu
 245 250 255

Arg Phe Lys Val Leu Phe Arg Leu Gln Ser Gln Trp Asp Leu Glu Asp
260 265 270

Ile Lys Pro Leu Ile Glu Glu Leu Asn Ser Arg Gly Met Lys Ile Asp
275 280 285

Ser Phe Ile Met Lys Tyr Ala Arg Arg Lys Arg Leu Gly Lys Lys Thr
290 295 300

Val Val Thr Ser Arg
305

<210> 27

<211> 1952

<212> DNA

<213> Candida albicans

<400> 27

```

gtcatcgaca gcaaattgct ggaagagttc aaggacaacg tgagatacac cttggaaaat 60
gacctgagag aaggagccga tgaggccact ctgcaacgca ggaggcagtt ggaacagatc 120
attacgggag acaacgctga ggaggagttg gaaagggtaca tccgtgctat ggtcagagag 180
cagatgctgg gccagggtc catggcggggt tccgggggacg aaccagattc caagagaaga 240
aaataacgac ccagcacaaa ggctcttaca gcttgctaaa agaaattgaa cgcgacgcta 300
catgaactac ttctttctct tacatagtct tttcccttat gtatcttttc tgtacattaa 360
tagacgttct tacaaggtaa aatttcaccg cgttttttaa tagaatgaaa aaaacgttgt 420
agagtgaag aaaagcaaca aatatacagt tcacaaggca gcttcgtata gtaatacagc 480
acgaaaaaca gtcatagaa atggtaacac agaccaatcc ggtccctgtt acatatccaa 540
cggatgctta tatccccacg tatctgcccg atgataaggt ctccaatctg gcagatttga 600
aaaaattgat agaaatggat tccagactag atttgtatct gacaagaagg aggctggata 660
cgtccatcaa tttacctaca aacaccaaga ccaaggacca tcccccaat aaagagatgc 720
tgaggattta cgtctacaac actacggaaa gcagccctcg cagcgattct ggcaccccag 780
cggactcagg caagactaca tggacactga gaatagaagg taagcttctg cacgagtcgc 840
caaacggaaa gcacccattt agtgagttt tgggaaggtgt cgcggtcgac tttaaaagac 900
tgaaaccgct gggcatgggc aagaagagga aacgcgattc gtcattgagc cttcctttga 960
atctgcaaca acccgaaatc aatgatcaag atagcaccat gggcgataac gacaacggcg 1020
aggatgagga cagtgcagag gcagaatcca gggaggaaat tgtagacgca ctggaatgga 1080
actacgatga aaacaacggt gtggagtttg atggtatcga catcaagagg caaggcaagg 1140
ataatttgcg atgcagtata accatccagt tgaggggtgt cgacggtgga aaagtacagt 1200
actcgcccaa cttagctacc ttgataggta tgcaaacggg ctccgttaat gacgcggttt 1260
attcgatcta caagtaacatt ttgatcaaca atctgtttgt tacggaacaa acagaggctc 1320
aagatggttc caacgatgcc gaagacagca gtaacgagaa taacaataaa aacggtgctg 1380
gtgacgatga tggcgctcgag ggaagtactc caaaggataa gcccgaattg ggtgaagtga 1440
agctagattc actcttacia aaggtatttg atacaaacgc cgcgcacctc cccttgatga 1500
atggttgta aaccgtgaac aaactgggtat caccctacc gcccatcatc ctagattata 1560
caattgatct ttccaaagat accacctatg gtgctaccac cttggatgta gatgtgtcgc 1620
acattctcca ccagcctcaa cccagccaa atttacaaaa agaggaagaa acagatgctg 1680
aagacacagc aaaactacgt gaaatcacia agcttgccct gcagttgaac tctagtgtc 1740
aaaaatacca gttttccac gaactgtctt tgcattccaag agaaacgctg actcactact 1800
tatggtcttc caagcaaaac gagcttgtgc tgcagggcga ccaatacttc aatgaagatg 1860
ctgcaagaac gagtgcata tacagtaaca acaacaatga caggtcacta atgggcaata 1920
tctcactact gtactccaa ggaagactat aa 1952

```

<210> 28

```

<400> 28
Met Val Thr Gln Thr Asn Pro Val Pro Val Thr Tyr Pro Thr Asp Ala
  1                               5                               10                               15

Tyr Ile Pro Thr Tyr Leu Pro Asp Asp Lys Val Ser Asn Leu Ala Asp
      20                               25                               30

Leu Lys Lys Leu Ile Glu Met Asp Ser Arg Leu Asp Leu Tyr Leu Thr
      35                               40                               45

Arg Arg Arg Leu Asp Thr Ser Ile Asn Leu Pro Thr Asn Thr Lys Thr
      50                               55                               60

Lys Asp His Pro Pro Asn Lys Glu Met Leu Arg Ile Tyr Val Tyr Asn
      65                               70                               75                               80

Thr Thr Glu Ser Ser Pro Arg Ser Asp Ser Gly Thr Pro Ala Asp Ser
      85                               90                               95

Gly Lys Thr Thr Trp Thr Leu Arg Ile Glu Gly Lys Leu Leu His Glu
      100                               105                               110

Ser Ala Asn Gly Lys His Pro Phe Ser Glu Phe Leu Glu Gly Val Ala
      115                               120                               125

Val Asp Phe Lys Arg Leu Lys Pro Leu Gly Met Gly Lys Lys Arg Lys
      130                               135                               140

Arg Asp Ser Ser Leu Ser Leu Pro Leu Asn Leu Gln Gln Pro Glu Tyr
      145                               150                               155                               160

Asn Asp Gln Asp Ser Thr Met Gly Asp Asn Asp Asn Gly Glu Asp Glu
      165                               170                               175

Asp Ser Ala Glu Ala Glu Ser Arg Glu Glu Ile Val Asp Ala Leu Glu
      180                               185                               190

Trp Asn Tyr Asp Glu Asn Asn Val Val Glu Phe Asp Gly Ile Asp Ile
      195                               200                               205

Lys Arg Gln Gly Lys Asp Asn Leu Arg Cys Ser Ile Thr Ile Gln Leu
      210                               215                               220

Arg Gly Val Asp Gly Gly Lys Val Gln Tyr Ser Pro Asn Leu Ala Thr
      225                               230                               235                               240

Leu Ile Gly Met Gln Thr Gly Ser Val Asn Asp Ala Val Tyr Ser Ile
      245                               250                               255

Tyr Lys Tyr Ile Leu Ile Asn Asn Leu Phe Val Thr Glu Gln Thr Glu
      260                               265                               270

Ala Gln Asp Gly Ser Asn Asp Ala Glu Asp Ser Ser Asn Glu Asn Asn

```

<400> 29							
aggtttttaac	gcgttatctt	tgttccgaaa	aaaaaaaaaa	acggaaaaaat	atatttttttc	60	
gcgtcgcgtt	ctcgcgtctg	ttttgttttt	tcgcgttcca	atgaccaaaa	tgggaaagtg	120	
gtcgtctttg	acgaaggaga	cgaaaacctc	ttctaaaacg	ttgggagaga	ga#aattaca	180	
tggccagaac	aatactgcaa	cgtgcatata	gtcgttagtc	tgtgcttgca	catccacggc	240	
agccgcagtg	gacgcactga	tggaaaggaca	cctgtgtgcc	ctttttgcgt	gcttcttctt	300	
ctaactgctg	acgaggcacc	ctgcagatgc	aagtgtcacc	gttgttatgt	tcgattcttt	360	
gaatcgtagc	cagacagcac	agtttttcat	aacctgtttt	gcgccatttg	gcaatttagca	420	
atztatcaqc	atacttttcc	tttatcaacc	aactcgtaaaq	gtcttttgaq	atqccctttc	480	


```
<210> 32
<211> 315
<212> PRT
<213> Candida albicans
```

<400> 32																
Met	Thr	Thr	Thr	Val	Pro	Lys	Ile	Phe	Ala	Phe	His	Glu	Phe	Ser	Asp	
1				5					10					15		
Val	Ala	Glu	Ala	Val	Ala	Asp	His	Val	Val	His	Ala	Gln	Asp	Gly	Ala	
			20					25					30			
Leu	Ala	Pro	Lys	Asn	Glu	Arg	Lys	His	Ser	Val	Pro	Asn	Ile	Ser	Met	
		35					40						45			
Asn	Ala	Leu	Asp	Met	Thr	Arg	Glu	Ala	Ser	Cys	Lys	Ser	Thr	Ala	Ser	
	50					55					60					
Ala	Ala	Glu	Gly	Lys	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ser	
65					70					75					80	
Lys	Pro	Lys	Lys	Glu	Lys	Arg	Phe	Lys	Ile	Ala	Leu	Ser	Gly	Gly	Ser	
				85					90					95		
Leu	Ile	Glu	Val	Leu	His	Glu	Gly	Leu	Leu	Lys	Arg	Asp	Asp	Val	Arg	
			100					105					110			
Trp	Gly	Asp	Trp	Asp	Ile	Tyr	Phe	Ala	Asp	Glu	Arg	Leu	Val	Pro	Phe	
		115					120					125				
Ser	Ser	Asn	Glu	Ser	Asn	Tyr	Gly	Cys	Ala	Lys	Arg	Lys	Ile	Leu	Asp	
		130				135					140					
Leu	Ile	Asp	Thr	Ala	Lys	Tyr	Gly	Thr	Pro	Lys	Val	Tyr	His	Ile	Asp	
145					150					155					160	

Glu Ser Leu Ile Asp Asp Pro Gln Glu Cys Val Asp Asn Tyr Glu Lys
165 170 175

Val Leu Ile Arg Gly Phe Ala Gly Arg Asp Ser Val Lys Leu Pro Met
180 185 190

Phe Asp Leu Phe Leu Leu Gly Cys Ala Pro Asp Gly His Ile Ala Ser
195 200 205

Leu Phe Pro Asn Phe Gln Asp Asn Leu Arg Glu Lys Leu Ala Trp Val
210 215 220

Val Pro Val Glu Asn Ala Pro Ser Gly Pro Ser Thr Arg Ile Ser Leu
225 230 235 240

Thr Ile Pro Val Ile Cys His Ser His Arg Val Thr Phe Val Val Glu
245 250 255

Gly Ala Thr Lys Ala Pro Ile Ile Lys Thr Ile Met Glu Arg Pro Glu
260 265 270

Lys Gly Leu Pro Ser Ser Ile Val Asn Glu Gly Ala Ala Gly Arg Val
275 280 285

Ser Trp Phe Val Asp Asp Asp Ala Leu Thr Asp Val Leu Val Thr Lys
290 295 300

Lys Lys Tyr Lys Phe His Gln Gly Leu Ser Ile
305 310 315

<210> 33

<211> 1196

<212> DNA

<213> Candida albicans

<400> 33

```

tagtaattag tttcttatga tggatttaat ggcgtagttc atccgcgttt aattttaacta 60
gaggataatc tacttgacgc atgaatgaaa atagtaagcc agtaaggatg cactgacaga 120
ctcagctacc gattagtgtt gttgactttt ccgcaagatc cttttctccc tctttggacc 180
tagtcatccc tccacacaag attcgctctt aagtagtggc gcaggctgtt cgcttttaag 240
catagtgcct aatgtcgaag gctttataga tcccaaatac tacgccttga gaaattgaat 300
gcactagcag ttagttaact ttctggaacg cgcatgacgc gtcccggggc gcctgaggcg 360
gagcggttcg gaaatcggga aaacattata ctgggaaaga tcactatcta ttctctaaat 420
gaacttttaa gcaaattatc gtaagataga aaagacgaaa ccttagcaac cttagcggttt 480
aatatagaaa caattttatt atgatacctt ccaataagag aaatgctaga attttaagca 540
ttacaacgct attattgttg ttagtggttt tcgtagcgca aaatgcgaac ttcttgacgg 600
tagagataaa agaggaaact tctaaagcat ttagtactaa tatggacaat atggctggag 660
gatcttccag ggaatatgct gctatgccga cttctaccac gaataagggg agctctgaag 720
tagacgaaga aattaatgaa ataaaacaga aggtgggact ccaacagccc atagcatcgg 780
ttgatgatag tttgtcgggc attaaaaacg ataaagggc gcgaataacc aaagctttta 840
atgttcaaaa agaatactcc ctcatactag acttgtctcc gattataata tttagtataa 900
gcacctgttc atatagcaag ggcattgaag aactgcttga aaatgagtat cagtttatcc 960
caaactacta tattatagaa cttgacaaac atggacatgg ggaagagctg caagaatata 1020
tcaagttggt gaccggtaga ggaactgttc caaacctttt ggtaaatgga gtatcaagag 1080
gaggtaatga agaaatcaag aaactgcaca ctcaagggaa acttttagaa tcattacaag 1140

```


tctggagtga tggtaaattc tcggttgagc aacgtgaaaa accttccaat aattga 1196

<210> 34

<211> 231

<212> PRT

<213> Candida albicans

<400> 34

Met Ile Pro Ser Asn Lys Arg Asn Ala Arg Ile Leu Ser Ile Thr Thr
1 5 10 15

Leu Leu Leu Leu Leu Val Phe Phe Val Ala Gln Asn Ala Asn Phe Leu
20 25 30

Thr Val Glu Ile Lys Glu Glu Thr Ser Lys Ala Phe Ser Thr Asn Met
35 40 45

Asp Asn Met Ala Gly Gly Ser Ser Arg Glu Tyr Ala Ala Met Pro Thr
50 55 60

Ser Thr Thr Asn Lys Gly Ser Ser Glu Val Asp Glu Glu Ile Asn Glu
65 70 75 80

Ile Lys Gln Lys Val Gly Leu Gln Gln Pro Ile Ala Ser Val Asp Asp
85 90 95

Ser Leu Ser Ala Ile Lys Asn Asp Lys Gly Ser Arg Ile Thr Lys Ala
100 105 110

Phe Asn Val Gln Lys Glu Tyr Ser Leu Ile Leu Asp Leu Ser Pro Ile
115 120 125

Ile Ile Phe Ser Lys Ser Thr Cys Ser Tyr Ser Lys Gly Met Lys Glu
130 135 140

Leu Leu Glu Asn Glu Tyr Gln Phe Ile Pro Asn Tyr Tyr Ile Ile Glu
145 150 155 160

Leu Asp Lys His Gly His Gly Glu Glu Leu Gln Glu Tyr Ile Lys Leu
165 170 175

Val Thr Gly Arg Gly Thr Val Pro Asn Leu Leu Val Asn Gly Val Ser
180 185 190

Arg Gly Gly Asn Glu Glu Ile Lys Lys Leu His Thr Gln Gly Lys Leu
195 200 205

Leu Glu Ser Leu Gln Val Trp Ser Asp Gly Lys Phe Ser Val Glu Gln
210 215 220

Arg Glu Lys Pro Ser Asn Asn
225 230

<210> 35

```

<400> 36
Met Gln Arg Asn Asn Arg Leu Arg Asn Leu Phe Thr Val Pro Val Ile
  1                      5                      10                      15

Met Ala Arg Gln Leu Lys Arg Asn Ala Leu Ser Ala Gly Leu Ala Phe
                20                      25                      30

Ala Gly Asn Ala Thr Ser Asn Glu Phe Asp Glu His Leu Gln Asn Glu
          35                      40                      45

Val Glu Arg Glu Arg Glu Ile Gln Lys Lys Lys Lys Ile Lys Arg Thr
    50                      55                      60

```

Gln	Ser	Lys	Lys	Ser	Pro	Asp	Leu	Ile	Asn	Lys	Ser	Thr	Phe	Gln	Ser		
65					70					75					80		
Arg	Thr	Ile	Gly	Ser	Lys	Lys	Glu	Lys	His	Arg	Gln	Leu	Asp	Pro	Glu		
				85					90					95			
Tyr	Glu	Ile	Val	Ile	Asp	Gly	Pro	Leu	Arg	Lys	Ile	Lys	Pro	Tyr	His		
			100					105					110				
Phe	Thr	Tyr	Arg	Thr	Phe	Cys	Lys	Glu	Arg	Trp	Arg	Asp	Lys	Lys	Leu		
		115					120					125					
Val	Asp	Val	Phe	Ile	Ser	Glu	Phe	Arg	Asp	Arg	Glu	Ser	Glu	Tyr	Tyr		
	130					135					140						
Lys	Arg	Thr	Ile	Glu	Asn	Gly	Asp	Val	His	Ile	Asn	Asp	Glu	Thr	Ala		
145					150					155					160		
Asp	Leu	Ser	Thr	Val	Ile	Arg	Asn	Gly	Asp	Leu	Ile	Thr	His	Gln	Val		
				165					170					175			
His	Arg	His	Glu	Pro	Pro	Val	Thr	Ser	Arg	Pro	Ile	Lys	Val	Ile	Phe		
			180					185					190				
Glu	Asp	Asp	Asn	Ile	Met	Val	Ile	Asp	Lys	Pro	Ser	Gly	Ile	Pro	Val		
		195					200					205					
His	Pro	Thr	Gly	Arg	Tyr	Arg	Phe	Asn	Thr	Ile	Thr	Lys	Met	Leu	Gln		
	210					215					220						
Asn	Asn	Leu	Gly	Phe	Val	Val	Asn	Pro	Cys	Asn	Arg	Leu	Asp	Arg	Leu		
225					230				235						240		
Thr	Ser	Gly	Leu	Met	Phe	Leu	Ala	Lys	Thr	Pro	Lys	Gly	Ala	Asp	Asn		
				245					250					255			
Ile	Gly	Asp	Gln	Leu	Lys	Ala	Arg	Glu	Val	Thr	Lys	Glu	Tyr	Val	Ala		
			260					265					270				
Lys	Val	Val	Gly	Glu	Phe	Pro	Glu	Thr	Glu	Val	Ile	Val	Glu	Lys	Pro		
		275					280					285					
Leu	Lys	Leu	Ile	Glu	Pro	Arg	Leu	Ala	Leu	Asn	Ala	Val	Cys	Gln	Met		
	290					295					300						
Asp	Glu	Lys	Gly	Ala	Lys	His	Ala	Lys	Thr	Val	Phe	Asn	Arg	Ile	Ser		
305					310					315					320		
Tyr	Asp	Gly	Lys	Thr	Ser	Ile	Val	Lys	Cys	Lys	Pro	Leu	Thr	Gly	Arg		
				325					330					335			
Ser	His	Gln	Ile	Arg	Val	His	Leu	Gln	Tyr	Leu	Gly	His	Pro	Ile	Ala		
			340					345					350				
Asn	Asp	Pro	Ile	Tyr	Ser	Asn	Asp	Glu	Val	Trp	Gly	Asn	Asn	Leu	Gly		
		355					360					365					

Lys Gly Gly Gln Ala Asp Phe Asp Ile Val Ile Thr Lys Leu Asp Glu
 370 375 380
 Ile Gly Lys Arg Lys Pro Ala Lys Ser Trp Phe His Ser Asn Gly Gly
 385 390 395 400
 Tyr Gly Glu Val Leu Arg Gln Glu Lys Cys Ser Ile Cys Glu Ser Asp
 405 410 415
 Leu Tyr Thr Asp Pro Gly Pro Asn Asp Leu Asp Leu Trp Leu His Ala
 420 425 430
 Tyr Leu Tyr Glu Ser Thr Glu Thr Glu Glu Gly Thr Glu Lys Lys Lys
 435 440 445
 Trp Cys Tyr Lys Thr Glu Tyr Pro Glu Trp Ala Leu Arg Arg
 450 455 460

<210> 37
 <211> 1364
 <212> DNA
 <213> Candida albicans

<400> 37
 tattccgact agaaaaaat taaattttct aactacaaaa aattgcctgc atatatgtaa 60
 ggatgtaaca ggaaatgtat gggtcacata ttaatagctt gttttactcc ataaaagagt 120
 ctgatattca gaaaaaacac ccatacatgt tgaaaaataa tgcattgtga aaaaaagtgg 180
 ttgaaaaatg tatgcatctt aggaaaaact gaattttcct taggttgctg ctccctctct 240
 agaaggatgc tgtggccttt gacctgggcg gaaattctct ctgtttccct ctagctgagg 300
 gaaacagaac tggtagcagt tcgttccggc caggccgcgt gagcctatac caccgaatat 360
 tatectagcg cagagagtaa cactggcaaa gtcaaaagta aatgccatgt aaaatgtata 420
 ggttacgcag tagactatct aatatatacc tttttattta gcagtgtttc gaaaaataca 480
 gcaagagaat aagcaacaag atgtctgccc tccaagtgt ccaagtatgt taaataatct 540
 aaacgatgtc acgaatttgt gagggatatt gaaacatgac agtgagataa tttcaattta 600
 agaaccatat cacctgaata agacgggtgg ggcaagcact agatgcgaat catagtttta 660
 gaacaacgga tcaccatttc acacgttaaa gaccgagtag aaataaccaa taaattgtgt 720
 gggaaaaatat tatacttaat ttctctgttg agtaaaagta tgagcgtctt ttgcggtctt 780
 atttattcat tcgtcccttg tgcaatgaat tttgaacaga atgctccaaa gaggaagtgc 840
 cagggtacct cacttgtttc acccttttac acagttcata atatttttga ggattttgaa 900
 tttctgtttt actaacatgt gacacgaaat gtttttcatt tttggtttta taacagactt 960
 ttggtaagaa gaaatcagct accgctgttg ccacggtcaa ggccggtgag ggtttgatta 1020
 aggtcaacgg ttctccaatc actttgggtg aaccagaaat cctaagattc aaggtctacg 1080
 aaccattatt gttgggttgg ttggacaagt tctccaacat cgatatcaga gtttagagtca 1140
 ctggtggtgg tcatgtttct caagtctacg ccacagaca agctattgct aagggtttag 1200
 tcgcttacca ccaaaagtac gttgacgaac aatccaagaa cgaattgaag aaggccttca 1260
 cctcttacga cagaactttg ttgatcgtg attctagaag accagaacca aagaaattcg 1320
 gtggtaaggg tgctcgttct agattccaaa aatcttaccg ttaa 1364

<210> 38
 <211> 143
 <212> PRT
 <213> Candida albicans

<400> 38

41

Met Ser Ala Val Pro Ser Val Gln Thr Phe Gly Lys Lys Lys Ser Ala
 1 5 10 15
 Thr Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Val Asn
 20 25 30
 Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val
 35 40 45
 Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp
 50 55 60
 Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala
 65 70 75 80
 Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr
 85 90 95
 Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr
 100 105 110
 Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys
 115 120 125
 Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg
 130 135 140

<210> 39

<211> 1088

<212> DNA

<213> Candida albicans

<400> 39

```

ttcaaaatac gagtaaagga gatcctaggt gtggattagt aaggggagtg tggcaacttc 60
ctttttccgg ttaattctcc gcgctttcgt tagactattt tgcaaggacc caaataggag 120
acgcatggag gcttctacaa aacagcgtgc cgttttgatg gcatgagcag ggggcgcaaa 180
ggaaacaccg gtaaatecgc caagaccttg ttggccacgt agcctcaaag gttgaattga 240
cacttgtcta cagaacttga aaagtacaaa aggaggtcac ataaaaacagt aagcttgaga 300
agctttaaga tatgggtgca atcgttacag aatattcctt gcagaaataa tggcgggtcc 360
gttctcttct gaagaagtta ccgcctact gaagcattgc tgtacgatcg tgtaatgtga 420
tgtgtgttcg actggaaagc ggagaacatt atgaagtaaa aggacaatca gcacgccttc 480
cagactttta agaaacattg atggagccat tgatatcggc accgtaccta acaacaacaa 540
aaatgtctgc tcctgctacg cttgatgctg cctgtatttt ttgcaagatt attaaaagta 600
tgtcacatta ctaataaaga gcttacctc acaccaatga tggcgatagt ctctatgtag 660
tacatataca taaagcagaa tactaacaat cgatccgcta tgcaacaggc gaaattccat 720
ccttcaaatt gattgaaaca aagtactcgt atgctttcct ggacatccaa cctactgctg 780
aaggtcatgc tttaatcatt cctaagtacc atgggtgcgaa gttgcatgac atcccggacg 840
aattccttac cgatgctatg ccgattgcc aagagactggc caaggcaatg aagttggaca 900
cttataatgt gttgcagaat aatggtaaaa ttgcgcatca agaagtgcac cacgtccact 960
tccatttgat tccaaagaga gatgagaaaa gtggtttgat ttaggggtgg ccagcccaag 1020
aaacggactt cgataagttg ggcaagctac acaaggaatt gcttgccaaa ctagaaggct 1080
ccgattag.

```

<210> 40

$\langle 210 \rangle$	42
$\langle 211 \rangle$	25

Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu
50 55 60

Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu
65 70 75 80

Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu
85 90 95

Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro
100 105 110

Gln Arg Lys Tyr Ala Ile Lys Ala
115 120

<210> 45

<211> 2660

<212> DNA

<213> Candida albicans

<400> 45

tgggtgtcgt	caaacaggat	gccgtggaat	catacgaacc	gcacattgtg	gtagagctac	60
aaagcgatac	gaaagaagat	atggtatcta	acgtatcccc	tattgttgct	tgggaaaaga	120
tgtggttaga	acaacatcca	gatggagtca	caaataaata	tcaagggcct	cgtagcgatg	180
acgaagacga	tgaagacagt	gagtaggcgt	tccataactt	tgtgtatcta	catatatata	240
tatataattg	taaattagta	acagtagtaa	tagtagtgcc	tattataaag	ggttttcttt	300
aagtaatgtc	atgtacttgt	ttaatgtgac	tttggttaata	tattttcatt	ctccgatgcc	360
gatgcccagt	ggaaaagttt	aaagtgaata	atTTTTcaac	acatacaagt	ttaataagtt	420
ggttttgatg	caaataagcat	tactaaagaa	gagcgctagg	ataattgtgc	attgctattg	480
tgatttttga	tacagaaatt	atgcactatg	tggtactaga	gctgcaagtt	gcgattttgc	540
cagatacccc	caaggatcaa	tgtcgcattg	cgaatatagc	atttcaaatt	gtgaatgctg	600
aaacattagt	atgccattat	gggaccaatt	ctttaccgag	cattgaagta	aacggggacga	660
caaagagttt	ggagagtgca	atggtgcaat	tggacaagga	tattcatgac	gttattggta	720
acgacgactt	tgttcttggt	tccctgtatt	caacatggca	tatccgtgtt	accttaccac	780
gtcaagcgag	agatgatggg	tttattctta	cttcttattt	acaacatccg	aaagtatttg	840
acttatggaa	ggaattcgat	agatgggtgtg	tcaaccatcc	ggagattttg	ggacaaaaga	900
aagcaattct	caacaacaat	tgtaataata	taagatttag	tattaatgca	gccaaaaata	960
cgaaggattt	ggacgaaata	gttagaatat	tgggaagttt	aatcccaact	gaagaggcag	1020
gctctgttcc	agagatatata	tctcttttaa	aaaggacaac	ggatatatta	atacaattgc	1080
acaaaaagtg	tacttccctt	gaagatatgg	aatctgtctt	aacaaaacca	tatgactcac	1140
acaccgatata	tagagcgttt	ttgcaagaga	aatctaagat	tttgtacatg	aacaattttac	1200
cgcccgacac	aactcaaagt	gagttggaat	catggtttac	ccaatatggt	gtagaccag	1260
ttgggttttg	gactgtcaaa	aacatcgtag	aagatacgtc	taacgttaat	aataacttga	1320
gtctaaataa	cagtccctat	gtggaagatc	aagatagtat	ctcaggattt	gttgtcttcc	1380
aaacacatga	agaagcaact	gaagtactag	cggtgaatgg	gagatcaatc	ctatctaata	1440
tggcaaacac	taagcaacca	aggggtgggtg	aacatgtcct	tgagcttcaa	ccttcttcca	1500
ccggagtact	cgataaggct	caagaaattt	tatcgctttt	ccctcaaagt	aaaaacaaac	1560
caagaccagg	tgactggaat	tgcccatctt	gtgggttttt	aaactttcaa	agacgtactg	1620
catgtttttg	atgttctttt	ccggcaccat	caaatagtca	aatacatact	gcgaactcaa	1680
acaataatgt	taacagttag	agaaataatt	taacaatacg	cgtgaactcg	ggatcttcaa	1740
gcaatattag	taacactgca	gcgaatcaac	cctatgggtg	ccctgagttc	aacatgattg	1800
ctaacaacac	gccagcagct	ttaacataca	atagagctca	ttttcctgca	attacgccat	1860
tgctcgcgaca	aaattcattg	aacatggcac	catcgaaacg	tgggtcgccg	ataattatag	1920
cggatcattt	ttcggaatat	aataatatag	ccccaaatta	tcgttataat	aataatatta	1980
acaataacaa	caataatatt	aacaatatga	ccaataatag	atataacatt	aataaaaaata	2040

tcaacggtaa tgggaatggt aatgggaaca acagtaataa caataacaat cataataaca 2100
 atcataataa caatcatcat aatggtagta tcaatagtaa tagtaatacc aataataata 2160
 ataataataa caatggtaac aatagtaata attgtaattc caatatcggg atgggaggat 2220
 gtggctccaa catgccattt agagcaggag attggaagtg ttccacgtgc acgtatcata 2280
 acttttgctaa aaacgtagtg tgcttacgct gtgggtgtcc aaaatcaata agcggcgatg 2340
 caagtgaac caatcattac atagattcat caacatttgg accagcgtcg cgtactccca 2400
 gtaataacaa tatttctggt aataactaatg gtggtagcaa tgctgggtcg accgatggga 2460
 acgataacaa aggtcgtgat attagtttga tgggaatttat gtcaccaccg ttatcgatgg 2520
 caacaaagtc aatgaaggag ggagatggga atggtagctc gtttaacgag ttcaaaagtg 2580
 acaaagctaa cgttaatttt tccaatgttg gtgataatag cgctttcggg aatgggttta 2640
 atagttcaat acgttggtag 2660

<210> 46

<211> 719

<212> PRT

<213> Candida albicans

<400> 46

Met His Tyr Val Val Leu Glu Leu Gln Val Ala His Leu Pro Asp Thr
 1 5 10 15

Pro Lys Asp Gln Cys Arg Ile Ala Asn Ile Ala Phe Gln Ile Val Asn
 20 25 30

Ala Glu Thr Leu Val Cys His Tyr Gly Thr Asn Ser Leu Pro Ser Ile
 35 40 45

Glu Val Asn Gly Thr Thr Lys Ser Leu Glu Ser Ala Met Val Gln Leu
 50 55 60

Asp Lys Asp Ile His Asp Val Ile Gly Asn Asp Asp Phe Val Leu Val
 65 70 75 80

Ser Leu Tyr Ser Thr Trp His Ile Arg Val Thr Leu Pro Arg Gln Ala
 85 90 95

Arg Asp Asp Gly Phe Ile Leu Thr Ser Tyr Leu Gln His Pro Lys Val
 100 105 110

Phe Asp Leu Trp Lys Glu Phe Asp Arg Trp Cys Val Asn His Pro Glu
 115 120 125

Ile Leu Gly Gln Lys Lys Ala Ile Ser Asn Asn Asn Cys Asn Thr Lys
 130 135 140

Ser Ile Ser Ile Asn Ala Ala Lys Asn Thr Lys Asp Leu Asp Glu Ile
 145 150 155 160

Val Arg Ile Leu Glu Val Ser Ile Pro Thr Glu Glu Ala Gly Ser Val
 165 170 175

Pro Glu Ile Tyr Ser Leu Leu Lys Arg Thr Thr Asp Ile Leu Ile Gln
 180 185 190

Leu His Lys Lys Cys Thr Ser Pro Glu Asp Met Glu Ser Val Leu Thr
 195 200 205

Lys Pro Tyr Asp Ser His Thr Asp Ile Arg Ala Phe Leu Gln Glu Lys
 210 215 220
 Ser Lys Ile Leu Tyr Met Asn Asn Leu Pro Pro Asp Thr Thr Gln Ser
 225 230 235 240
 Glu Leu Glu Ser Trp Phe Thr Gln Tyr Gly Val Arg Pro Val Gly Phe
 245 250 255
 Trp Thr Val Lys Asn Ile Val Glu Asp Thr Ser Asn Val Asn Asn Asn
 260 265 270
 Trp Ser Leu Asn Asn Ser Pro Tyr Val Glu Asp Gln Asp Ser Ile Ser
 275 280 285
 Gly Phe Val Val Phe Gln Thr His Glu Glu Ala Thr Glu Val Leu Ala
 290 295 300
 Leu Asn Gly Arg Ser Ile Leu Ser Asn Leu Ala Asn Thr Lys Gln Pro
 305 310 315 320
 Arg Val Val Glu His Val Leu Glu Leu Gln Pro Ser Ser Thr Gly Val
 325 330 335
 Leu Asp Lys Ala Gln Glu Ile Leu Ser Pro Phe Pro Gln Ser Lys Asn
 340 345 350
 Lys Pro Arg Pro Gly Asp Trp Asn Cys Pro Ser Cys Gly Phe Ser Asn
 355 360 365
 Phe Gln Arg Arg Thr Ala Cys Phe Arg Cys Ser Phe Pro Ala Pro Ser
 370 375 380
 Asn Ser Gln Ile His Thr Ala Asn Ser Asn Asn Asn Val Asn Ser Ser
 385 390 395 400
 Arg Asn Asn Leu Asn Asn Arg Val Asn Ser Gly Ser Ser Ser Asn Ile
 405 410 415
 Ser Asn Thr Ala Ala Asn His Pro Tyr Gly Ala Pro Glu Phe Asn Met
 420 425 430
 Ile Ala Asn Asn Thr Pro Ala Ala Leu Thr Tyr Asn Arg Ala His Phe
 435 440 445
 Pro Ala Ile Thr Pro Leu Ser Arg Gln Asn Ser Leu Asn Met Ala Pro
 450 455 460
 Ser Asn Ser Gly Ser Pro Ile Ile Ile Ala Asp His Phe Ser Gly Asn
 465 470 475 480
 Asn Asn Ile Ala Pro Asn Tyr Arg Tyr Asn Asn Asn Ile Asn Asn Asn
 485 490 495
 Asn Asn Asn Ile Asn Asn Met Thr Asn Asn Arg Tyr Asn Ile Asn Asn
 500 505 510

Asn	Ile	Asn	Gly	Asn	Gly	Asn	Gly	Asn	Gly	Asn	Asn	Ser	Asn	Asn	Asn
		515					520					525			
Asn	Asn	His	Asn	Asn	Asn	His	Asn	Asn	Asn	His	His	Asn	Gly	Ser	Ile
		530				535					540				
Asn	Ser	Asn	Ser	Asn	Thr	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Gly	Asn
545					550					555					560
Asn	Ser	Asn	Asn	Cys	Asn	Ser	Asn	Ile	Gly	Met	Gly	Gly	Cys	Gly	Ser
				565					570					575	
Asn	Met	Pro	Phe	Arg	Ala	Gly	Asp	Trp	Lys	Cys	Ser	Thr	Cys	Thr	Tyr
			580					585					590		
His	Asn	Phe	Ala	Lys	Asn	Val	Val	Cys	Leu	Arg	Cys	Gly	Gly	Pro	Lys
		595					600					605			
Ser	Ile	Ser	Gly	Asp	Ala	Ser	Glu	Thr	Asn	His	Tyr	Ile	Asp	Ser	Ser
		610				615					620				
Thr	Phe	Gly	Pro	Ala	Ser	Arg	Thr	Pro	Ser	Asn	Asn	Asn	Ile	Ser	Val
625					630					635					640
Asn	Thr	Asn	Gly	Gly	Ser	Asn	Ala	Gly	Arg	Thr	Asp	Gly	Asn	Asp	Asn
				645					650					655	
Lys	Gly	Arg	Asp	Ile	Ser	Leu	Met	Glu	Phe	Met	Ser	Pro	Pro	Leu	Ser
			660					665				670			
Met	Ala	Thr	Lys	Ser	Met	Lys	Glu	Gly	Asp	Gly	Asn	Gly	Ser	Ser	Phe
		675					680					685			
Asn	Glu	Phe	Lys	Ser	Asp	Lys	Ala	Asn	Val	Asn	Phe	Ser	Asn	Val	Gly
		690				695					700				
Asp	Asn	Ser	Ala	Phe	Gly	Asn	Gly	Phe	Asn	Ser	Ser	Ile	Arg	Trp	
705					710					715					

```
<210> 47
<211> 578
<212> DNA
<213> Candida albicans
```

<400> 47						
aacaagaaaa	cccttcggtt	gatcttagat	ttcttagagg	ttcatgaact	agaaagcgac	60
ttgaacaaag	tcatccttca	agaatcgaaa	tctcaagaga	aaaacaaaat	ttaatgtaga	120
ttgtccacta	tctcatgtaa	atatacataa	caggatttcc	tgagcggttcg	aaaatttagac	180
tgtacttttt	tgatgcgctc	ccgtacacct	ttgacatata	caaacatccg	cacatttttat	240
agcttttctt	ctagaatttt	ttccacgcgc	tctcgatcaa	tgaactctta	aaagtaactg	300
acccctaact	ttttcccagg	caaggctggc	ctcattaccc	tacccgaaag	tttcacttta	360
ccccattgca	gatggacgat	atttttaaca	gacgaaactg	acctcgtctt	ctataaaaat	420
ggacttctaa	gcaactctca	tttatcttat	attcgtttca	ttttgtacta	aaagaaccag	480
accacatcga	ttcaatcgaa	atgaagacca	agtggagaaa	gaagagaact	aqaagactta	540

48

agagaaagag acggaagggtg agagccagat ccaaataa

578

<210> 48

<211> 25

<212> PRT

<213> Candida albicans

<400> 48

Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Arg Arg Leu Lys Arg Lys
 1 5 10 15

Arg Arg Lys Val Arg Ala Arg Ser Lys
 20 25

<210> 49

<211> 1354

<212> DNA

<213> Candida albicans

<400> 49

tattgacggt tcgctctcag gtccaccgtg ttctcaaaaag atactttttaa aacctaataaac 60
 acacgaaatc atattatgat aattcagaat gatagtgtgg tactgtgtca attgactggt 120
 caagactgaa gaggatcttt gatttggtgt tactcaacaa ataatcttca cgaaaacttt 180
 ctcaatctgg ggactgtatt aatctcagac ccatacatat ctacacccat aactttttac 240
 atttaatttt ttatcacata ataggtagct taaattgtaa agtcgcaaaa aaaaatggca 300
 gcgcagcctc tccgggtgaa ccccacgaca acttacctgg cactccatgc actaacgggc 360
 ggggtttgggc aggattccag catcaatttt gcaaaattca cacctgagta attcatatat 420
 gtaatataat gttaagcata cgctgtcgat tagcactatt attgaccgta gaatagggtac 480
 agtgagacag tatattcgaa atgggtatgt tgagatgaac aaaataataa agactgacaa 540
 ctgcagaaca gagaggatca tagcaacctg gtgcaagaaa gagcctcgaa gcgttaaaact 600
 tttggaacgt aattcatccg ttggctatgt ctattcaata cagttagaat acgaaagctg 660
 taatcaagta tatcggatta ttcgcaagca aagaatcaag gaaaagaaa tgaaaatagc 720
 atacatcttt aaattcagag gttttgctga attttaatag ggaagtttac gttatgattg 780
 ttggccgtag atcgccctagc gtttgaccaa atttaattct cctaattttt ttattgtaaa 840
 aaagccttcc aacgaaataa attagttatt ggtttttttt ctctgttacg agggatatat 900
 gatgcctgtg cttgttagtt cattataagt gctaataaaa tactaacgtt aataaaaatt 960
 tggaatatta ttteattttt tatectatta ataggccggt gttaaagctt acgaactaag 1020
 aaccaaatcc aaggaacaat tggcttctca attgggttgac ttgaaaaagg agttggctga 1080
 attgaaggtc caaaagttgt ccagaccatc tttgccaaag atcaagaccg tcagaaagag 1140
 tatcgccctg gtcttgaccg tcatcaacga acaacaaaga gaagctgtta gacaattata 1200
 caagggtaag aagtaccaac caaaggactt gagagccaag aagaccagag ctttgagaag 1260
 agctttgacc aaattcgaag cttcccaagt taccgaaaag caaagaaaga agcaaatcgc 1320
 tttccacaa agaaagtacg ctattaaggc ttaa 1354

<210> 50

<211> 120

<212> PRT

<213> Candida albicans

<400> 50

Met Ala Gly Val Lys Ala Tyr Glu Leu Arg Thr Lys Ser Lys Glu Gln
 1 5 10 15

Leu Ala Ser Gln Leu Val Asp Leu Lys Lys Glu Leu Ala Glu Leu Lys
20 25 30
Val Gln Lys Leu Ser Arg Pro Ser Leu Pro Lys Ile Lys Thr Val Arg
35 40 45
Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu
50 55 60
Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu
65 70 75 80
Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu
85 90 95
Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro
100 105 110
Gln Arg Lys Tyr Ala Ile Lys Ala
115 120

<210> 51
<211> 3254
<212> DNA
<213> Candida albicans

<400> 51
atcaagtttc ctttaaaggg atatataaca gattctaaaa ctgacagaaa tatttcgagt 60
gaagaagaag cgttaaatat tggatctttc cgcagttcta ctctgataca tttttgaagt 120
aggagagtca tttagaaggc gtattgctca atagtagaaa gcaggcctgt gcacatgaat 180
taattaaaaa atataaagggt agtgattaga cgacacatgt ccataggtaa cctgtcataa 240
ttttgaacaa tttcccttct tttctttttt ttttttgggt gcggcgatat gtagcttggt 300
aatttacaca tcatgtactt ttctgcatca aaatatgaaa ggcgatagta gctaaagaaa 360
ataccgagaa tttcctcgaa aagttgacga caaaagaaag gcataaaaaa gtaatttgaa 420
aatattttta aactgtttta acccatctag catccgcgct aaaaaaggaa gatacaggat 480
acagcggaaa caacttttaa atgatggaaa ctcttacaga caatatagtt tccccttttc 540
acaatttttg tagctcgaca caatatagtg gtaccttgct gagaactccc aaccaaataa 600
tagagctaga gaagcccagt actctatccc cattgtcaag agggaaaaaa tggacggaaa 660
agttagccag gttccaaaga agtagtgcta aaaagaaaag attctcacct tctcctattt 720
cctcctctac attttctgtt tcacccaaat ctagggtcac ttcttcaaac tcttctggca 780
atgaagacgg taacctaatg aatacacctt ctacggtttc cactgattat ttgccacaac 840
accctcacag aacatcgtct ttgccaagac ctaattccaa tctctttcac gcaagtaata 900
gtaacctatc ccgagcaaat gagcccccaa gggccgaaaa tttatcagat aatataccac 960
ccaaggtcgc tccatttggc tatccaatac aaagaacctc tattaaaaaa tcctttttga 1020
atgcttcttg tacgttatgt gacgagccta tttctaacag aagaaaaggga gagaaaatta 1080
tagagcttgc atgtggccac ttaagtcacc aagaatgtct tattatctct tttggcacca 1140
cttcaaaggc agacgttcgt gcgctatttc cttttgtac caaatgtaaa aaagatacta 1200
acaaagccgt tcaatgcatt ccagaaaatg atgaactaaa ggatattcta atttctgatt 1260
ttttgattca taagattcct gattctgagt tatcaatcac acctcagtcg cgctttcctc 1320
cttattccac actcttgctt ccttttgggt tatcctatac acctgttgaa agacaaacga 1380
tatattctca agctccaagt ctaaacccaa atctcatatt ggctgcaccc cccaaggaaa 1440
gaaaccaaat tccacaaaaa aaatcaaaact atacattttt acattcaccc ctggggcaca 1500
gaagaattcc gtccggagca aactctatct tagcagacac ctctgtagcg ttgtcagcta 1560
atgattctat ttctgctgtt tccaattcgg taagagcaaaa ggatgacgaa accaaaacaa 1620
cgttgccgct gttaaggtca tattttattc aaattctttt gaacaatttc caggaagaat 1680

<400> 52																
Met	Met	Glu	Thr	Pro	Thr	Asp	Asn	Ile	Val	Ser	Pro	Phe	His	Asn	Phe	
1				5					10					15		
Gly	Ser	Ser	Thr	Gln	Tyr	Ser	Gly	Thr	Leu	Ser	Arg	Thr	Pro	Asn	Gln	
			20					25					30			
Ile	Ile	Glu	Leu	Glu	Lys	Pro	Ser	Thr	Leu	Ser	Pro	Leu	Ser	Arg	Gly	
		35					40					45				
Lys	Lys	Trp	Thr	Glu	Lys	Leu	Ala	Arg	Phe	Gln	Arg	Ser	Ser	Ala	Lys	
	50					55					60					
Lys	Lys	Arg	Phe	Ser	Pro	Ser	Pro	Ile	Ser	Ser	Ser	Thr	Phe	Ser	Phe	
65					70					75					80	
Ser	Pro	Lys	Ser	Arg	Val	Thr	Ser	Ser	Asn	Ser	Ser	Gly	Asn	Glu	Asp	
				85					90					95		
Gly	Asn	Leu	Met	Asn	Thr	Pro	Ser	Thr	Val	Ser	Thr	Asp	Tyr	Leu	Pro	
			100					105					110			
Gln	His	Pro	His	Arg	Thr	Ser	Ser	Leu	Pro	Arg	Pro	Asn	Ser	Asn	Leu	

115	120	125
Phe His Ala Ser Asn Ser Asn Leu Ser Arg Ala Asn Glu Pro Pro Arg 130 135 140		
Ala Glu Asn Leu Ser Asp Asn Ile Pro Pro Lys Val Ala Pro Phe Gly 145 150 155 160		
Tyr Pro Ile Gln Arg Thr Ser Ile Lys Lys Ser Phe Leu Asn Ala Ser 165 170 175		
Cys Thr Leu Cys Asp Glu Pro Ile Ser Asn Arg Arg Lys Gly Glu Lys 180 185 190		
Ile Ile Glu Leu Ala Cys Gly His Leu Ser His Gln Glu Cys Leu Ile 195 200 205		
Ile Ser Phe Gly Thr Thr Ser Lys Ala Asp Val Arg Ala Leu Phe Pro 210 215 220		
Phe Cys Thr Lys Cys Lys Lys Asp Thr Asn Lys Ala Val Gln Cys Ile 225 230 235 240		
Pro Glu Asn Asp Glu Leu Lys Asp Ile Leu Ile Ser Asp Phe Leu Ile 245 250 255		
His Lys Ile Pro Asp Ser Glu Leu Ser Ile Thr Pro Gln Ser Arg Phe 260 265 270		
Pro Pro Tyr Ser Pro Leu Leu Pro Pro Phe Gly Leu Ser Tyr Thr Pro 275 280 285		
Val Glu Arg Gln Thr Ile Tyr Ser Gln Ala Pro Ser Leu Asn Pro Asn 290 295 300		
Leu Ile Leu Ala Ala Pro Pro Lys Glu Arg Asn Gln Ile Pro Gln Lys 305 310 315 320		
Lys Ser Asn Tyr Thr Phe Leu His Ser Pro Leu Gly His Arg Arg Ile 325 330 335		
Pro Ser Gly Ala Asn Ser Ile Leu Ala Asp Thr Ser Val Ala Leu Ser 340 345 350		
Ala Asn Asp Ser Ile Ser Ala Val Ser Asn Ser Val Arg Ala Lys Asp 355 360 365		
Asp Glu Thr Lys Thr Thr Leu Pro Leu Leu Arg Ser Tyr Phe Ile Gln 370 375 380		
Ile Leu Leu Asn Asn Phe Gln Glu Glu Leu Gln Asp Trp Arg Ile Asp 385 390 395 400		
Gly Asp Tyr Gly Leu Leu Arg Leu Val Asp Lys Leu Met Ile Ser Lys 405 410 415		
Asp Gly Gln Arg Tyr Ile Gln Cys Trp Cys Phe Leu Phe Glu Asp Ala		

420	425	430
Phe Val Ile Ala Glu Val Asp Asn Asp Val Asp Val Leu Glu Ile Arg		
435	440	445
Leu Lys Asn Leu Glu Val Phe Thr Pro Ile Ala Asn Leu Arg Met Thr		
450	455	460
Thr Leu Glu Ala Ser Val Leu Lys Cys Thr Leu Asn Lys Gln His Cys		
465	470	475
Ala Asp Leu Ser Asp Leu Tyr Ile Val Gln Asn Ile Asn Ser Asp Glu		
485	490	495
Ser Thr Thr Val Gln Lys Trp Ile Ser Gly Ile Leu Asn Gln Asp Phe		
500	505	510
Val Phe Asn Glu Asp Asn Ile Thr Ser Thr Leu Pro Ile Leu Pro Ile		
515	520	525
Ile Lys Asn Phe Ser Lys Asp Val Gly Asn Gly Arg His Glu Thr Ser		
530	535	540
Thr Phe Leu Gly Leu Ile Asn Pro Asn Lys Val Val Glu Val Gly Asn		
545	550	555
Val His Asp Asn Asp Thr Val Ile Ile Arg Arg Gly Phe Thr Leu Asn		
565	570	575
Ser Gly Glu Cys Ser Arg Gln Ser Thr Val Asp Ser Ile Gln Ser Val		
580	585	590
Leu Thr Thr Ile Ser Ser Ile Leu Ser Leu Lys Arg Glu Lys Pro Asp		
595	600	605
Asn Leu Ala Ile Ile Leu Gln Ile Asp Phe Thr Lys Leu Lys Glu Glu		
610	615	620
Asp Ser Leu Ile Val Val Tyr Asn Ser Leu Lys Ala Leu Thr Ile Lys		
625	630	635
Phe Ala Arg Leu Gln Phe Cys Phe Val Asp Arg Asn Asn Tyr Val Leu		
645	650	655
Asp Tyr Gly Ser Val Leu His Lys Ile Asp Ser Leu Asp Ser Ile Ser		
660	665	670
Asn Leu Lys Ser Lys Ser Ser Ser Thr Gln Phe Ser Pro Ile Trp Leu		
675	680	685
Lys Asn Thr Leu Tyr Pro Glu Asn Ile His Glu His Leu Gly Ile Val		
690	695	700
Ala Val Ser Asn Ser Asn Met Glu Ala Lys Lys Ser Ile Leu Phe Gln		
705	710	715
Asp Tyr Arg Cys Phe Thr Ser Phe Gly Arg Arg Arg Pro Asn Glu Leu		

Glu	Leu	Thr	Leu	Asp	Ile	Leu	Arg	Val	Leu	Asn	Ala	Glu	Asp	Leu	Asp	325	330	335	
Val	Arg	Ser	Lys	Ala	Leu	Asp	Ile	Ser	Met	Asp	Leu	Ala	Thr	Ser	Arg	340	345	350	
Asn	Ala	Glu	Asp	Val	Val	Gln	Leu	Lys	Lys	Glu	Leu	Gln	Thr	Thr		355	360	365	
Val	Asn	Asn	Pro	Asp	Gln	Asp	Lys	Ala	Met	Gln	Tyr	Arg	Gln	Leu	Leu	370	375	380	
Ile	Lys	Thr	Ile	Arg	Thr	Val	Ala	Val	Asn	Phe	Val	Glu	Met	Ala	Ala	385	390	395	400
Ser	Val	Val	Ser	Leu	Leu	Leu	Asp	Phe	Ile	Gly	Asp	Leu	Asn	Ser	Val	405	410	415	
Ala	Ala	Ser	Gly	Ile	Ile	Ala	Phe	Ile	Lys	Glu	Val	Ile	Glu	Lys	Tyr	420	425	430	
Pro	Gln	Leu	Arg	Ala	Asn	Ile	Leu	Glu	Asn	Met	Val	Gln	Thr	Leu	Asp	435	440	445	
Lys	Val	Arg	Ser	Ala	Lys	Ala	Tyr	Arg	Gly	Ala	Leu	Trp	Ile	Met	Gly	450	455	460	
Glu	Tyr	Ala	Glu	Gly	Glu	Ser	Glu	Ile	Gln	His	Cys	Trp	Lys	His	Ile	465	470	475	480
Arg	Asn	Ser	Val	Gly	Glu	Val	Pro	Ile	Leu	Gln	Ser	Glu	Ile	Lys	Lys	485	490	495	
Leu	Thr	Gln	Asn	Gln	Glu	His	Thr	Glu	Glu	Asn	Glu	Val	Asp	Ala	Thr	500	505	510	
Ala	Lys	Pro	Thr	Gly	Pro	Val	Ile	Leu	Pro	Asp	Gly	Thr	Tyr	Ala	Thr	515	520	525	
Glu	Ser	Ala	Phe	Asp	Val	Lys	Thr	Ser	Gln	Lys	Ser	Val	Thr	Asp	Glu	530	535	540	
Glu	Arg	Asp	Ser	Arg	Pro	Pro	Ile	Arg	Arg	Phe	Val	Leu	Ser	Gly	Asp	545	550	555	560
Phe	Tyr	Thr	Ala	Ala	Ile	Leu	Ala	Asn	Thr	Ile	Ile	Lys	Leu	Val	Leu	565	570	575	
Lys	Phe	Glu	Asn	Val	Ser	Lys	Asn	Lys	Thr	Val	Ile	Asn	Ala	Leu	Lys	580	585	590	
Ala	Glu	Ala	Leu	Leu	Ile	Leu	Val	Ser	Ile	Val	Arg	Val	Gly	Gln	Ser	595	600	605	
Ser	Leu	Val	Glu	Lys	Lys	Ile	Asp	Glu	Asp	Ser	Leu	Glu	Arg	Val	Met	610	615	620	

Thr Ser Ile Ser Ile Leu Leu Asp Glu Val Asn Pro Glu Glu Lys Lys
 625 630 635 640
 Glu Glu Val Lys Leu Leu Glu Val Ala Phe Leu Asp Thr Thr Lys Ser
 645 650 655
 Ser Phe Lys Arg Gln Ile Glu Ile Ala Lys Lys Asn Lys His Lys Arg
 660 665 670
 Ala Leu Lys Asp Ser Cys Lys Asn Ile Glu Pro Ile Asp Thr Pro Ile
 675 680 685
 Ser Phe Arg Gln Phe Ala Gly Val Asp Ser Thr Asn Val Gln Lys Asp
 690 695 700
 Ser Ile Glu Glu Asp Leu Gln Leu Ala Met Lys Gly Asp Ala Ile His
 705 710 715 720
 Ala Thr Ser Ser Ser Ser Ile Ser Lys Leu Lys Lys Ile Val Pro Leu
 725 730 735
 Cys Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Cys Ile Thr Asn Asn
 740 745 750
 Gln Phe Asp Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Lys Glu
 755 760 765
 Thr Leu Lys Asn Leu His Val Gln Phe Ala Thr Leu Gly Asp Leu Lys
 770 775 780
 Ile Ile Asp Thr Pro Gln Lys Thr Asn Val Ile Pro His Gly Phe His
 785 790 795 800
 Lys Phe Thr Val Thr Val Lys Val Ser Ser Ala Asp Thr Gly Val Ile
 805 810 815
 Phe Gly Asn Ile Ile Tyr Asp Gly Ala His Gly Glu Asp Ala Arg Tyr
 820 825 830
 Val Ile Leu Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro
 835 840 845
 Ala Thr Ala Asp Asp Glu His Phe Arg Thr Met Trp Asn Ala Phe Glu
 850 855 860
 Trp Glu Asn Lys Ile Ser Val Lys Ser Gln Leu Pro Thr Leu His Ala
 865 870 875 880
 Tyr Leu Arg Glu Leu Val Lys Gly Thr Asn Met Gly Ile Leu Thr Pro
 885 890 895
 Ser Glu Ser Leu Gly Glu Asp Asp Cys Arg Phe Leu Ser Cys Asn Leu
 900 905 910
 Tyr Ala Lys Ser Ser Phe Gly Glu Asp Ala Leu Ala Asn Leu Cys Ile
 915 920 925

Ser Ser Met Ala Thr Tyr Asn Ala Ser Glu Lys Asn Leu Asn Glu His
 20 25 30
 Pro Ser Pro Gln Ile Ala Gln Pro Ser Thr Ser Gln Lys Leu Pro Tyr
 35 40 45
 Arg Ile Asn Pro Thr Thr Thr Asn Gly Asp Thr Asp Ile Ser Val Asn
 50 55 60
 Ser Asn Pro Ile Gln Pro Pro Leu Pro Asn Leu Met His Leu Ser Gly
 65 70 75 80
 Pro Ser Asp Tyr Arg Ser Met His Gln Ser Pro Ile His Pro Ser Tyr
 85 90 95
 Ile Ile Pro Pro His Ser Asn Glu Arg Lys Gln Ser Ala Ser Tyr Asn
 100 105 110
 Arg Pro Gln Asn Ala His Val Ser Ile Gln Pro Ser Val Val Phe Pro
 115 120 125
 Pro Lys Ser Tyr Ser Ile Ser Tyr Ala Pro Tyr Gln Ile Asn Pro Pro
 130 135 140
 Leu Pro Asn Gly Leu Pro Asn Gln Ser Ile Ser Leu Asn Lys Glu Tyr
 145 150 155 160
 Ile Ala Glu Glu Gln Leu Ser Thr Leu Pro Ser Arg Asn Thr Ser Val
 165 170 175
 Thr Thr Ala Pro Pro Ser Phe Gln Asn Ser Ala Asp Thr Ala Lys Asn
 180 185 190
 Ser Ala Asp Asn Asn Asp Asn Asn Asp Asn Val Thr Lys Pro Val Pro
 195 200 205
 Asp Lys Asp Thr Gln Leu Ile Ser Ser Ser Gly Lys Thr Leu Arg Asn
 210 215 220
 Thr Arg Arg Ala Ala Gln Asn Arg Thr Ala Gln Lys Ala Phe Arg Gln
 225 230 235 240
 Arg Lys Glu Lys Tyr Ile Lys Asn Leu Glu Gln Lys Ser Lys Ile Phe
 245 250 255
 Asp Asp Leu Leu Ala Glu Asn Asn Asn Phe Lys Ser Leu Asn Asp Ser
 260 265 270
 Leu Arg Asn Asp Asn Asn Ile Leu Ile Ala Gln His Glu Ala[^] Ile Arg
 275 280 285
 Asn Ala Ile Thr Met Leu Arg Ser Glu Tyr Asp Val Leu Cys Asn Glu
 290 295 300
 Asn Asn Met Leu Lys Asn Glu Asn Ser Ile Ile Lys Asn Glu His Asn
 305 310 315 320

[illegible]

tagacgcatt atacaagttg ggtccaggag aggataccgc caccaagtag

2270

<210> 58

<211> 589

<212> PRT

<213> Candida albicans

<400> 58

Met	Ser	Gly	Val	Ser	Asn	Lys	Thr	Val	Ser	Ile	Asn	Gly	Trp	Tyr	Gly
1				5					10					15	

Met	Pro	Ile	His	Leu	Leu	Arg	Glu	Glu	Gly	Asp	Phe	Ala	Gln	Phe	Met
			20					25					30		

Ile	Leu	Thr	Ile	Asn	Glu	Leu	Lys	Ile	Ala	Ile	His	Gly	Tyr	Leu	Arg
		35					40					45			

Asn	Thr	Pro	Trp	Tyr	Asn	Met	Leu	Lys	Asp	Tyr	Leu	Phe	Val	Ile	Phe
	50					55					60				

Cys	Tyr	Lys	Leu	Ile	Ser	Asn	Phe	Phe	Tyr	Leu	Leu	Lys	Val	Tyr	Gly
65					70					75					80

Pro	Val	Arg	Leu	Ala	Val	Arg	Thr	Tyr	Glu	His	Ser	Ser	Arg	Arg	Leu
			85						90					95	

Phe	Arg	Trp	Leu	Leu	Asp	Ser	Pro	Phe	Leu	Arg	Gly	Thr	Val	Glu	Lys
		100						105					110		

Glu	Val	Thr	Lys	Val	Lys	Gln	Ser	Ile	Glu	Asp	Glu	Leu	Ile	Arg	Ser
		115				120						125			

Asp	Ser	Gln	Leu	Met	Asn	Phe	Pro	Gln	Leu	Pro	Ser	Asn	Gly	Ile	Pro
	130					135					140				

Gln	Asp	Asp	Val	Ile	Glu	Glu	Leu	Asn	Lys	Leu	Asn	Asp	Leu	Ile	Pro
145					150					155					160

His	Thr	Gln	Trp	Lys	Glu	Gly	Lys	Val	Ser	Gly	Ala	Val	Tyr	His	Gly
			165						170					175	

Gly	Asp	Asp	Leu	Ile	His	Leu	Gln	Thr	Ile	Ala	Tyr	Glu	Lys	Tyr	Cys
			180				185						190		

Val	Ala	Asn	Gln	Leu	His	Pro	Asp	Val	Phe	Pro	Ala	Val	Arg	Lys	Met
		195					200					205			

Glu	Ser	Glu	Val	Val	Ser	Met	Val	Leu	Arg	Met	Phe	Asn	Ala	Pro	Ser
	210					215					220				

Asp	Thr	Gly	Cys	Gly	Thr	Thr	Thr	Ser	Gly	Gly	Thr	Glu	Ser	Leu	Leu
225					230					235					240

Leu	Ala	Cys	Leu	Ser	Ala	Lys	Met	Tyr	Ala	Leu	His	His	Arg	Gly	Ile
			245						250					255	

Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
 260 265 270
 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
 275 280 285
 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
 290 295 300
 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
 305 310 315 320
 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
 325 330 335
 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
 340 345 350
 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
 355 360 365
 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
 370 375 380
 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
 385 390 395 400
 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
 405 410 415
 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
 420 425 430
 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
 435 440 445
 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
 450 455 460
 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
 465 470 475 480
 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
 485 490 495
 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
 500 505 510
 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
 515 520 525
 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
 530 535 540
 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
 545 550 555 560

Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
565 570 575

Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys
580 585

<210> 59

<211> 3470

<212> DNA

<213> Candida albicans

<400> 59

```

acgtcatttt gttcttgtgg agctgggtgg tcttgtggag cagattcctg tggagcagat 60
tcctgtggaa cttgtgggtc ttgtggagca tctggagcct gtggtgggtc ttggtgctgt 120
tcttcgactg gggcatcgac aacagattct ggtagttgct ctacgtgagt ttcttgagct 180
tcagacatta tccttatggg tttagcgtaa ttgcttaatt ttgattcctt caaaagtata 240
tatatttaga agagaggaaa ttatttttct catgtccttt ttaaaccctt ttgggtggcg 300
aaaaaaaaaga atgtaaaaaa ttttgccctt cgtttacagt gataaatata cggaggggct 360
ctatgataaa ggtagtagta aatcattgaa ttgttgaaac agcattgaca gatatgataa 420
caagcaattg taatcaataa gccaccaatt agaaggctac tcaaaagaat aaagttacta 480
taaaatatac tgcggtatat atgttgcggt ttcagcgatt tgcgtcctcg tatgcccag 540
cacaggccgt tagaaaatat ccagttggag gtatattcca tggttatgaa gtgagaagaa 600
ttctaccggg tccggagctg agactcactg cggtagattt ggtgcactcc cagacaggag 660
ccgagcattt gcatattgat agagacgaca agaataatgt gttcagcatt gcttttaaaa 720
ccaaccctcc agattccact ggggtccctc atattctaga gcatacaacg ttgtgtgggt 780
ctgttaaata tccagttagg gacccttttt tcaaaatgct aaataaatct ctagctaatt 840
tcatgaacgc tatgacaggt ccagattata cattttttcc cttttccact acgaaccctc 900
aagatttcgc taatttaaga ggtgtttatt tagactccac cttgaatccg ctacttaaac 960
aagaagattt tgatcaggag ggttggaggg tggagcataa aaacatcaca gacccgaga 1020
gtaacattgt tttcaaaggt gttgtctata acgaaatgaa aggtcaaata tcaaatgcc 1080
attactatth ctggagtaaa tttcaacagt ctatttatcc ttcctgaat aactccggcg 1140
gagatcctat gaaaattaca gacttgagat acggcgatct cttggatttc catcacaaaa 1200
attaccatcc ctccaatgca aaaactttca cgtacggtaa cttgccattg gtggatacgt 1260
taaagcaatt aaatgagcag ttcagtggtt acgggaagag agctcgaaag gataagttgt 1320
taatgcctat tgatttataa aaagacatag atgtcaagtt actgggtcaa atagatacta 1380
tgcttccacc ggagaagcag acaaaagcct caatgacgtg gatttgtgga gcgccacagg 1440
acacatatga tacctttttg ttaaaagtac tggggaattt attaatggat ggccattctt 1500
ctgtaatgta tcaaaaatta atagaatcag gaattgggtt ggagttctcc gtaaattcag 1560
gtgttgaacc aactacagca gtaaatttgc taactgttgg tatacagggc gtgagtata 1620
ttgaaatatt taaagacact gtaaataata tttttcaaaa cctgttgga acagaacatc 1680
cttttgaccg caagcgtatc gatgccataa ttgaacaatt ggaattatct aagaaggatc 1740
aaaaggctga ctttggaact caattactct attctatact acctggttgg acaaaacaaa 1800
tcgatccttt tgagagcttg ttgtttgagg acgttttgca aagatttaga ggtgacttag 1860
aaacgaaagg tgatacttta ttccaagatt taatccgtaa atatatcgtt cataaacctt 1920
gtttcacgtt ttccattcag ggatctgaag agttctctaa atctttggat gatgaagaac 1980
aaacaagact gagagaaaaa attactgcct tggatgaaca agacaagaaa aacatcttta 2040
aacgtgggat actgttacag gagaaacaaa atgaaaaaga agatttatcc tgtttaccta 2100
ccttacaaat aaaagacatc ccaagagctg gtgataaata ttcaatcgaa cagaagaata 2160
atacaatgtc taggattact gataccaatg gtatcacata tgtcagaggt aaacgtttac 2220
taaatagacat aatacccttt gaactcttcc catacttacc tttatttgc gaatcgtaa 2280
ctaaccatag gacaacaaca gaatccttta gtgaaataga agatcagata aaattacata 2340
cgggtgggat atcaacacat gtgaggtta catctgacct taacaccaca gagcctcgcc 2400
tgattttcgg gtttgaccga tgggtcttaa attcgaagac cgaccacatt tttgaattct 2460
gggtctaagat cttactagaa actgatttcc ataaaaacag cgataaattg aaagttctta 2520
tccgcttatt agcatcttca aacacatctt ctgtagcaga tgccggtcat gcatttgcaa 2580

```


[illegible]

785		790		795		800
Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr						
		805		810		815
Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala						
		820		825		830
Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu						
		835		840		845
Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Gly Ala Ser Tyr Ser Ala						
		850		855		860
Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu						
		865		870		875
Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp						
		885		890		895
Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe						
		900		905		910
Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr						
		915		920		925
Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln						
		930		935		940
Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr						
		945		950		955
Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu						
		965		970		975
Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu						
		980		985		

<210> 61

<211> 1612

<212> DNA

<213> Candida albicans

<400> 61

```

cttttctcag cacctgtcca gagacataac atcacaatca catcgcccca gtaaattgcat 60
acgcaagata agatacaaac tggctacggg aacactacgc caacgtgatt ggcaattgtg 120
ctctaatagt tactctatta ttgctgttaa ttgacaatgt ttagtcacgt gcaacacaat 180
tcaagtcacg tggaaaggcc ttccatggt gatccatctt ctacatcttc atcgggtcctg 240
cataaagtca taatatgggg ctactggaat gtatgcactt aacagtacta ttatatgggtg 300
aggctgtaat gcttaccgtt ttgtggctat tctcgtattc ttagggcccc ccatacaca 360
tttttcggta actgcgccat atagatgaaa gttgaaatga atattcaaaa gaatatatat 420
aataatgcag gagatcaagg aagaattaga tatgtataag agtgatggta gagggcaaaaa 480
ataaaaagta agcaggagaa tgaatcgtgt tggatatagac gtagatcata tgataggggtg 540
cctgcttctg gccgtagtgg tgggtgtttg ggttggcgct tcgtgtttga ctaatgaatt 600
gctcgagaca aacgcgtaca ataaaccttt cttccttact tatctaaaca tatcatcggt 660

```

```

tgctctttat ttgacgccag atctatggag gataatccaa tcaagaagga agagcttgca 720
ggaacggaca gaacgaacat tacctattca cacacaagaa tctttttcag agttcctacc 780
tttactatct tcaactcctt ctacttcttc aaatttgtct tcgatagcgg acacgaaagt 840
gaaggatata atgagggtga gtctgctatt ttgcgtcttg tggttcgtgg caaatattggc 900
ggctaacgct gctttgtcgt ataccacagt ggcttcgtca acaattcttt catcgacatc 960
ctcatttttt accttatttc ttgccactag tctaggaata gaaacttttt cgacaaaaaa 1020
actgctgggg ttatttgtgt ctttgttttg aattatctta attgtgatgc aatcctcgaa 1080
gcaacaggat tctgtgagtg cttoctcctt tttggtagg aacactttag cactgctggg 1140
gtcattgggt tacagtgtct atacaaccct tttgaaatac gaaatatcat ccaaaggctc 1200
cagactagac attcagatgt ttcttggtta tgttggtatc ttcacgtttc tgttgttttg 1260
gccaatttta ataactcgtg atataacaca tatggaaact tttgaactac caagtaactt 1320
ccacatttct tttcttggtca tgttaaattg tatcattatc tttgttagtg actatttttg 1380
gtgtaaagcc ctcattttga catcaccctt ggtggttacc gttgccttaa cttttactat 1440
cccgtagacc atgttcgctg attttgtatg gcgagaggca ttttttacgc cttggtatat 1500
cattggtgtt attttcattt ttgtttcatt ctttctagtt aaccatcggg gagaatctgc 1560
tggtgaaaag gactgtgctg cgggtgaaaa aggacctatc ttggatgcct aa 1612

```

<210> 62

<211> 370

<212> PRT

<213> Candida albicans

<400> 62

```

Met Asn Arg Val Gly Ile Asp Val Asp His Met Ile Gly Val Leu Leu
  1             5             10             15

```

```

Leu Ala Val Val Val Val Phe Trp Val Gly Ala Ser Cys Leu Thr Asn
      20             25             30

```

```

Glu Leu Leu Glu Thr Asn Ala Tyr Asn Lys Pro Phe Phe Leu Thr Tyr
      35             40             45

```

```

Leu Asn Ile Ser Ser Phe Ala Leu Tyr Leu Thr Pro Asp Leu Trp Arg
      50             55             60

```

```

Ile Ile Gln Ser Arg Arg Lys Ser Leu Gln Glu Arg Thr Glu Arg Thr
      65             70             75             80

```

```

Leu Pro Ile His Thr Gln Glu Ser Phe Ser Glu Phe Leu Pro Leu Leu
      85             90             95

```

```

Ser Ser Thr Pro Ser Thr Ser Ser Asn Leu Ser Ser Ile Ala Asp Thr
      100             105             110

```

```

Lys Val Lys Asp Thr Met Arg Leu Ser Leu Leu Phe Cys Val Leu Trp
      115             120             125

```

```

Phe Val Ala Asn Leu Ala Ala Asn Ala Ala Leu Ser Tyr Thr Thr Val
      130             135             140

```

```

Ala Ser Ser Thr Ile Leu Ser Ser Thr Ser Ser Phe Phe Thr Leu Phe
      145             150             155             160

```

```

Leu Ala Thr Ser Leu Gly Ile Glu Thr Phe Ser Thr Lys Lys Leu Leu
      165             170             175

```


Gly Leu Phe Val Ser Leu Phe Gly Ile Ile Leu Ile Val Met Gln Ser
 180 185 190
 Ser Lys Gln Gln Asp Ser Val Ser Ala Ser Ser Phe Leu Val Gly Asn
 195 200 205
 Thr Leu Ala Leu Leu Gly Ser Leu Gly Tyr Ser Val Tyr Thr Thr Leu
 210 215 220
 Leu Lys Tyr Glu Ile Ser Ser Lys Gly Leu Arg Leu Asp Ile Gln Met
 225 230 235 240
 Phe Leu Gly Tyr Val Gly Ile Phe Thr Phe Leu Leu Phe Trp Pro Ile
 245 250 255
 Leu Ile Ile Leu Asp Ile Thr His Met Glu Thr Phe Glu Leu Pro Ser
 260 265 270
 Asn Phe His Ile Ser Phe Leu Val Met Leu Asn Cys Ile Ile Ile Phe
 275 280 285
 Val Ser Asp Tyr Phe Trp Cys Lys Ala Leu Ile Leu Thr Ser Pro Leu
 290 295 300
 Val Val Thr Val Ala Leu Thr Phe Thr Ile Pro Leu Ala Met Phe Ala
 305 310 315 320
 Asp Phe Val Trp Arg Glu Ala Phe Phe Thr Pro Trp Tyr Ile Ile Gly
 325 330 335
 Val Ile Phe Ile Phe Val Ser Phe Phe Leu Val Asn His Arg Gly Glu
 340 345 350
 Ser Ala Val Glu Lys Asp Cys Ala Ala Val Glu Lys Gly Pro Ile Leu
 355 360 365
 Asp Ala
 370

<210> 63

<211> 1376

<212> DNA

<213> Candida albicans

<400> 63

cggcccatga gcataaattg agaacgatat tattaattct agtatatttt aggaacagca 60
 ggccattata tccaaaactt ttttaaaata gcatccacat cacttactgg cgtacagttt 120
 cgtgtctggc aacaaaaaag tacattttaat ttcaatgatt aaaaagacat taaacatccg 180
 tacattacgc acccatgcat gctatctgaa aatattctac atgctgcttt tagaaatttg 240
 aagcggcata tgggtgtttcc ttgcgagac gcgcgctcag gggaaactgcg attccgaaag 300
 atgcctttcc cagtcccata tgcccatccc aagatcatgc ccgggagagc aaatgtcgcc 360
 ccagccaggt cggacacatc tgtcattcga ccactaagta ttgtcaaagc tagggttaat 420
 tgaagatagc tctacatggt attagtagag tttttaaacg ttgagatact agtgaacgta 480
 tacacaagag cggataaaaag atgtcttttag ttgtccaaga acaagggtcc ttccaacaca 540
 ttttacggta tgtttattat tactagttag ctatgacaaa atcggtctaaa aacttaaaaa 600

```
<210> 65
<211> 1289
<212> DNA
<213> Candida albicans
```

<400> 65

```

actgcataca caataactgt agatgtagcc caaggcacta ccacagggtat ttctgctcac 60
gacagggtcga tgactttagg ggctcttgca gactcttcct ctacgccaaa atcattttta 120
aaaccagggc acatctgtcc cttgagagcc gctgatggcg gtgttttgca gagaagaggc 180
cacactgagg ccggtgtcga tttgtgtaaa ctaagtggac taagtcccgt cgctgttatt 240
ggcgaattgg ttaacgatga cgaacaagga actatgatga gattaaatga ctgccaaagc 300
tttggtgaaga aacatggcat tcctttgatc tccatcgaag aattggccca atatttgaag 360
aaataatctg gtgaacattt tctccattca ttctatcaca acagactcac acatatatac 420
atgtatatat ttgtaacttt gtatatatct tttgtttttt gacctttttc ttcctctatg 480
tttttcagcc atacaaaaat atgggatttt tagcaagaga aaaagtacat ctaaaaaaag 540
tagtaatagg aggaagccaa gattggttga aacacagtta taaactcttc aaggcaatta 600
tgaacaggat tttcggatat gggaacaaaa agagccatga tcagctctta caagagtcga 660
atcagtccat gaatcaggcc caacaatcac tatcgaacag aatatcccag ttagatactc 720
aaatcgccca gttaaaactc cagctgcaaa atattcaaaa gaatttgcaa agatcaaaca 780
acaagcaacc ctcgttaaga aaacaggcctt tgaagatttt aaataaacgt aaacagttag 840
aaaatatgaa ggattcttta gattctcaat cctgggtccat gacgcaagcc cagttaacaa 900
atgataaact acagaacaca atgatcacta taaacgcact aaagcaaaca aacaatgcca 960
tgaaggctca atacggcaag ataaatatcg acaaaactaca ggacatgcag gatgagatgc 1020
tggaattaat agaacaaggg gatgagctgc aagaagtctt ggcaatgaat aataacagtg 1080
gagagctcga cgacattagt gatgcagagc tggatgcaga gctggatgct ctggcacaag 1140
aggatttcac tttgccaaac agcgaaaact cattaggtaa cgatatgccc agttacttac 1200
taggtgcgaa tgcgccaccg gctttttattg atgaagagcc aaacttagat actgaagaca 1260
aaaataaagc tttagaaagc gctcagtga 1289

```

<210> 66

<211> 262

<212> PRT

<213> *Candida albicans*

<400> 66

```

Met Gly Phe Leu Ala Arg Glu Lys Val His Leu Lys Lys Val Val Ile
  1           5           10           15

Gly Gly Ser Gln Asp Trp Leu Lys His Ser Tyr Lys Leu Phe Lys Ala
      20           25           30

Ile Met Asn Arg Ile Phe Gly Tyr Gly Asn Lys Lys Ser His Asp Gln
      35           40           45

Leu Leu Gln Glu Ser Asn Gln Ser Met Asn Gln Ala Gln Gln Ser Leu
      50           55           60

Ser Asn Arg Ile Ser Gln Leu Asp Thr Gln Ile Ala Gln Leu Asn Phe
      65           70           75           80

Gln Leu Gln Asn Ile Gln Lys Asn Leu Gln Arg Ser Asn Asn Lys Gln
      85           90           95

Pro Ser Leu Arg Lys Gln Ala Leu Lys Ile Leu Asn Lys Arg Lys Gln
      100          105          110

Leu Glu Asn Met Lys Asp Ser Leu Asp Ser Gln Ser Trp Ser Met Thr
      115          120          125

Gln Ala Gln Leu Thr Asn Asp Asn Leu Gln Asn Thr Met Ile Thr Ile

```

<400>	67						
ggcaaatcaa	ttaaaattcc	ttttctctct	acctttgcta	atattaaaaa	ccatagttgt	60	
aaaggggtact	taatgctata	ttcctgttaa	gtttcctatt	tcaccttggt	ttttccaatt	120	
cttaccaat	tgaagcatat	gttttttaac	acccaatcat	tttccaccca	cacatatatt	180	
accctttttt	tgggtgaaga	gaagttagtat	tttgtttttc	atggggagtgg	aagtcctttc	240	
aaaactaatc	cgagcagtag	tgctgtctag	gcgggagatta	ttgaaagtcg	cgattggctg	300	
cagctagcgt	tttgtttttg	gtactacctg	tcaaaccggg	cgctcgcta	gattgcgcgg	360	
aggggtacgtt	gaaacttttg	cctttccacg	tcagtttata	atatcaaaag	cagcaatata	420	
cacattttaat	ggtttgccct	tagtgactat	tagggcgttt	tggtgaaaag	aaagagtcgc	480	
tcaaagaaat	caataatacc	atggctaaat	ttttgaaagc	aggtaaagtt	ggtagctaaa	540	
tttaacagag	caaacgctct	aattaagata	tccaataaaa	gggactttc	aggtgcataa	600	
gatgggaaat	tgtacaatct	gagggacaaa	caatatggaa	agcagtacat	gattgtattg	660	
tcattgtagg	aggtaccaat	tgtgccagta	aaaaagagag	ggcccgggga	gcaccacatt	720	
cacgaccaat	cgtgtcgatc	tgcaaaaaag	gcacatggaa	aatgtaattt	atcagtgttc	780	
aacactgagt	tgaacagata	gctatcta	caatgttaac	tttccaggga	acaaaaagct	840	
aaatccactt	ctcttttatt	tcaaaata	attagaata	gaaaaattta	ctacaaatt	900	
ttcgtattat	cgtagctgtc	gttgttcgtg	gtcgttacgc	tgaagaag	gttgtgatcg	960	
ttaagccaca	cgatgaggtt	tctaaatctc	atccattcgg	tcacgctttg	gttgccggta	1020	
ttgaaaggta	cccatcaaag	gtcaccaaga	agcacgggtc	caagaaggtc	gctaagagaa	1080	
ctaaaatcaa	gccattcatc	aaagtcgtca	actacaacca	cttattgcc	accagataca	1140	
ccttggtagt	tgaagccttc	aagagctgtt	tatctacaga	gacttttgaa	caaccatccc	1200	
aacgtgaaga	agccaagaag	gttgtaaga	aggtcatgtga	agaaagacat	caagctggta	1260	
aaaaccaatg	gttcttctcc	aagttgagat	tctaa			1295	

<210> 68
 <211> 136
 <212> PRT
 <213> Candida albicans

<400> 68
 Met Ala Lys Phe Leu Lys Ala Gly Lys Val Ala Val Val Val Arg Gly
 1 5 10 15
 Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
 20 25 30
 Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg
 35 40 45
 Tyr Pro Ser Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys
 50 55 60
 Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu
 65 70 75 80
 Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val
 85 90 95
 Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys
 100 105 110
 Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln
 115 120 125
 Trp Phe Phe Ser Lys Leu Arg Phe
 130 135

<210> 69
 <211> 2744
 <212> DNA
 <213> Candida albicans

<400> 69
 taacaataga aaaaaataca cacacattag attggaatta gagcttaagt ggtacaaact 60
 agggctaata aagaggtaac ggtcggttct ctactaaggt tcgtattgtg tggcaccgat 120
 gttaagcact tttaagcggg ataactcgag tggaaatttt atgtttagtt aggttttacc 180
 ttgaattttt ttaaaaaaaaa aagagtcaga caggctcgct ctttctact aaatattagg 240
 agcaaagcag taaaaagtct ctgaataagg atagtaacct gtagtaactc caaaatttat 300
 cttacaaaga gctattagta tcttggttct tctattttct tcgattattg gtgatttttc 360
 ccgcctctag ccaaattccga gcgttccatc gatttttttg ggaaaacagc acatgcaata 420
 aaataaaaag caaacaaata cgcgatagtg cagcaaacgt caacacaatc atcaaactct 480
 tttgcatatt tctattatag atgagacgag aaacgggtggg tgaattttct tcagatgacg 540
 atgatgatat tcttttggaa ttaggcacca ggcctccaag gtttactcaa ataccgcat 600
 catcagcagc attacaaaca caaattccca ctactttgga gggtacaacg accacattaa 660
 acaataaaca gagtaaaaat gataaccaac tgggttaacca actgaataaa gctcaagggtg 720
 aagcaagcat gcttcgtgat aaaataaact ttttgaacat tgaaagggaa aaggaaaaga 780
 atattcaagc cgtcaaagtt aatgaattgc aagtcaagca tcttcaagag ttggctaaat 840
 taaaacaaga attacagaaa ctggaagatg agaagaagtt cttacagatg gaagcgagag 900

```

<400> 70
Met Arg Arg Glu Thr Val Gly Glu Phe Ser Ser Asp Asp Asp Asp Asp
  1                               10                      15

Ile Leu Leu Glu Leu Gly Thr Arg Pro Pro Arg Phe Thr Gln Ile Pro
  20                      25                      30

Pro Ser Ser Ala Ala Leu Gln Thr Gln Ile Pro Thr Thr Leu Glu Val
  35                      40                      45

Thr Thr Thr Thr Leu Asn Asn Lys Gln Ser Lys Asn Asp Asn Gln Leu
  50                      55                      60

Val Asn Gln Leu Asn Lys Ala Gln Gly Glu Ala Ser Met Leu Arg Asp
  65                      70                      75                      80

Lys Ile Asn Phe Leu Asn Ile Glu Arg Glu Lys Glu Lys Asn Ile Gln
  85                      90                      95

```


Phe Val Tyr Lys Leu Ala Leu Thr Ile Ser Tyr Lys Pro Met Val Asn
 405 410 415
 Val Ile Phe Ser Ala Val Glu Val Val Asn Ile Ile Thr Ser Ile Ile
 420 425 430
 Leu Asn Met Asp Asn Ser Ser Asp Leu Lys Ser Leu Ile Ser Gly Ser
 435 440 445
 Trp Trp Arg Asp Cys Ile Thr Arg Leu Tyr Ala Leu Leu Glu Lys Glu
 450 455 460
 Ile Lys Ser Gly Asp Val Tyr Asn Glu Asn Val Asp Thr Thr Thr Leu
 465 470 475 480
 His Met Ser Lys Tyr His Asp Phe Phe Gly Leu Ile Arg Asn Ile Gly
 485 490 495
 Asp Asn Glu Leu Gly Gly Leu Ile Ser Lys Leu Ile Tyr Thr Asp Arg
 500 505 510
 Leu Gln Ser Val Pro Arg Val Ile Ser Lys Glu Asp Ile Gly Met Asp
 515 520 525
 Ser Asp Lys Phe Thr Ala Pro Ile Ile Gly Tyr Lys Met Glu Lys Trp
 530 535 540
 Leu Leu Lys Leu Lys Asp Glu Val Leu Asn Ile Phe Glu Asn Leu Leu
 545 550 555 560
 Met Ile Tyr Gly Asp Asp Ala Thr Ile Val Asn Gly Glu Met Leu Ile
 565 570 575
 His Ser Ser Lys Phe Leu Ser Arg Glu Gln Ala Leu Met Ile Glu Arg
 580 585 590
 Tyr Val Gly Gln Asp Ser Pro Asn Leu Asp Leu Arg Cys His Leu Ile
 595 600 605
 Glu His Thr Leu Thr Ile Ile Tyr Arg Leu Trp Lys Asp His Phe Lys
 610 615 620
 Gln Leu Arg Glu Glu Gln Ile Lys Gln Val Glu Ser Gln Leu Ile Met
 625 630 635 640
 Ser Leu Trp Arg Phe Leu Val Cys Gln Thr Glu Thr Val Thr Ala Asn
 645 650 655
 Glu Arg Glu Met Arg Asp His Arg His Leu Val Asp Ser Leu His Asp
 660 665 670
 Leu Thr Ile Lys Asp Gln Ala Ser Tyr Tyr Glu Asp Ala Phe Glu Asp
 675 680 685
 Leu Pro Glu Tyr Ile Glu Glu Glu Leu Lys Met Gln Leu Asn Lys Arg
 690 695 700

Thr Gly Arg Ile Met Gln Val Lys Tyr Asp Glu Lys Phe Gln Glu Met
705 710 715 720

Ala Arg Thr Ile Leu Glu Ser Lys Ser Phe Asp Leu Thr Thr Leu Glu
725 730 735

Glu Ala Asp Ser Leu Tyr Ile Ser Met Gly Leu
740 745

<210> 71
<211> 3929
<212> DNA
<213> Candida albicans

<400> 71
ctcttttaaat attctatgta ctttgtgcaa acatcattgt catcacataa atgcattcct 60
actattacta acttgaactt cacttcaactg gaagaactgg gttattcaag gtaaagaaat 120
catttgtttt gcgccaagtt tcgtctgaca agaatttttt attattattt cccacttttc 180
atcgaaggaa acgcgtcaaa tccattcggt actacgcgca atctgcgtta tttccttttt 240
cggcatacca tcgcgaaata tcaacggcca caccatagat tccttttgat gttaaattaa 300
aagcgactga atgaagtgc cacttttttt atttcttctt gattttcttt tctattttgt 360
tttgctttct cttctgtcga caacgtctca actgtactca ccattagtat tctcgaaggc 420
tttagcagac ttgtgaataa ttaattgccc actttgatca agaaagatat tcgcagcaca 480
atacaataat aacattcaaa atggcaatca atggtaacag tattcctgcc ataaaggata 540
ataccatcgg tccatggaaa ctaggtgaaa ctctcggtct agggagcact ggtaaagtcc 600
agcttgctcg taatggatcc acaggacaag aggcggcagt taaggtaata tcaaaagcag 660
tattcaatac cggtaatgtc agcggtagct cgattgttgg ctccaccacc ccagatgctc 720
taccatatgg tatagaacgc gaaataatca ttatgaagtt gttaaaccac ccaaagtgtg 780
tacgtttata tgatgtctgg gaaacaaata cagatttata ccttgtttta gaatacgcgg 840
agaaaggtag gttgttcaaa ttattgggtg agagaggtcc tctgccagag catgaagcta 900
tcaggttttt tagacaaatt attattgggtg tgcgtactg tcatgcgttg ggtattgtcc 960
atcgtgatct aaaaccggaa aatctattat tagatcataa atataacatc aagattgcag 1020
attttggtat ggctgctttg gaaactgaag gaaagctact ggagacgtcg tgcggatcac 1080
cacattatgc tgcaccagaa attgtatctg gtataccgta tcaagggttc gcaagtgatg 1140
tgtggtcatg cgggtgtgatc ctattcgccc ttcttactgg tcggttaccc tttgacgagg 1200
aagatggaag tataagaaca ctattactta aagttcaaaa aggtgagttc gaaatgcctt 1260
ctgatgatga aatttcgcgt gaagctcagg atttgattag aaaaatctta accgttgatc 1320
ctgaaagaag aatcaagacc agagatatat tcaaaccatcc gctattacaa aaatatccaa 1380
gtataagaga ttctaaaagt attagaggct taccaagaga agacacatat ctcacgccat 1440
tatcagaaag taattcttct attgacgcta cgattttgca aaatttagta atattatggc 1500
atggaagaga tcctgaagga attaaggaaa aactaagaga acctggcgct aatgcagaaa 1560
agacattata tgcactactg tatagattta agtgtgacac tcaaaaagag cttattaagc 1620
aacagcaagt taagaagagg cagtcaatta gtacggtttc tgtttcccca tctaaaaaag 1680
tatcgacaac tccacaacgc agaagaaata gagaatcttt aattagtgtg acatcttctc 1740
gtaaaaagcc aatatccttc aacaaattca ctgcctccag tgcctcctcc agcaatctaa 1800
ctacaccggg ttcttcaaaa cgcctttcaa aaaacttctc ttcaaagaag aaattatcta 1860
caatcgttaa ccaatcttct ccaacaccag catcacgtaa taaaagagct tcggttataa 1920
atgtggaaaa gaatcaaaaa agagcctcta tcttttctac taccaagaag aacaaaagat 1980
cttctagatc tatcaagaga atgtcattga taccaagcat gaaacgtgaa tcggtgacaa 2040
caaaattaat gtcaacatat gcgaaattgg cagaggatga cgattgggaa tacattgaga 2100
aggaaacaaa gagaacgagc tcaaattttg caactttgat agatgaaatt tttgagtacg 2160
aaaagtcga acaaaataag aaagagaagg aagagctaga acgtaaagtg agagaagcaa 2220
aagcacgtga agagctggaa cgtagaagac gtaaacaaga agaaaaagaa cgtgcaagaa 2280
aattactaga aaaggaagat ctgaaaagaa aacaggagga actcaagaag caaattgaaa 2340
ttgatataag tgatctagag caagagctgt ccaaacacaa agaggaaaaa ctggatggta 2400

```

atattagatc tatctctgct cctatggaaa atgaagagaa aaatatcaat catttgagg 2460
ttgatattga caatattctc cgtcgcogca acttttcttt acaaactaga cctgtgtcaa 2520
ggcttgatcc ggggtataatg ttctccagtc caactgagga agtaagtcca gtggaaccaa 2580
agagaacaga aaatgaaaga cttacaacag aaaagaaaat tttagaaact atcagaagat 2640
caaaattctt ggggttcatca tttaatatcg ataaagagtt gaaattgtct aaaatggaat 2700
atccaagtat aattgcacca caaagattgt cagaggagcg agtgggtgtca gattctaata 2760
atggatatga atctttgatc ctcccgaagg atgggaatgg cgtatctcaa ttaaaggata 2820
gtaccgcaac aactgctccc gtctctgatg gtaggttgag gaagatctct gaaattagag 2880
taccacaatt tactagaaaa tcaaggcatt ttagtgagtc caataaaaagg ctatctgtcc 2940
tgctgatgta ctctaccaag gagtcgttta ccaacttggg tgatattttg aaaaacggta 3000
accttgatgt caataaccaa caaagccaaa gaattccaac accaagaagt gcggatgatt 3060
cagaatttct ttttgaaact gtcaacgaag aagctgaata tacaggaaat agttcgaacg 3120
atgagagatt gtacgatgtc ggtgattcca ctatcaaaga caaatccgcg ttaaagctga 3180
actttgcaga tcggttttaat ggatcgaacg aagcgaaaca aactgataac ttacatcttc 3240
cgatccttcc tccgcttaat ggtgacaatg aattgcgtaa acagaatagc caagagggtg 3300
accaggcaca tccaaagatt aaatcgatga taccagaatc aggtctcttc tcacatactg 3360
aaaaggaaga agaaaatgag gaaaaaggaag agaaaaagcc agaacaacac aaacaagaag 3420
aggatcaaga aaaaagagag aaagtagtag atgatatgga gccaccattg aacaaatctg 3480
tgcaaaaaat tagggaaaaa aatgctggct cgcaggcaaa ggatcattca aaagatcact 3540
taaaagagca taagcaggat aaaaatacag caattggaaa tggttccttc ttagaaaaat 3600
tctcaaaatc ttcggacaaa acaatggaat tgatgccaa gatttctgca aaacaattgt 3660
ttaatggttt agagaagctg ttgctgggtt ggactcagta tggtttaaaa aatataaaaat 3720
cgcaccccaa caatctgacc ttaacgggta aactatcgag tgataatata ttctcactac 3780
gttcaacact ctttgaggtt aatatttata cgagaggtaa gatgagcgtt gtgcagttca 3840
agaaagtttc tggttcattc aaagctgtca aaaagtgggt caatgaagtt gagaacgtcc 3900
tgaataagga aggcgttcta caaaaatag 3929

```

<210> 72
 <211> 1142
 <212> PRT
 <213> Candida albicans

<400> 72
 Met Ala Ile Asn Gly Asn Ser Ile Pro Ala Ile Lys Asp Asn Thr Ile
 1 5 10 15
 Gly Pro Trp Lys Leu Gly Glu Thr Leu Gly Leu Gly Ser Thr Gly Lys
 20 25 30
 Val Gln Leu Ala Arg Asn Gly Ser Thr Gly Gln Glu Ala Ala Val Lys
 35 40 45
 Val Ile Ser Lys Ala Val Phe Asn Thr Gly Asn Val Ser Gly Thr Ser
 50 55 60
 Ile Val Gly Ser Thr Thr Pro Asp Ala Leu Pro Tyr Gly Ile Glu Arg
 65 70 75 80
 Glu Ile Ile Ile Met Lys Leu Leu Asn His Pro Asn Val Leu Arg Leu
 85 90 95
 Tyr Asp Val Trp Glu Thr Asn Thr Asp Leu Tyr Leu Val Leu Glu Tyr
 100 105 110
 Ala Glu Lys Gly Glu Leu Phe Asn Leu Leu Val Glu Arg Gly Pro Leu
 115 120 125

Pro Glu His Glu Ala Ile Arg Phe Phe Arg Gln Ile Ile Ile Gly Val
 130 135 140
 Ser Tyr Cys His Ala Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu
 145 150 155 160
 Asn Leu Leu Leu Asp His Lys Tyr Asn Ile Lys Ile Ala Asp Phe Gly
 165 170 175
 Met Ala Ala Leu Glu Thr Glu Gly Lys Leu Leu Glu Thr Ser Cys Gly
 180 185 190
 Ser Pro His Tyr Ala Ala Pro Glu Ile Val Ser Gly Ile Pro Tyr Gln
 195 200 205
 Gly Phe Ala Ser Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala Leu
 210 215 220
 Leu Thr Gly Arg Leu Pro Phe Asp Glu Glu Asp Gly Asn Ile Arg Thr
 225 230 235 240
 Leu Leu Leu Lys Val Gln Lys Gly Glu Phe Glu Met Pro Ser Asp Asp
 245 250 255
 Glu Ile Ser Arg Glu Ala Gln Asp Leu Ile Arg Lys Ile Leu Thr Val
 260 265 270
 Asp Pro Glu Arg Arg Ile Lys Thr Arg Asp Ile Leu Lys His Pro Leu
 275 280 285
 Leu Gln Lys Tyr Pro Ser Ile Arg Asp Ser Lys Ser Ile Arg Gly Leu
 290 295 300
 Pro Arg Glu Asp Thr Tyr Leu Thr Pro Leu Ser Glu Ser Asn Ser Ser
 305 310 315 320
 Ile Asp Ala Thr Ile Leu Gln Asn Leu Val Ile Leu Trp His Gly Arg
 325 330 335
 Asp Pro Glu Gly Ile Lys Glu Lys Leu Arg Glu Pro Gly Ala Asn Ala
 340 345 350
 Glu Lys Thr Leu Tyr Ala Leu Leu Tyr Arg Phe Lys Cys Asp Thr Gln
 355 360 365
 Lys Glu Leu Ile Lys Gln Gln Gln Val Lys Lys Arg Gln Ser Ile Ser
 370 375 380
 Ser Val Ser Val Ser Pro Ser Lys Lys Val Ser Thr Thr Pro Gln Arg
 385 390 395 400
 Arg Arg Asn Arg Glu Ser Leu Ile Ser Val Thr Ser Ser Arg Lys Lys
 405 410 415
 Pro Ile Ser Phe Asn Lys Phe Thr Ala Ser Ser Ala Ser Ser Ser Asn
 420 425 430


```

atttactcgt tctaacagag aagaaattta aatcattcat cgaatctcat ccgttagtc 660
tcgtcgagtt ttttgctcca tgggtgttgc attctcagat cttacgccct cacttagaag 720
aggccgcctc tatttttaaag gagcataacg tcccagttgt tcaaattgat tgtgaggcta 780
acagtatggt ttgcctgcaa caaactataa atacctaccc aaccttgaaa atctttaaaa 840
atgggtcgat ttttgatggt caagtctatc gcggtgtcaa gatcaccgat gaaatcactc 900
agtacatgat tcagctatac gaggcttctg tcatTTtatt aaattccgaa gatgaaatcc 960
aaccatactt ggaaaatgca actttaccag tagtaataaa cagaggcttg acaggcttga 1020
atgaaacgta tcaagaagtc gcaactggacc ttgctgagga ttacgtcttt ttatcccttc 1080
tagattcaga agataagtca ttatcaatcc acttgccaaa cactacagaa ccaattctgt 1140
ttgatggaaa tgtagactct ttggtcggaa attccgttgc tctaactcag tgggttaaaag 1200
tggtaatttt accttacttt accgacatcg aacctgatct cttccccaag tacatttcta 1260
gcaatttgcc gttggcttac ttcttttata cttctgagga agaattggaa gattacactg 1320
atcttttcac gcagttaggt aaggaaaatc gtggccaaat aaatttcatt gcattaaact 1380
ctacaatggt cccacaccac gtttagattcc taaatatgag agaacagttc ccattatttg 1440
ctatccataa tatgatcaat aatctgaaat atggtttacc acaactacca gaagaagagt 1500
acgcgaaatt agaaaaacca caaccactag acagagatat gatcgttcag ttggtaaaag 1560
attaccgtga aggtactgcc aagccaattg ttaagtcaga agagattcca aaagaacaaa 1620
agtccaatgt ttataaaata gttgggaaga cacatgacga cattgttcat gatgatgaca 1680
aggatgtcct tgtcaaatat tacgcgacat ggtgtattca tagtaaaagg tttgcgccta 1740
tttacgaaga aattgcaaat gtcttagcat ctgatgaatc tgttcgcgat aaaatcttga 1800
tcgccgaagt agattcaggg gcaaatagata tcttaagttt tcctgtgaca ggatatccaa 1860
ccattgcttt gtatcctgcc ggaaataact ctaagcctat tatcttcaat aaaattagaa 1920
atttgaaga tgttttcgaa tttatcaagg aatcaggtac acatcacatt gacggccagg 1980
caatttatga taaattgcac caggccaagg attctgaagt gtctactgaa gataccgtac 2040
atgatgaatt ataa 2054

```

<210> 76

<211> 517

<212> PRT

<213> Candida albicans

<400> 76

Met Gln Val Thr Thr Arg Phe Ile Ser Ala Ile Val Ser Phe Cys Leu
1 5 10 15

Phe Ala Ser Phe Thr Leu Ala Glu Asn Ser Ala Arg Ala Thr Pro Gly
20 25 30

Ser Asp Leu Leu Val Leu Thr Glu Lys Lys Phe Lys Ser Phe Ile Glu
35 40 45

Ser His Pro Leu Val Leu Val Glu Phe Phe Ala Pro Trp Cys Leu His
50 55 60

Ser Gln Ile Leu Arg Pro His Leu Glu Glu Ala Ala Ser Ile Leu Lys
65 70 75 80

Glu His Asn Val Pro Val Val Gln Ile Asp Cys Glu Ala Asn Ser Met
85 90 95

Val Cys Leu Gln Gln Thr Ile Asn Thr Tyr Pro Thr Leu Lys Ile Phe
100 105 110

Lys Asn Gly Arg Ile Phe Asp Gly Gln Val Tyr Arg Gly Val Lys Ile
115 120 125

Thr Asp Glu Ile Thr Gln Tyr Met Ile Gln Leu Tyr Glu Ala Ser Val
 130 135 140
 Ile Tyr Leu Asn Ser Glu Asp Glu Ile Gln Pro Tyr Leu Glu Asn Ala
 145 150 155 160
 Thr Leu Pro Val Val Ile Asn Arg Gly Leu Thr Gly Leu Asn Glu Thr
 165 170 175
 Tyr Gln Glu Val Ala Leu Asp Leu Ala Glu Asp Tyr Val Phe Leu Ser
 180 185 190
 Leu Leu Asp Ser Glu Asp Lys Ser Leu Ser Ile His Leu Pro Asn Thr
 195 200 205
 Thr Glu Pro Ile Leu Phe Asp Gly Asn Val Asp Ser Leu Val Gly Asn
 210 215 220
 Ser Val Ala Leu Thr Gln Trp Leu Lys Val Val Ile Leu Pro Tyr Phe
 225 230 235 240
 Thr Asp Ile Glu Pro Asp Leu Phe Pro Lys Tyr Ile Ser Ser Asn Leu
 245 250 255
 Pro Leu Ala Tyr Phe Phe Tyr Thr Ser Glu Glu Glu Leu Glu Asp Tyr
 260 265 270
 Thr Asp Leu Phe Thr Gln Leu Gly Lys Glu Asn Arg Gly Gln Ile Asn
 275 280 285
 Phe Ile Ala Leu Asn Ser Thr Met Phe Pro His His Val Arg Phe Leu
 290 295 300
 Asn Met Arg Glu Gln Phe Pro Leu Phe Ala Ile His Asn Met Ile Asn
 305 310 315 320
 Asn Leu Lys Tyr Gly Leu Pro Gln Leu Pro Glu Glu Glu Tyr Ala Lys
 325 330 335
 Leu Glu Lys Pro Gln Pro Leu Asp Arg Asp Met Ile Val Gln Leu Val
 340 345 350
 Lys Asp Tyr Arg Glu Gly Thr Ala Lys Pro Ile Val Lys Ser Glu Glu
 355 360 365
 Ile Pro Lys Glu Gln Lys Ser Asn Val Tyr Lys Ile Val Gly Lys Thr
 370 375 380
 His Asp Asp Ile Val His Asp Asp Asp Lys Asp Val Leu Val Lys Tyr
 385 390 395 400
 Tyr Ala Thr Trp Cys Ile His Ser Lys Arg Phe Ala Pro Ile Tyr Glu
 405 410 415
 Glu Ile Ala Asn Val Leu Ala Ser Asp Glu Ser Val Arg Asp Lys Ile
 420 425 430

Leu Ile Ala Glu Val Asp Ser Gly Ala Asn Asp Ile Leu Ser Phe Pro
 435 440 445
 Val Thr Gly Tyr Pro Thr Ile Ala Leu Tyr Pro Ala Gly Asn Asn Ser
 450 455 460
 Lys Pro Ile Ile Phe Asn Lys Ile Arg Asn Leu Glu Asp Val Phe Glu
 465 470 475 480
 Phe Ile Lys Glu Ser Gly Thr His His Ile Asp Gly Gln Ala Ile Tyr
 485 490 495
 Asp Lys Leu His Gln Ala Lys Asp Ser Glu Val Ser Thr Glu Asp Thr
 500 505 510
 Val His Asp Glu Leu
 515

<210> 77
 <211> 908
 <212> DNA
 <213> Candida albicans

<400> 77
 ggggcaaatg atatcttaag ttttcctgtg acaggatatc caaccattgc tttgtatcct 60
 gccggaataa actctaagcc tattatcttc aataaaatta gaaatttgga agatgttttc 120
 gaatttatca aggaatcagg tacacatcac attgacggcc aggcaattta tgataaattg 180
 caccaggcca aggattctga agtgtctact gaagataccg tacatgatga attataatca 240
 ataaataaag catatataat gcacattttt aacatctgat tactcgcatc gtttctggaa 300
 gaaaatagct aatattcggt atttatggca tcacgattat tctcaccagt taccggttta 360
 tgctcttgaa gagatttagc attactgcca gcgcattctc aaatacagggt ttatatgaga 420
 cccattacta taaccctaag aagagaaaaa ggagtgtctt cgttttcaat cacattctag 480
 tttacagtaa ttgagtctcg atgatgttta atatttacct tttcgtcact tttttttcca 540
 ccattcttgc aggttccctg tcagatttgg aaatcggtat tatcaagaga ataccggtag 600
 aagattgctt aattaaggca atgccagggtg ataaagttaa gggttcattat acaggatcct 660
 tattagaatc gggaactgta tttgactcaa gttattcaag aggctctcct atcgcttttg 720
 aacttggcgt tggcagagta attaaagggt gggatcaagg tggtgccggc atgtgcgttg 780
 gcgaaaaaag aaagctgcaa attccaagtt ctttggccta cggagaaaga ggtgtcccag 840
 gcgtcattcc tccaagtgtt gatttgggtg ttgatgtcga attggtagac gtgaaatcag 900
 ccgcctag 908

<210> 78
 <211> 135
 <212> PRT
 <213> Candida albicans

<400> 78
 Met Met Phe Asn Ile Tyr Leu Phe Val Thr Phe Phe Ser Thr Ile Leu
 1 5 10 15
 Ala Gly Ser Leu Ser Asp Leu Glu Ile Gly Ile Ile Lys Arg Ile Pro
 20 25 30
 Val Glu Asp Cys Leu Ile Lys Ala Met Pro Gly Asp Lys Val Lys Val

<400>	81						
accctatatg	ggaggacaac	tcgcccactg	tttgggctgt	gttagcgata	aggtccgaag	60	
tagaagcgga	aagagaagga	gctgaagagg	ttaattcatc	gatggaaggc	aactgggttt	120	
ggattttccga	gacatcgttg	gcatttgggc	ccgtcgaatt	aaactctttt	gcctgaaaaa	180	
agatccatga	cggatggggc	cggggcaata	ctatggttcg	agcgggtggc	agtcgtgaag	240	
aggcagcaaaa	ccttgacgtg	acgagtcgag	aggtgagttt	gaacatcgtc	ggggaggtta	300	
ttctgtggct	ccgcttgtag	gtgaacagat	acgtatagag	ggcgagccac	tggttaaatt	360	
tttcatggct	cggattactt	ccgtactgct	ggctaaaatc	gaaatctcgg	cctgctgaga	420	
gtgttttgag	caatcaaggg	aacatctgaa	cgtggaagag	cagacgaggc	attagctcga	480	
acataaagaac	ggaacacgct	atgttgacta	tcacgaaaaa	actggtgacc	accgatgtgc	540	
ggtcgcgaat	actgttaagc	agtttaaacg	ggaaaatgtc	cgatgcactg	gcgctgtcgc	600	
gtcagcagca	gcagaccagc	gtggatgtgg	agctgctgca	cacgatgcta	gcgcgagccg	660	
ctcgccttgc	ccatgccgac	actatagcat	acatgtggta	tcagcatgtg	atgccacgcc	720	

<400> 82															
Met	Leu	Thr	Ile	Thr	Lys	Arg	Leu	Val	Thr	Thr	Asp	Val	Arg	Ser	Arg
1				5					10					15	
Ile	Leu	Leu	Ser	Ser	Leu	Asn	Gly	Lys	Met	Ser	Asp	Ala	Leu	Ala	Leu
			20					25					30		
Leu	Arg	Gln	Gln	Gln	Gln	Thr	Ser	Val	Asp	Val	Glu	Leu	Leu	His	Thr
		35					40					45			
Met	Leu	Ala	Arg	Ala	Ala	Ala	Leu	Ala	His	Ala	Asp	Thr	Ile	Ala	Tyr
	50					55					60				
Met	Trp	Tyr	Gln	His	Val	Met	Pro	Arg	Arg	Leu	Pro	Val	Glu	Gly	Arg
65					70					75					80
Leu	Leu	Cys	Glu	Met	Ala	Gly	Val	Ala	Leu	Tyr	Gln	Asp	Arg	Leu	Phe
				85					90					95	
Leu	Pro	Ala	Gln	Phe	Leu	Gln	His	Tyr	Gln	Ala	Met	Asn	Arg	Asp	Arg
			100					105					110		
Arg	Thr	Ser	Pro	Glu	Asp	Glu	Leu	Ile	Glu	Tyr	Glu	Leu	Arg	Arg	Ile
		115					120					125			
Lys	Val	Glu	Ala	Phe	Ala	Arg	Gly	Thr	Met	His	Ser	Thr	Ala	Leu	Arg
	130					135					140				
Glu	Lys	Trp	Lys	Val	Phe	Leu	Gln	Glu	Met	Asp	Thr	Leu	Pro	Gly	Gln
145					150					155					160
Pro	Pro	Leu	Arg	Leu	Arg	Asp	Phe	Pro	Gln	Met	Thr	Lys	Ala	Met	Gly
				165					170					175	
Ile	Ala	Leu	Met	Gln	Gln	Asp	Glu	Gln	Ala	Ala	Ala	Leu	Ala	Leu	Phe
			180					185					190		
Gly	Arg	Gln	Pro	Leu	Val	Ile	Lys	Asn	Glu	Trp	Ser	Leu	Pro	Leu	Leu
		195					200					205			

Leu Ala Gly Val Leu Trp His Val Pro Gly Pro Ala Gln Ala Arg Arg
 210 215 220

Val Leu Ala Glu Phe Arg Gln Ser Tyr Arg Gly Leu Pro Leu Leu Asp
 225 230 235 240

Ala Glu Leu Val Ile Lys Arg Arg Gly Phe Glu Ile Asn Thr
 245 250

<210> 83
 <211> 830
 <212> DNA
 <213> Candida albicans

<400> 83
 ggactagaag ccaaaagcca gaggcggtaa aaatagcaag actagaatat tgctggcatc 60
 tggttaagggg atatgttgca acttgcaggg ggcggcacaa aataacatag aaacgtagta 120
 aagaggggaa aaggaaaagg aaaaggaaaa ggaaggaaaa aaaccattg acgtagaaat 180
 tgaaagaagg aaaggtatac gcaagcatta atacaacca caaacacaga ccagaagcac 240
 tctagacgga gagtaactag atctacagcc cctggaaaaat cgtttggtca actttgaggt 300
 tccggtcgtc cccctcttga tctgaaaggt ctttctctaa atctatatta aaacgtataa 360
 ataggacggg gaattgcgtt ctacttcctc aattgcgttt gatcttattt aatctctctc 420
 taatatatag aaaaaaaaaac catctgatta ttcgataatc tcaaacaaac aactcaaaac 480
 aaaaaaaact aaatacaaca atgtctgacg caggtagaaa aggattcggg gaaaaagctt 540
 ctgaagcttt gaagccagac tctcaaaagt catacgtga acaaggtaag gaatacatca 600
 ctgacaaggc cgacaaggtc gctggtaagg ttcaaccaga agacaacaag ggtgtcttcc 660
 aaggtgtcca cgactctgcc gaaaaaggca aggataacgc tgaagggtcaa ggtgaatctt 720
 tggcagacca agctagagat tacatgggag ccgccaaagtc caagttgaac gatgccgtcg 780
 aatatgtttc cggctcgtgc cacggtgaag aagacccaac caagaagtaa 830

<210> 84
 <211> 109
 <212> PRT
 <213> Candida albicans

<400> 84
 Met Ser Asp Ala Gly Arg Lys Gly Phe Gly Glu Lys Ala Ser Glu Ala
 1 5 10 15

Leu Lys Pro Asp Ser Gln Lys Ser Tyr Ala Glu Gln Gly Lys Glu Tyr
 20 25 30

Ile Thr Asp Lys Ala Asp Lys Val Ala Gly Lys Val Gln Pro Glu Asp
 35 40 45

Asn Lys Gly Val Phe Gln Gly Val His Asp Ser Ala Glu Lys Gly Lys
 50 55 60

Asp Asn Ala Glu Gly Gln Gly Glu Ser Leu Ala Asp Gln Ala Arg Asp
 65 70 75 80

Tyr Met Gly Ala Ala Lys Ser Lys Leu Asn Asp Ala Val Glu Tyr Val
 85 90 95

Phe Thr Trp Ile Cys Ala Ser Pro Phe Phe Leu His Ser Leu Thr Pro
 115 120 125
 Pro Thr Phe Ser His Phe Ser Val Tyr Gln Glu Glu Lys Lys Glu Lys
 130 135 140
 Arg Arg Thr Pro Lys Asn Thr Glu Gln Glu Gly Asn Arg Met Cys Ile
 145 150 155 160
 Trp Met Ser Gly

<210> 87
 <211> 2702
 <212> DNA
 <213> Candida albicans

<400> 87
 ctgccttccg tacgtcacaa cgcatacaca atatagttta tataaactcc tgcgtataat 60
 ctatcctttt gcataatatt ttcgtcacca ttatcttggt gcggtgtttt tattttaaaac 120
 aatagaactc gcctaaaggg gaaatttttcg atataaaaaat tcaaaaaaat ggctttcatg 180
 gatcgagtat ttgtttgtcg aaaaaggatc actggagtga cgttactacg ctacgaagcc 240
 tccttcgggc ttagecctgt tgattacgaa tttggatcag ttggtatttg attcctcgga 300
 agagttaact tcacgcgggt aaatcacttg tgatgcggta tattctctat acggctaata 360
 gatgaatcag ggtgttttaa agtgcgtata aacccttttg ctattttcgt ttatataatt 420
 ggcgttgata aagagccaat atctattgtt gctacataga ggcagctctc ttagcaaaat 480
 aaaaatacaa aaagttcgac atgggcttca gtagcggtaa atcaactaag aaaaagcctc 540
 tgcttttcga tatcagactt aaaaatggtg acaacgatgt aatactcctc aaaggtcctc 600
 caaacgaggc cccctcgggtg cttttatctg gttgcacgtt tttatcgatt aacgaacca 660
 tgcagatcaa aagcatatca ttgagacttt atgggaagat acaaataagac gtaccattag 720
 agaggcccca ggacgctagt tcttcgtcgt tgtcttcac gccgccaaag atcagaaagt 780
 acaacaagtg tttttataat tacgcatggg ataattgtta cctcaaggag tatctgagtg 840
 gtttaagagg gcaatctggc cttgcgggca gtagctcatc aagtaatatc ttggggcactc 900
 gccaaagagc tcagtcacaa agttccttga agtcttttaa ggggtcctcc tcaccctctt 960
 catgtacttt agataagggc aactacgatt ttcccttttag tgctattttg cctgggttcgt 1020
 taccagagag cgtagaatct ttgccaaatt gcttcgtgac atatagcatg gaatccgtta 1080
 ttgaacgcag caaaaattat agtgatttga tctgtaggaa aaatattaga gttctgagaa 1140
 ccatttcacc cgcagcagtg gagttatcag aaactgtttg tgtagataac tcatggcccg 1200
 acaaagtgga ttattctatt tcagtaacca acaaagccgt agctattggg tcagccaccc 1260
 ctataaatat ttccattgta cctctttcga aagggttgaa attgggctca atcaaagtcg 1320
 tattatttga gaattatcaa tattgtgacc ccttccctcc agtaatttct gaaaataggc 1380
 aagtgcacaga actaaatctt gaagatccct tgaacgagtc atctggagaa tttaatggta 1440
 atgggttgctt tgtaaataac cccttttttc agcctgatca ttcatcccaa gacaagtggg 1500
 agattgatac catcctgcaa atcccgaaca gcttatcaaa ctgtgtgcaa gattgtgatg 1560
 tccgctctaa cattaagggt cgccataagc tcaaattttt catcatccta attaacccag 1620
 atggtcataa atctgagtta agagcgctct taccgattca actttttatt tcaccatttg 1680
 tggcactttc aataaaaacca ttgtcatcct cgaatttgta ttcgcttttt agcaccacta 1740
 accagaaaga cgaaaactca tcacaagaag aggaagagga atatctgttt tctagatcag 1800
 catcagtcac aggggttgaa ttattagcgg atatgcgtag cggtggctct gttcctacca 1860
 tttcagactt gatgacgcc ccaaattatg aaatgcacgt atatgatcgt ctttatagcg 1920
 gttctttcac tcgcacggct gtggaaacgt ctggaacatg tactcctttg ggaagcgaat 1980
 gttcgactgt cgaggatcag caacaggatt tagaagattt acgtatacgg ttgacaaaaa 2040
 ttagaaatca acgtgacaat ctagggtctac caccgtctgc ctgctctgct gccgcttcca 2100
 gatcgctatc tccattacta aacgttccag caccagagga tggcacggag agaattcttac 2160
 ctcagagtgc tcttggtccc aatagtggtc ctgtgccagg agtacatagt aacgtatcac 2220

```

ctgttttact ttcaagatcc ccagcccca gcggtgcagc ccatgaagtg ttaccagtgc 2280
cctcgggctt aaattatcca gagactcaaa acctgaacaa gggtccatcg tatggcaagg 2340
caatgaaata tgatatcatt ggtgaggacc ttctccttc ctacccttgt gcgatacaaa 2400
atgtgcaacc aagaaaaccc agtagggtag attccaggaa ctcttcgaca acattgtcat 2460
cttctatacc aactagcttt cattcctcta gttttatgag tagcactgct tcccctattt 2520
ccataattaa tggctctaga agtagttcta gtgggggtatc tcttaataca cttaatgagt 2580
taacttcgaa aacttcgaat aacccatcca gtaatagtat gaaaagggtca ccaacaagac 2640
ggaggggtac ttcttttagct gggtttatgg gaggttttct atcaaagggt aacaaaacgat 2700
ag 2702

```

<210> 88

<211> 733

<212> PRT

<213> Candida albicans

<400> 88

```

Met Gly Phe Ser Ser Gly Lys Ser Thr Lys Lys Lys Pro Leu Leu Phe
  1             5             10             15

Asp Ile Arg Leu Lys Asn Val Asp Asn Asp Val Ile Leu Leu Lys Gly
      20             25             30

Pro Pro Asn Glu Ala Pro Ser Val Leu Leu Ser Gly Cys Ile Val Leu
      35             40             45

Ser Ile Asn Glu Pro Met Gln Ile Lys Ser Ile Ser Leu Arg Leu Tyr
      50             55             60

Gly Lys Ile Gln Ile Asp Val Pro Leu Glu Arg Pro Gln Asp Ala Ser
      65             70             75             80

Ser Ser Ser Leu Ser Ser Ser Pro Pro Lys Ile Arg Lys Tyr Asn Lys
      85             90             95

Val Phe Tyr Asn Tyr Ala Trp Asp Asn Val Asn Leu Lys Glu Tyr Leu
      100            105            110

Ser Gly Leu Arg Gly Gln Ser Gly Leu Ala Gly Ser Ser Ser Ser Ser
      115            120            125

Asn Ile Leu Gly Thr Arg Gln Arg Ala Gln Ser Thr Ser Ser Leu Lys
      130            135            140

Ser Leu Lys Gly Ser Ser Ser Pro Ser Ser Cys Thr Leu Asp Lys Gly
      145            150            155            160

Asn Tyr Asp Phe Pro Phe Ser Ala Ile Leu Pro Gly Ser Leu Pro Glu
      165            170            175

Ser Val Glu Ser Leu Pro Asn Cys Phe Val Thr Tyr Ser Met Glu Ser
      180            185            190

Val Ile Glu Arg Ser Lys Asn Tyr Ser Asp Leu Ile Cys Arg Lys Asn
      195            200            205

Ile Arg Val Leu Arg Thr Ile Ser Pro Ala Ala Val Glu Leu Ser Glu

```

210	215	220
Thr Val Cys Val Asp 225	Asn Ser Trp Pro Asp 230	Lys Val Asp Tyr Ser Ile 235 240
Ser Val Pro Asn Lys 245	Ala Val Ala Ile Gly 250	Ser Ala Thr Pro Ile Asn 255
Ile Ser Ile Val Pro 260	Leu Ser Lys Gly 265	Leu Lys Leu Gly Ser Ile Lys 270
Val Val Leu Phe Glu 275	Asn Tyr Gln Tyr Cys 280	Asp Pro Phe Pro Pro Val 285
Ile Ser Glu Asn Arg 290	Gln Val Thr Glu Leu 295	Asn Leu Glu Asp Pro Leu 300
Asn Glu Ser Ser Gly 305	Glu Phe Asn Gly Asn 310 315	Gly Cys Phe Val Asn Asn 320
Pro Phe Phe Gln Pro 325	Asp His Ser Phe Gln 330	Asp Lys Trp Glu Ile Asp 335
Thr Ile Leu Gln Ile 340	Pro Asn Ser Leu Ser 345	Asn Cys Val Gln Asp Cys 350
Asp Val Arg Ser Asn 355	Ile Lys Val Arg His 360	Lys Leu Lys Phe Phe Ile 365
Ile Leu Ile Asn Pro 370	Asp Gly His Lys Ser 375	Glu Leu Arg Ala Ser Leu 380
Pro Ile Gln Leu Phe 385	Ile Ser Pro Phe Val 390 395	Ala Leu Ser Ile Lys Pro 400
Leu Ser Ser Ser Asn 405	Leu Tyr Ser Leu Phe 410	Ser Thr Thr Asn Gln Lys 415
Asp Glu Asn Ser Ser 420	Gln Glu Glu Glu Glu 425	Tyr Leu Phe Ser Arg 430
Ser Ala Ser Val Thr 435	Gly Leu Glu Leu Leu 440	Ala Asp Met Arg Ser Gly 445
Gly Ser Val Pro Thr 450	Ile Ser Asp Leu Met 455	Thr Pro Pro Asn Tyr Glu 460
Met His Val Tyr Asp 465	Arg Leu Tyr Ser Gly 470 475	Ser Phe Thr Arg Thr Ala 480
Val Glu Thr Ser Gly 485	Thr Cys Thr Pro Leu 490	Gly Ser Glu Cys Ser Thr 495
Val Glu Asp Gln Gln 500	Gln Asp Leu Glu Asp 505	Leu Arg Ile Arg Leu Thr 510
Lys Ile Arg Asn Gln 515	Arg Asp Asn Leu Gly 520	Leu Pro Pro Ser Ala Ser 525


```

gaaaaaaaca tattacaatc atgtcgggtg ctgctgctgc atctgctgct ggttatgaca 540
ggcacatcac tatcttttcc cccgaggggc gtttatatca agtagaatat gccttttaaag 600
cgactaatca aactaacata aactcactag cggtcagagg taaagattgt acagtgggtga 660
taagtcagaa aaaggtcctt gataaactgt tggatccaac tactgtttcg tatatttttt 720
gtatttcaag aacaattggg atggtagtga acggaccaat accggatgca agaaatgcgg 780
ccctaagagc caaggctgag gctgcagaat tccgttataa atatgggtat gatatgccat 840
gcgatgtatt ggctaagaga atggctaacc tttcccaa atatactcaa agagcatata 900
tgagaccatt aggtgttata ctcacatttg tttcggtaga tgaagaattg ggctccctcca 960
tttacaaaac tgaccctgca gggtattacg ttggctacaa agctactgcg acaggacca 1020
aacaacagga gatcacaaca aacttagaaa accatttcaa aaagagtaaa atcgaccata 1080
ttaatgaaga atcatgggag aagggtgtag aafttgctat tactcatatg attgacgcac 1140
tgggtaccga attttcaaag aatgacttgg aagtcggtgt cgctacaaag gacaaattct 1200
ttaccttgag tgctgagaac atcgaagaaa ggctagtagc aattgctgaa caagattaa 1259

```

<210> 90

<211> 252 *

<212> PRT

<213> Candida albicans

<400> 90

```

Met Ser Gly Ala Ala Ala Ala Ser Ala Ala Gly Tyr Asp Arg His Ile
  1              5              10              15

```

```

Thr Ile Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Phe
      20              25              30

```

```

Lys Ala Thr Asn Gln Thr Asn Ile Asn Ser Leu Ala Val Arg Gly Lys
      35              40              45

```

```

Asp Cys Thr Val Val Ile Ser Gln Lys Lys Val Pro Asp Lys Leu Leu
      50              55              60

```

```

Asp Pro Thr Thr Val Ser Tyr Ile Phe Cys Ile Ser Arg Thr Ile Gly
      65              70              75              80

```

```

Met Val Val Asn Gly Pro Ile Pro Asp Ala Arg Asn Ala Ala Leu Arg
      85              90              95

```

```

Ala Lys Ala Glu Ala Ala Glu Phe Arg Tyr Lys Tyr Gly Tyr Asp Met
      100              105              110

```

```

Pro Cys Asp Val Leu Ala Lys Arg Met Ala Asn Leu Ser Gln Ile Tyr
      115              120              125

```

```

Thr Gln Arg Ala Tyr Met Arg Pro Leu Gly Val Ile Leu Thr Phe Val
      130              135              140

```

```

Ser Val Asp Glu Glu Leu Gly Pro Ser Ile Tyr Lys Thr Asp Pro Ala
      145              150              155              160

```

```

Gly Tyr Tyr Val Gly Tyr Lys Ala Thr Ala Thr Gly Pro Lys Gln Gln
      165              170              175

```

```

Glu Ile Thr Thr Asn Leu Glu Asn His Phe Lys Lys Ser Lys Ile Asp
      180              185              190

```


100

50 55 60
 Val Ser Asn Cys Gly Ser His Pro Ser Thr Thr Ser Lys Gly Ser Pro
 65 70 75 80
 Ile Asn Thr Gln Tyr Val Phe
 85

<210> 95
 <211> 1430
 <212> DNA
 <213> Candida albicans

<400> 95
 tcgggatggt ggggttgttct gtacccccgc attcacaccg ctctgcctat tcattttatc 60
 gttttcgtct tttctttcaa tgtattgata attaacgtgt ctatgtgatg ctattggtat 120
 atagcctttc ttgtatatcc ctctaacaat tattacaagt gtttctgttt aaagcaagtg 180
 ctagaagtga ctcggttctc ttaggaaatt ctaaaccgaa gatttctctt atgggtgattg 240
 taacaattat gagatacttc actagcccac cttaacttta cggaccttct tttgaaacga 300
 tgcttcgaat gacaacgcct ttttgatata taatatccaa tttcattata gggaaatttt 360
 caactcttac ccgccccact gtgctgatat gaccaagtga tcactcgatg atggggactac 420
 gtattgaaaa atattgaatg aaaaattact caagcagcag aacattcaca gtgtagtcag 480
 tccgcataag agcattcatc atggatagta aggaagtact ggtacatggt aagaatctag 540
 aaaagaacaa aagtaatgat gctgcagttc tagaaatctt acatgtcttg gataaagaat 600
 tcgtccccac tgaaaagtta ctgagagaaa caaaagttgg tgtggaagtc aacaagttta 660
 aaaaatccac taatgtagag atcagcaaac tcgtgaagaa aatgattagc tcttggaag 720
 acgcaattaa taaaaataag cgttccaggc aagcacagca gcatcatcaa gatcatgcgc 780
 caggcaatgc agaggacaag acaactgtag gtgagtcctg gaatggtgtt caacagccgg 840
 cctcctccca gtcagatgcc atgaaacaag acaagtacgt cagcactaaa ccaagaaata 900
 gtaagaacga tgggtgtggat acagctatat accaccacaa attacgtgat cagggtactaa 960
 aagcactcta cgacgttttg gccaaaggaaa gtgagcatcc acctcaatct attttgcata 1020
 ctgcaaaggc catagaaagt gaaatgaata aagttaacaa ctgtgacacc aacgaagccg 1080
 cttacaaagc caggtatcgt ataattttatt caaacgtcat atcaaagaat aaccagatc 1140
 tcaaacataa aattgccaac ggtgatataa cacctgaatt cttagctaca tgcgatgcca 1200
 aggatctggc accagcgccc ttaaagcaaa agatagaaga aattgccaaag caaaacttat 1260
 acaacgcaca ggggtgccacc atagaaaggt cagtcaccga tagatttaca tgtggtaaat 1320
 gtaaagagaa gaaggtatct tactatcaat tgcaaacaag atctgcggat gaaccattga 1380
 ccactttctg tacatgtgaa gcatgtggtg acagatggaa attctcttag 1430

<210> 96
 <211> 309
 <212> PRT
 <213> Candida albicans

<400> 96
 Met Asp Ser Lys Glu Val Leu Val His Val Lys Asn Leu Glu Lys Asn
 1 5 10 15
 Lys Ser Asn Asp Ala Ala Val Leu Glu Ile Leu His Val Leu Asp Lys
 20 25 30
 Glu Phe Val Pro Thr Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val
 35 40 45

<212> DNA

<213> Candida albicans

<400> 99

```

aacaagctat aatattgtta aatatagttg atcaacagca ttgtaatgat tacaagagac 60
gaggtggaat gaaccttatg aaatgcgtat tatatataaa ctgtaataag agctaagttg 120
aattgaaatc tacgatactt gatgttgaca ttatagcact agttcccagg aaaccctttc 180
gaaaaacaca gcaaaaacaa gagtactgta accaatgtaa catctgtaca ccagggaccc 240
acacattacc aaaatcaaaa ttatttttct aatgcctgtt atttttccta tttttcctct 300
ggcgcgtgaa tagcccgag agacgcaaac aattttcctc gcagtttttc gcttgtttaa 360
tgcgtatttt cccagatagg ttcaaacctt tcactctgtat cccgtatatt taagatggcg 420
tttgctttct cegtgtattt ttttccttct tagtgatttt tttgcattaa atcccagaac 480
aatcatccaa ctaatcaaga atgccttcca gattcactaa gactagaaag cacagaggtc 540
acgtctcagg tatgtagttc catttggaag agggaatgaa agaaccaaga cggtgacttt 600
tttttttagtg ttgtgcaacc aatatgtcgt gtgtatatca tggtagagga gaatgtcaat 660
cagctaagtg tactcaacat atttctttgt gttttgattg cgaactttgt attaccatct 720
cactgttgag acggcttatt tgaggtaata gctcgagtaa atgtactctt ccatcgcaaa 780
ctgagcaaaa agaaagtgtg catagccttt gtcatacttc tcctttatta taccatgata 840
ttcagaacag tcatactgtc tactcatttt acggctataa aaggtaactt tcatttagat 900
tatggaaagc actaattatc gctgtatcaa atgggtgtag agagcgcaat tatgaaaaag 960
agttaccacg tttcttttgt ttcgataaaa tgtccagttg aaaacctgtt ttactaacga 1020
tttaaaaatt gtatttcatt acaatatattt ttttgtacag ccggtaaagg tcgtatcggg 1080
aagcacagaa agcaccgccg tggtagaggt atggccgggtg gtcaacatca ccacagaatt 1140
aacatggata aataccatcc aggttatattc ggtaagggtg gtatgagata cttccacaag 1200
caacaagctc atttctggaa gccagtccttg aacttggaca aattgtggac attgatccca 1260
gaagacaaga gagaccaata cttgaaatct gcttctaagg aaactgctcc agttattgac 1320
actttggcag ccggttacgg taagatcttg ggtaagggtg gaattccaaa tgttccagtt 1380
atcgtcaaag ctagattcgt ctccaagttg gctgaagaaa aaatcagagc tgctgggtgg 1440
gttggtgaat tgatcgctta a 1461

```

<210> 100

<211> 149

<212> PRT

<213> Candida albicans

<400> 100

```

Met Pro Ser Arg Phe Thr Lys Thr Arg Lys His Arg Gly His Val Ser
  1                      5                      10                      15

```

```

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg
      20                      25                      30

```

```

Gly Met Ala Gly Gly Gln His His His Arg Ile Asn Met Asp Lys Tyr
  35                      40                      45

```

```

His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg Tyr Phe His Lys Gln
  50                      55                      60

```

```

Gln Ala His Phe Trp Lys Pro Val Leu Asn Leu Asp Lys Leu Trp Thr
  65                      70                      75                      80

```

```

Leu Ile Pro Glu Asp Lys Arg Asp Gln Tyr Leu Lys Ser Ala Ser Lys
      85                      90                      95

```

```

Glu Thr Ala Pro Val Ile Asp Thr Leu Ala Ala Gly Tyr Gly Lys Ile
  100                      105                      110

```

Leu Gly Lys Gly Arg Ile Pro Asn Val Pro Val Ile Val Lys Ala Arg
 115 120 125

Phe Val Ser Lys Leu Ala Glu Glu Lys Ile Arg Ala Ala Gly Gly Val
 130 135 140

Val Glu Leu Ile Ala
 145

<210> 101
 <211> 1880
 <212> DNA
 <213> Candida albicans

<400> 101
 ttttgggtact tgaattttctc gtttctacta gctggattgc ttgtcctttt acaattcctg 60
 ggagtttggc tattgctacc cttgggtctta gcaccacttt ttccgctat ttgtatttgt 120
 tgaactaatt tagtatctat ttccatttca ttataattca cgtttttagc agcctctctt 180
 cttctaggta attggaaatc ttcttcttta ggcatacggt gaccagctga aaggcagatg 240
 atctcaatat gtcccgatag gccaattttg ccaccagata gttcgatggc attttatttt 300
 tagtcctttt gaaagcaata tcataaaata tatatagttc tccatgatgt tcgggtcagt 360
 cgctccgaag cgtaacctag tataataaat agttcattgc agaaaataac gaaagaaatg 420
 gtggaatacg atctgttata tctaaactaa agctaactaa cggaataagc aaatacgaat 480
 cgaccgctaa tttaacaaat atgggttttag caatggaaag tagagtggca ccggaaattc 540
 ctgggctcat tcaacctggg aatgtcacgc aagacttgaa gatgatggc tgtaaattat 600
 tgaattcccc aaaacctacg aaaacattcc ctgggtccca gcctgtgtcc ttccagcatt 660
 ctgatgtgga agagaagctg cttgcgcagt attactacgt ttgtgagaaa acagatgggc 720
 tgccgggtgtt gatgtttata gtgataaatc ctgtgacggg tgagcaagga tgctttatga 780
 ttgataggga aaataactat tatctgggta atggatttag gtttcccaga ttaccccaaa 840
 agaagaaaga agagctgcta gagactcttc aagatggcac cttatttagat ggtgaacttg 900
 tcatacaaac taaccaatg acaaaattac aagagttagc ttatttaatg ttcgattgtc 960
 ttgctatcaa tggtagatgt ctcacacaat caccaacaag ttctagacta gccacacctg 1020
 gaaaagaatt ttttaaacca tacttcgatt taagagcagc gtaccctaact cgttgtacta 1080
 cttttccgtt caaaatttcc atgaaacata tggatttcag ttaccaatta gtaaaagttg 1140
 ctaaaagttt agataaacta ccacatcttt ctgatgggtc gatatttact cctgtgaagg 1200
 caccttacac tgccggcgga aaagattcat tgttattaaa atggaagcca gaacaagaaa 1260
 acaccgtgga cttcaaattg attttagata tcccaatggg ggaggatcct tctttgccta 1320
 aagatgatcg gaacaggtgg tattacaatt atgacgttaa gccagttttc agcttatatg 1380
 tctggcaagg cggagctgat gtcaattcac gtttaaaaca ttccgaccag cctttcgata 1440
 ggaaggaatt tgaaatatta gaaagaacat acagaaaatt tgcagagttg agcgtttcag 1500
 atgaggaatg gcaaaatttg aagaacctag aacagccatt aaatggtaga atagtagagt 1560
 gcgcaaaaaa ccaagagact ggggcgtggg aaatgttaag attcagggat gataagttaa 1620
 atggtaatca tacatcggtg gtccagaaag ttttgagag tatcaacgat tcagtttcat 1680
 tggaggacct cgaggaaatt gttggtgata ttaaaagggt ctgggacgag agaagagcaa 1740
 atatggctgg tggtagtggg agaccactac cgtctcaaag tcaaaatgag acattatcta 1800
 cctctaagcc agtccattca cagcccccac gtaatgataa ggagccaaaa tatgtagacg 1860
 aggatgatgt gtcggattag 1880

<210> 102
 <211> 459
 <212> PRT
 <213> Candida albicans

<400> 102

Met	Val	Leu	Ala	Met	Glu	Ser	Arg	Val	Ala	Pro	Glu	Ile	Pro	Gly	Leu
1				5					10					15	
Ile	Gln	Pro	Gly	Asn	Val	Thr	Gln	Asp	Leu	Lys	Met	Met	Val	Cys	Lys
			20					25					30		
Leu	Leu	Asn	Ser	Pro	Lys	Pro	Thr	Lys	Thr	Phe	Pro	Gly	Ser	Gln	Pro
		35					40					45			
Val	Ser	Phe	Gln	His	Ser	Asp	Val	Glu	Glu	Lys	Leu	Leu	Ala	His	Asp
	50					55					60				
Tyr	Tyr	Val	Cys	Glu	Lys	Thr	Asp	Gly	Leu	Arg	Val	Leu	Met	Phe	Ile
65					70					75					80
Val	Ile	Asn	Pro	Val	Thr	Gly	Glu	Gln	Gly	Cys	Phe	Met	Ile	Asp	Arg
				85					90					95	
Glu	Asn	Asn	Tyr	Tyr	Leu	Val	Asn	Gly	Phe	Arg	Phe	Pro	Arg	Leu	Pro
			100					105					110		
Gln	Lys	Lys	Lys	Glu	Glu	Leu	Leu	Glu	Thr	Leu	Gln	Asp	Gly	Thr	Leu
		115						120				125			
Leu	Asp	Gly	Glu	Leu	Val	Ile	Gln	Thr	Asn	Pro	Met	Thr	Lys	Leu	Gln
	130					135					140				
Glu	Leu	Arg	Tyr	Leu	Met	Phe	Asp	Cys	Leu	Ala	Ile	Asn	Gly	Arg	Cys
145					150					155					160
Leu	Thr	Gln	Ser	Pro	Thr	Ser	Ser	Arg	Leu	Ala	His	Leu	Gly	Lys	Glu
				165					170					175	
Phe	Phe	Lys	Pro	Tyr	Phe	Asp	Leu	Arg	Ala	Ala	Tyr	Pro	Asn	Arg	Cys
			180					185					190		
Thr	Thr	Phe	Pro	Phe	Lys	Ile	Ser	Met	Lys	His	Met	Asp	Phe	Ser	Tyr
		195					200					205			
Gln	Leu	Val	Lys	Val	Ala	Lys	Ser	Leu	Asp	Lys	Leu	Pro	His	Leu	Ser
	210					215					220				
Asp	Gly	Leu	Ile	Phe	Thr	Pro	Val	Lys	Ala	Pro	Tyr	Thr	Ala	Gly	Gly
225					230					235					240
Lys	Asp	Ser	Leu	Leu	Leu	Lys	Trp	Lys	Pro	Glu	Gln	Glu	Asn	Thr	Val
			245						250					255	
Asp	Phe	Lys	Leu	Ile	Leu	Asp	Ile	Pro	Met	Val	Glu	Asp	Pro	Ser	Leu
			260					265					270		
Pro	Lys	Asp	Asp	Arg	Asn	Arg	Trp	Tyr	Tyr	Asn	Tyr	Asp	Val	Lys	Pro
		275					280					285			
Val	Phe	Ser	Leu	Tyr	Val	Trp	Gln	Gly	Gly	Ala	Asp	Val	Asn	Ser	Arg
			290			295					300				

130		135		140
Asp Val Lys Gly Thr Thr Tyr Ile Trp Lys Phe His Pro Phe Ala Asp				
145		150		155
Glu Ser Asn Ser Leu Thr Leu Asn Trp Ser Pro Thr Leu Glu Leu Gln				
	165		170	175
Gly Thr Val Glu Ser Pro Met Thr Pro Ser Gln Phe Ala Thr Ser Val				
	180		185	190
Asp Ile Ser Glu Arg Gly Leu Ile Ala Thr Gly Phe Asn Asn Gly Thr				
	195		200	205
Val Gln Ile Ser Glu Leu Ser Thr Leu Arg Pro Leu Tyr Asn Phe Glu				
	210		215	220
Ser Gln His Ser Met Ile Asn Asn Ser Asn Ser Ile Arg Ser Val Lys				
225		230		235
Phe Ser Pro Gln Gly Ser Leu Leu Ala Ile Ala His Asp Ser Asn Ser				
	245		250	255
Phe Gly Cys Ile Thr Leu Tyr Glu Thr Glu Phe Gly Glu Arg Ile Gly				
	260		265	270
Ser Leu Ser Val Pro Thr His Ser Ser Gln Ala Ser Leu Gly Glu Phe				
	275		280	285
Ala His Ser Ser Trp Val Met Ser Leu Ser Phe Asn Asp Ser Gly Glu				
	290		295	300
Thr Leu Cys Ser Ala Gly Trp Asp Gly Lys Leu Arg Phe Trp Asp Val				
305		310		315
Lys Thr Lys Glu Arg Ile Thr Thr Leu Asn Met His Cys Asp Asp Ile				
	325		330	335
Glu Ile Glu Glu Asp Ile Leu Ala Val Asp Glu His Gly Asp Ser Leu				
	340		345	350
Ala Glu Pro Gly Val Phe Asp Val Lys Phe Leu Lys Lys Gly Trp Arg				
	355		360	365
Ser Gly Met Gly Ala Asp Leu Asn Glu Ser Leu Cys Cys Val Cys Leu				
	370		375	380
Asp Arg Ser Ile Arg Trp Phe Arg Glu Ala Gly Gly Lys				
385		390		395

<210> 107

<211> 1037

<212> DNA

<213> Candida albicans

<400> 111
 tccttacttt agtctattat caatatctct tccccctcct aaatatgtac tcttttattt 60
 tttttaattg tgaaggaaca attcaagtta gaactctttt gataggaaac attatttcct 120
 gtgtagccta atgtttaatg cctaattttt ttctaaaatg cagcaacata catatgttga 180
 gtcgtataga catctatata taacaagcac agaaccgtct aattgggtatt tttcaggaca 240
 ttttaaacad ccgtacaacg agaaccata cattactttt tttaatattc tttttgtttt 300
 caccgccttc tttttatttt tatccgaaga tcttttgga cccgctctgc gaatagcgaa 360
 gctaggatac caaattgaaa cttggacata actcatcatt aaagaagtat actgttaaga 420
 gaggcattca tttcgtgtat tataacgttt agcatcagtt acccttgaaa gcccaacata 480
 tacaaaaata cgcgtccaag atgtctacta aagcccaaaa ccctatgcgt gatttgaaga 540
 tcgagaaatt ggtcctgaac atctccgttg gtgaatctgg tgacagatta accagagcct 600
 ccaagggtttt agaacaatta tctgggtcaaa ctccagttca atccaaggcc agatacactg 660
 tcagaacttt cggtatcaga agaaacgaaa aaattgctgt tcacgttacc gtcagagggtc 720
 caaaggctga agaaattttg gaaagaggtt tgaagggtcaa ggaataccaa ttgagagaca 780
 gaaacttctc tgctaccggt aacttcggtt tcggtattga cgaacacatt gacttgggtta 840
 tcaagtatga cccatccatc ggtatttttcg gtatggattt ctatgtcgtc atgaacagac 900
 caggtgctag agtcactaga agaaagagat gtaagggtac tgttggtaac tcccacaaga 960
 caactaagga agacaccgtc tcttggttca agcaaaagta cgacgctgat gtgctcgata 1020
 aataa 1025

<210> 112

<211> 174

<212> PRT

<213> Candida albicans

<400> 112

Met Ser Thr Lys Ala Gln Asn Pro Met Arg Asp Leu Lys Ile Glu Lys
 1 5 10 15
 Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg
 20 25 30
 Ala Ser Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser
 35 40 45
 Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys
 50 55 60
 Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu
 65 70 75 80
 Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Asp Arg Asn Phe
 85 90 95
 Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu
 100 105 110
 Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Phe Gly Met Asp Phe Tyr
 115 120 125
 Val Val Met Asn Arg Pro Gly Ala Arg Val Thr Arg Arg Lys Arg Cys
 130 135 140
 Lys Gly Thr Val Gly Asn Ser His Lys Thr Thr Lys Glu Asp Thr Val
 145 150 155 160

Ser Trp Phe Lys Gln Lys Tyr Asp Ala Asp Val Leu Asp Lys
 165 170

<210> 113
 <211> 1258
 <212> DNA
 <213> Candida albicans

<400> 113
 agccatgctg gtcgcactag actttttcttc tcaactgtcac ttacctgttt gaaatcatgt 60
 cctttttttt ttgtccattc ttatacattt tcttttccttc tgaaattaac tgtacaccca 120
 taccctatat acaccatac cctatttttta aatataaaaa gtaaacttca ttttgaaaga 180
 ccactctgca tcagcacgcg ggctctggaa ggaagaaatg acgtttcggc ggaataccct 240
 ttcagaagggt ctgctcttgt ggctgggttca tgggagacac ccagcggagc tctctccgag 300
 aaaggccccct tcactctctgc cgattgctga cggaaagcag tagcggagggt ttgagttctc 360
 tacgccgaga gtacactgcc gtaatatcac aatgtttcga ctaacgggtta cagtacgtta 420
 aattagatac tgcctatgaa ttgacatatt agataatgtc aaattttaca aaaacctaag 480
 acaacaggaa ataaacaaag atgggttaaag gtaagccaag aggtttgaac tctgctagaa 540
 agctacgtgt ccacagaaga aacaagtatg ttgactattt caaaattaaa aaaaactatc 600
 aaccccctat tgtgatatcg ttttaggtga aggaaatgtt gtgagctctg gagtataaaa 660
 tttatcaagt aacatatacct ggcgcaaatac agtttggaga ggcttaaaat gacacgtcac 720
 agtgataaaa agtaatgaat agtgaacgggt cagcttcggc cattcttccc aatctatagt 780
 gtggaaaata aaccttttct tcccaaaaata actcagaaag tcacaggagg ccgtttttta 840
 caacggaatc atttttttac taacagtttt tttttattat tatagccgtt gggccgaaaa 900
 caactacaag aagagattgt tgggtactgc cttcaagtct tctccattcg gtggttcttc 960
 tcatgccaaag ggtatcgtct tggaaaaaatt gggatcga tccaagcaac ctaactctgc 1020
 tatcagaaaag tgtgttagag ttcaattaat caagaacgggt aagaagggtca ctgctttcgt 1080
 tccaaacgat ggttggttga actttgtcga cgaaaatgat gaagtcttgc tagcagggtt 1140
 cggtagaaaag ggtaaagcta agggtgatat tccagggtgt agattcaagg tcgttaagggt 1200
 ctctgggtgtc tccttggttg ctttgtggaa agaaaagaag gaaaagccaa gatcataa 1258

<210> 114
 <211> 145
 <212> PRT
 <213> Candida albicans

<400> 114
 Met Gly Lys Gly Lys Pro Arg Gly Leu Asn Ser Ala Arg Lys Leu Arg
 1 5 10 15
 Val His Arg Arg Asn Asn Arg Trp Ala Glu Asn Asn Tyr Lys Lys Arg
 20 25 30
 Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His
 35 40 45
 Ala Lys Gly Ile Val Leu Glu Lys Leu Gly Ile Glu Ser Lys Gln Pro
 50 55 60
 Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly
 65 70 75 80
 Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val
 85 90 95

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Lys Gly Lys
 100 105 110

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser
 115 120 125

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg
 130 135 140

Ser
 145

<210> 115
 <211> 1733
 <212> DNA
 <213> Candida albicans

<400> 115
 ggactacttt acagggtaat gaatatttgg gcgtttttcg ctatttttagc atgctgtagt 60
 gtatgtactg tgcacgtca ttagcacta tttcagccgt atttttcttt ttttctttcg 120
 caccgtctgt ggttgtaaag ttactgacac ttttttttct agaaagtcc ggaaaattgc 180
 gacactcggg ggagctcgag agttgtatcc agttttcttg ttcggcgata ttccgaacca 240
 ggtcgggttg ggctaacagc cgcccaggat ggaagaatta agaatttcat agaagccttc 300
 agttcttggc gaagtaaagt ggcaaaacaa atggaagatc tattgcatta catatataaa 360
 agcattagaa caatcttttc tcattgacag gtattctcat tgctctatat atattttctt 420
 cttcttgaaa gaaatatcag tattacaatc ataacaacaa ccaaaagaaa ataactaata 480
 gaccccatata caatatagaa atgtttttcca tattcaattc accatgtgtt tttgaacagc 540
 tgccatcttt tagtcagccc ctacattcgc gttattttga ttgcagttct ccagtgaagt 600
 attatccaga atgtaaaagg aggaaagcaa taaaagctaa cctaagagct ccaaaaaaaa 660
 gcgatgcaaa ttgttcagaa cctttgaggt atgcacttgc tgaaacacca aatgggtata 720
 cattaagctt gtctaagcgg attccatatg aacttttttc aaagtacgtt aatgagaaat 780
 taggtgagct aaaggagaac cattacagac caacttacca tgttgtccaa gatttttttg 840
 gaaaccagta ttatgttgaa gatgaagcgg atgaagatgc tctattgaga tctgcattga 900
 aagatctgga ttttagagcc ataggaaaga aaattgctaa ggatcttttc caagactacg 960
 aaatagaatt gaatcataga ggtgatgaat tgagcatatt gagtaagaag gataaaatct 1020
 ttaaggaatt ctctctagac caagtgtttg aagatgtttt tgttattggc tgtggagtgt 1080
 aaaacataga tgatggctcg agagaaaaat atgcactttt aaagattggt ttagttaagc 1140
 atgaggaaga aatttccgaa ggtggcatca acgaaccaaa gatgccaaata attgaatcca 1200
 aaatagacga gtctcacgat gatgttaaca tgtctgaatc tttgaaggag gaagaagcgg 1260
 agaaagcgaa agaaccacta accaaagaag accaaataaa aaaatggata gaggaagaaa 1320
 gattgatgca ggaggaaagc agaaaatcag aacaggaaaa agctgccaaag gaagatgaag 1380
 aaaggcaaaa gaaagagaag gaagccagat tgaaggcaag gaaagaatct ttgataaata 1440
 agcaaaaaac caagaggtcc cagcaaaaaa aattgcaaaa ttccaaatca ttgcctatct 1500
 ctgagattga ggccagcaat aaaaataata atagcaattc tggttcagca gaaagtgata 1560
 atgaaagtat aaacagtgat tctgatacga ctttgatttt ctctgtgtct ggtaatacac 1620
 taataaaaca cgcttcaccc ctattagaag acgttgagga tgaggaagtt gacagataca 1680
 acgagtccct aagcagatct cccaagggaa actctattat tgaggagata taa 1733

<210> 116
 <211> 410
 <212> PRT
 <213> Candida albicans

<400> 116

Met Phe Ser Ile Phe Asn Ser Pro Cys Val Phe Glu Gln Leu Pro Ser
 1 5 10 15
 Phe Ser Gln Pro Leu His Ser Arg Tyr Phe Asp Cys Ser Ser Pro Val
 20 25 30
 Ser Tyr Tyr Pro Glu Cys Lys Arg Arg Lys Ala Ile Lys Ala Asn Leu
 35 40 45
 Arg Ala Pro Lys Lys Ser Asp Ala Asn Cys Ser Glu Pro Leu Arg Tyr
 50 55 60
 Ala Leu Ala Glu Thr Pro Asn Gly Tyr Thr Leu Ser Leu Ser Lys Arg
 65 70 75 80
 Ile Pro Tyr Glu Leu Phe Ser Lys Tyr Val Asn Glu Lys Leu Gly Glu
 85 90 95
 Leu Lys Glu Asn His Tyr Arg Pro Thr Tyr His Val Val Gln Asp Phe
 100 105 110
 Phe Gly Asn Gln Tyr Tyr Val Glu Asp Glu Ala Asp Glu Asp Ala Leu
 115 120 125
 Leu Arg Ser Ala Leu Lys Asp Leu Asp Phe Arg Ala Ile Gly Lys Lys
 130 135 140
 Ile Ala Lys Asp Leu Phe Gln Asp Tyr Glu Ile Glu Leu Asn His Arg
 145 150 155 160
 Gly Asp Glu Leu Ser Ile Leu Ser Lys Lys Asp Lys Ile Phe Lys Glu
 165 170 175
 Phe Ser Leu Asp Gln Val Phe Glu Asp Val Phe Val Ile Gly Cys Gly
 180 185 190
 Val Glu Asn Ile Asp Asp Gly Ser Arg Glu Lys Tyr Ala Leu Leu Lys
 195 200 205
 Ile Gly Leu Val Lys His Glu Glu Glu Ile Ser Glu Gly Gly Ile Asn
 210 215 220
 Glu Pro Lys Met Pro Ile Ile Glu Ser Lys Ile Asp Glu Ser His Asp
 225 230 235 240
 Asp Val Asn Met Ser Glu Ser Leu Lys Glu Glu Glu Ala Glu Lys Ala
 245 250 255
 Lys Glu Pro Leu Thr Lys Glu Asp Gln Ile Lys Lys Trp Ile Glu Glu
 260 265 270
 Glu Arg Leu Met Gln Glu Glu Ser Arg Lys Ser Glu Gln Glu Lys Ala
 275 280 285
 Ala Lys Glu Asp Glu Glu Arg Gln Lys Lys Glu Lys Glu Ala Arg Leu
 290 295 300

Lys Ala Arg Lys Glu Ser Leu Ile Asn Lys Gln Lys Thr Lys Arg Ser
305 310 315 320

Gln Gln Lys Lys Leu Gln Asn Ser Lys Ser Leu Pro Ile Ser Glu Ile
325 330 335

Glu Ala Ser Asn Lys Asn Asn Asn Ser Asn Ser Gly Ser Ala Glu Ser
340 345 350

Asp Asn Glu Ser Ile Asn Ser Asp Ser Asp Thr Thr Leu Asp Phe Ser
355 360 365

Val Ser Gly Asn Thr Leu Lys Lys His Ala Ser Pro Leu Leu Glu Asp
370 375 380

Val Glu Asp Glu Glu Val Asp Arg Tyr Asn Glu Ser Leu Ser Arg Ser
385 390 395 400

Pro Lys Gly Asn Ser Ile Ile Glu Glu Ile
405 410

<210> 117

<211> 890

<212> DNA

<213> Candida albicans

<400> 117

```
caaaaaagtt ttcggatgaa cccgattaat acaagtaaaa tcagcaaaga tatagaagac 60
aaaataagcg tgaaaacaat cataaaccac tcacaacggg gggttttcagc tggtactcct 120
ccatacatatc attttgataa agatataatg ttatatattct tttcgtaatt ttgttttact 180
tcggtttgct ctatagattt catcagccgc accgaaaagg gagatcaata aggtaccctt 240
taaaagggat aagaagccta catcacccca ataaatggag taatggccag cattggatga 300
agagaagaat tacgggatac tgggataaca ctgttaaaaa atgcttcgcg acgtgagggt 360
cttcttcata taaattgaac tgccaaatct ctttcacatt atccaggata gtttggaatg 420
tgtgttactg aaggatcaga atcaataaat acaatcaata caaatattta gcgcataaaa 480
ttcaaacaaa gtttactgaa atgaagttag attcaggaat atactcagag gcacaaagag 540
ttgtgagaac tccaaagttt agatatatta tgttagggct ggtgggcgct gctgtggtac 600
cgaccgcata catgaggaga ggctatacgg ttccctgcaca tagcttagac aacatcaacg 660
gcgtagacac aactaaggcg tctgttatgg gtacagaaca gagagcagct atgacgaagg 720
gtaagagttt acaagagatg atggatgatg atgaagtaac gtatttgatg ttcctcttca 780
atcatgtaag ggaatttgta cttgggtccc tgcatttatg ttctttgcat tttgttttcg 840
catttaatca tagtacgaca aacggggaag gggattgtga ttttacataa 890
```

<210> 118

<211> 129

<212> PRT

<213> Candida albicans

<400> 118

Met Lys Leu Asp Ser Gly Ile Tyr Ser Glu Ala Gln Arg Val Val Arg
1 5 10 15

Thr Pro Lys Phe Arg Tyr Ile Met Leu Gly Leu Val Gly Ala Ala Val

20	25	30
Val Pro Thr Ala Tyr Met Arg Arg Gly Tyr Thr Val Pro Ala His Ser		
35	40	45
Leu Asp Asn Ile Asn Gly Val Asp Thr Thr Lys Ala Ser Val Met Gly		
50	55	60
Thr Glu Gln Arg Ala Ala Met Thr Lys Gly Lys Ser Leu Gln Glu Met		
65	70	75
Met Asp Asp Asp Glu Val Thr Tyr Leu Met Phe Leu Phe Asn His Val		
85	90	95
Arg Glu Phe Val Leu Gly Ser Leu His Leu Cys Ser Leu His Phe Val		
100	105	110
Phe Ala Phe Asn His Ser Thr Thr Asn Gly Glu Gly Asp Cys Asp Phe		
115	120	125
Thr		

<210> 119
 <211> 1418
 <212> DNA
 <213> Candida albicans

<400> 119
 aatctttgcg attgaattgc tgcacgaaca ttaacattag ttcttttgct aaagtttctc 60
 caatatctgg aatatcagaa tttagcaagg caatcaaagc ggataaagca gggattagcc 120
 tgccattctg tttgttcaga gtaaaatcca caacattttt acaaattatg ttgcggccaa 180
 taagtatat gacttgaaat aagtctctgt gcgattcctg taagttgtcc attgttaa 240
 tggatattat gggtgaaacg tgtgacctta tcatttccca gttttctctc tgaaatttaa 300
 tgtcttcac ctgtatggta gcggtagaca tgctgggttg tagcctttttt attccttttt 360
 aggtttctta ctcaaatgc caaaataaat atcagtgtaa tataattttt caagagtacg 420
 taatggaaaa agataaaaaat aaggaccgct ataaaaagag acgtgattaa acctaaaaat 480
 ctaaagtaaa gaagtgtgag atggttgagg aaaattccag agttttgatt gttcttctt 540
 atacaccgcc tagtgctact ttgcagagga ttatagggca aactattccg ttcttaagag 600
 aatgtcaaag tcaactagac atcgtgattg tacctgaatt caaaacctca ttccagttgg 660
 attctgcgct aggggaagatg tacagtatta ccagggatgt ccttttgggc tatggaatga 720
 tcaacagcgg aatcaacatc atattcaaca atattcattt cgtcgagagt aatttgcaat 780
 ggaaagtgg tttattgcca caggaatcca cttttgaaac ttggaagcta gagttgggac 840
 aaggacaata ccatagtata gaacattatg caccacaga taatataatg gaagagatag 900
 aaggtcccaa agatgctaac aaatttcatt tcaccgcatt gggcggaacg ttcgaccaca 960
 ttcacgatgg acataaaaata ttgttgagcg tctctacatt catcacgtca caaagggttaa 1020
 tttgtggaat tacgtgcgat gagctcttgc aaaacaagaa atacaaagag ttgattgaac 1080
 cttatgatac acgatgcagg cacgtacatc aattcatcaa gttgttaaaa ccggatctct 1140
 ccgtagaact agttccctta agggacgtgt gcggccccac agggaaagta cccgagatag 1200
 aatgtttagt tgtgagtaga gaaaccgtca gtggggcaga gactgtgaat aagactagga 1260
 ttgaaaaagg catgagccca ttggcagtac atgtgggttaa tgtacttggg ggaagggagg 1320
 aagacggctg gagecgagaag ttaagcagca cggaaatcag acgcctactt aagtcctctg 1380
 cttcgccaac gtgcactcca caaaaccctt gcgtataa 1418

<210> 120
 <211> 305
 <212> PRT
 <213> Candida albicans

<400> 120
 Met Val Glu Glu Asn Ser Arg Val Leu Ile Val Leu Pro Tyr Thr Pro
 1 5 10 15
 Pro Ser Ala Thr Leu Gln Arg Ile Ile Gly Gln Thr Ile Pro Phe Leu
 20 25 30
 Arg Glu Cys Gln Ser Gln Leu Asp Ile Val Ile Val Pro Glu Phe Lys
 35 40 45
 Thr Ser Phe Gln Leu Asp Ser Ala Leu Gly Lys Met Tyr Ser Ile Thr
 50 55 60
 Arg Asp Val Leu Leu Gly Tyr Gly Met Ile Asn Ser Gly Ile Asn Ile
 65 70 75 80
 Ile Phe Asn Asn Ile His Phe Val Glu Ser Asn Leu Gln Trp Lys Val
 85 90 95
 Val Leu Leu Pro Gln Glu Ser Thr Phe Glu Thr Trp Lys Leu Glu Leu
 100 105 110
 Gly Gln Gly Gln Tyr His Ser Ile Glu His Tyr Ala Leu His Asp Asn
 115 120 125
 Ile Met Glu Glu Ile Glu Gly Pro Lys Asp Ala Asn Lys Phe His Val
 130 135 140
 Thr Ala Leu Gly Gly Thr Phe Asp His Ile His Asp Gly His Lys Ile
 145 150 155 160
 Leu Leu Ser Val Ser Thr Phe Ile Thr Ser Gln Arg Leu Ile Cys Gly
 165 170 175
 Ile Thr Cys Asp Glu Leu Leu Gln Asn Lys Lys Tyr Lys Glu Leu Ile
 180 185 190
 Glu Pro Tyr Asp Thr Arg Cys Arg His Val His Gln Phe Ile Lys Leu
 195 200 205
 Leu Lys Pro Asp Leu Ser Val Glu Leu Val Pro Leu Arg Asp Val Cys
 210 215 220
 Gly Pro Thr Gly Lys Val Pro Glu Ile Glu Cys Leu Val Val Ser Arg
 225 230 235 240
 Glu Thr Val Ser Gly Ala Glu Thr Val Asn Lys Thr Arg Ile Glu Lys
 245 250 255
 Gly Met Ser Pro Leu Ala Val His Val Val Asn Val Leu Gly Gly Arg
 260 265 270

Glu Glu Asp Gly Trp Ser Glu Lys Leu Ser Ser Thr Glu Ile Arg Arg
 275 280 285

Leu Leu Lys Ser Ser Ala Ser Pro Thr Cys Thr Pro Gln Asn Pro Cys
 290 295 300

Val
 305

<210> 121
 <211> 1433
 <212> DNA
 <213> Candida albicans

<400> 121
 agagagccat ccgtaactct gctaaggaag ctgactactt tggatgatgct gacaaggcca 60
 ccacgattga cgaacaagtt ggtttgatcg ttgacagttt gaatgacgaa gagttagtgt 120
 ccaccgccga taagatcaag gccaatgctg ctgggtgccaa ggaagttttg aaggaatctg 180
 caaagactat tgtcgattct ggcaaaactac catccagctt gttgtcctac ttcgtgtgaa 240
 taccgtaaga aatggaatag aatatatacg aatgtatacg aatattatag agaacgttct 300
 cttttatttc tataatgaat aggttcgggt aacgggtccc tttttaggta tttctagaag 360
 atgagagaag aggggaataat gagaaaggcg aaaaataaag gacaccttta acgaaagatc 420
 aaaggtgtcc ttatttactt acaatagctg caattagtac gactcaaaaa aagtgaatac 480
 aaaactgaaa ggatagatca atgtcttaca gaggacctat tggaaatttt ggcggtatgc 540
 caatgtcatc atcgcaagga ccatactctg gcgggtgcaca attcagatca aaccagaacc 600
 aatccacttc tggcatctta aagcaatgga agcattcttt tgaaaagttt gcctccagaa 660
 ttgaggggct cactgacaat gcagttgttt ataaattgaa gccttacatt ccaagtttgt 720
 caagattttt cattgtggcc accttttatg aagattcgtt taggatctta tcacaatggt 780
 cagatcaaat tttttatctg aataagtgga agcattaccc atacttcttt gtcgttgtgt 840
 ttctagtggg tgttaccggt tccatgttga ttggcgccag tttgttagtt ttaagaaagc 900
 aaaccaatta tgccaccggt gtgttatgtg cttgcgttat ttctcaagca ttagtttatg 960
 ggttggtttac gggttcatca tttgtcctaa gaaacttttag tgttattggt gggttgttaa 1020
 ttgcattcag cgattcaatt gttcaaaaca agacaacatt cggtatgctt cctgaattaa 1080
 acagcaaaaa cgacaaagcg aagggttacc tggtgtttgc tggtagaatt ttaattgttt 1140
 taatgtttat cgctttcact ttcagtaaat catgggtttac tggtgttttg accattatcg 1200
 gcacaatatg ttctgccatt gggttacaaga caaaattcgc atccattatg ttgggtttga 1260
 tactaacttt ttacaatatc acgctaaaca actactgggt ttataacaat actaagagag 1320
 atttcttgaa gtatgagttt taccagaact taagcatcat tgggtgggctt ctattagtta 1380
 ctaatactgg cgctgggtgaa ttatccgttg atgaaaagaa gaagatttac tag 1433

<210> 122
 <211> 310
 <212> PRT
 <213> Candida albicans

<400> 122
 Met Ser Tyr Arg Gly Pro Ile Gly Asn Phe Gly Gly Met Pro Met Ser
 , 1 5 10 15
 Ser Ser Gln Gly Pro Tyr Ser Gly Gly Ala Gln Phe Arg Ser Asn Gln
 20 25 30
 Asn Gln Ser Thr Ser Gly Ile Leu Lys Gln Trp Lys His Ser Phe Glu
 35 40 45

Lys Phe Ala Ser Arg Ile Glu Gly Leu Thr Asp Asn Ala Val Val Tyr
 50 55 60
 Lys Leu Lys Pro Tyr Ile Pro Ser Leu Ser Arg Phe Phe Ile Val Ala
 65 70 75 80
 Thr Phe Tyr Glu Asp Ser Phe Arg Ile Leu Ser Gln Trp Ser Asp Gln
 85 90 95
 Ile Phe Tyr Leu Asn Lys Trp Lys His Tyr Pro Tyr Phe Phe Val Val
 100 105 110
 Val Phe Leu Val Val Val Thr Val Ser Met Leu Ile Gly Ala Ser Leu
 115 120 125
 Leu Val Leu Arg Lys Gln Thr Asn Tyr Ala Thr Gly Val Leu Cys Ala
 130 135 140
 Cys Val Ile Ser Gln Ala Leu Val Tyr Gly Leu Phe Thr Gly Ser Ser
 145 150 155 160
 Phe Val Leu Arg Asn Phe Ser Val Ile Gly Gly Leu Leu Ile Ala Phe
 165 170 175
 Ser Asp Ser Ile Val Gln Asn Lys Thr Thr Phe Gly Met Leu Pro Glu
 180 185 190
 Leu Asn Ser Lys Asn Asp Lys Ala Lys Gly Tyr Leu Leu Phe Ala Gly
 195 200 205
 Arg Ile Leu Ile Val Leu Met Phe Ile Ala Phe Thr Phe Ser Lys Ser
 210 215 220
 Trp Phe Thr Val Val Leu Thr Ile Ile Gly Thr Ile Cys Phe Ala Ile
 225 230 235 240
 Gly Tyr Lys Thr Lys Phe Ala Ser Ile Met Leu Gly Leu Ile Leu Thr
 245 250 255
 Phe Tyr Asn Ile Thr Leu Asn Asn Tyr Trp Phe Tyr Asn Asn Thr Lys
 260 265 270
 Arg Asp Phe Leu Lys Tyr Glu Phe Tyr Gln Asn Leu Ser Ile Ile Gly
 275 280 285
 Gly Leu Leu Leu Val Thr Asn Thr Gly Ala Gly Glu Leu Ser Val Asp
 290 295 300
 Glu Lys Lys Lys Ile Tyr
 305 310

<210> 123

<211> 1802

<212> DNA

Ala	Asp	Glu	Asp	Leu	Leu	Thr	His	Asp	Ala	Arg	Asp	Trp	Lys	Thr	Ala	
				85					90					95		
Asp	Leu	Tyr	Ala	Ala	Met	Gly	Leu	Ser	Lys	Leu	Arg	Phe	Arg	Ala	Thr	
				100					105					110		
Glu	Ser	Gln	Ile	Ile	Lys	Ala	His	Arg	Lys	Gln	Val	Val	Lys	Tyr	His	
				115					120					125		
Pro	Asp	Lys	Gln	Ser	Ala	Ala	Gly	Gly	Ser	Leu	Asp	Gln	Asp	Gly	Phe	
				130					135					140		
Phe	Lys	Ile	Ile	Gln	Lys	Ala	Phe	Glu	Thr	Leu	Thr	Asp	Ser	Asn	Lys	
				145					150					155		
Arg	Ala	Gln	Tyr	Asp	Ser	Cys	Asp	Phe	Val	Ala	Asp	Val	Pro	Pro	Pro	
				165					170					175		
Lys	Lys	Gly	Thr	Asp	Tyr	Asp	Phe	Tyr	Glu	Ala	Trp	Gly	Pro	Val	Phe	
				180					185					190		
Glu	Ala	Glu	Ala	Arg	Phe	Ser	Lys	Lys	Thr	Pro	Ile	Pro	Ser	Leu	Gly	
				195					200					205		
Asn	Lys	Asp	Ser	Ser	Lys	Lys	Glu	Val	Glu	Gln	Phe	Tyr	Ala	Phe	Trp	
				210					215					220		
His	Arg	Phe	Asp	Ser	Trp	Arg	Thr	Phe	Glu	Phe	Leu	Asp	Glu	Asp	Val	
				225					230					235		
Pro	Asp	Asp	Ser	Ser	Asn	Arg	Asp	His	Lys	Arg	Tyr	Ile	Glu	Arg	Lys	
				245					250					255		
Asn	Lys	Ala	Ala	Arg	Asp	Lys	Lys	Lys	Thr	Ala	Asp	Asn	Ala	Arg	Leu	
				260					265					270		
Val	Lys	Leu	Val	Glu	Arg	Ala	Val	Ser	Glu	Asp	Pro	Arg	Ile	Lys	Met	
				275					280					285		
Phe	Lys	Glu	Glu	Glu	Lys	Lys	Glu	Lys	Glu	Arg	Arg	Lys	Trp	Glu	Arg	
				290					295					300		
Glu	Ala	Gly	Ala	Arg	Ala	Glu	Ala	Glu	Ala	Lys	Ala	Lys	Ala	Glu	Ala	
				305					310					315		
Glu	Ala	Lys	Ala	Lys	Ala	Glu	Ser	Glu	Ala	Lys	Ala	Asn	Ala	Ser	Ala	
				325					330					335		
Lys	Ala	Asp	Lys	Lys	Lys	Ala	Lys	Glu	Ala	Ala	Lys	Ala	Ala	Lys	Lys	
				340					345					350		
Lys	Asn	Lys	Arg	Ala	Ile	Arg	Asn	Ser	Ala	Lys	Glu	Ala	Asp	Tyr	Phe	
				355					360					365		
Gly	Asp	Ala	Asp	Lys	Ala	Thr	Thr	Ile	Asp	Glu	Gln	Val	Gly	Leu	Ile	
				370					375					380		

Val Asp Ser Leu Asn Asp Glu Glu Leu Val Ser Thr Ala Asp Lys Ile
385 390 395 400

Lys Ala Asn Ala Ala Gly Ala Lys Glu Val Leu Lys Glu Ser Ala Lys
405 410 415

Thr Ile Val Asp Ser Gly Lys Leu Pro Ser Ser Leu Leu Ser Tyr Phe
420 425 430

Val

<210> 125
<211> 1472
<212> DNA
<213> Candida albicans

<400> 125
gactcggacg gaaccgtctc atattatacg ttcagtgaat atttttcacg gaagaatgga 60
aagggcctcg aaagacgtta atgcatccgt acacctacat ctttacattt tttgctgttg 120
cacctacact gttttttttt ttttcacett atgagtcctg tatttcttga aagagccgat 180
aacaatattc caggtggagt cccgaggcag aatcaaggct gcggagagaa gttcctctca 240
aactaatggg agtgatccgc tcagttctcc catcacgaca gaactgtctg agacaaagtc 300
ttccagcag agtccgccta cgctcttgct gcagagattc gcccgaaggc aggtttcctg 360
aaattctttt cactagtaaa gtgttcgttc atgtaaaaca tactgccgta gttttgagct 420
aaaattaaag atatattaga tttttagaat ttcttagata gtctcaacgt gttaaaacaa 480
aagcataacc aaagaaaaaa atggctaagt tcttgaaagc tggtaaagtt ggtacgtatc 540
attttcagtt tttggacatc aacaaaaaac cgtgcaactg tggattatga aatccaagtt 600
attagcagtt gatgttgtat aatttgagtt tgaattcgag tattgtatct tcatatggga 660
gtagggagga aaaagcgtgg agatgttaga tctgggaaaa aaccttttaa tttgaatgat 720
agcttattaa tagaaatatt ggacaaaaag atgaatgatt taggagcgaa actaacgatt 780
attcatattc attgagctat acgaggcagt ggaagggtta tcaaaaagtt gtaatttaaa 840
agaaaaaagc atcaatagcc accaaataag atggtgaaag ttccgcgata tatttgctaa 900
gaccataggc acatgtacgc aggcgaccag ggccttttat ttactgtagt tctttccatg 960
ccctattaaa aattcgtggg cctatgataa tttttctctc cctagtattg aagaacaaaa 1020
ttgagaattc gccaaacttt aagaagggtt cacattttact aactatttct tttccttctc 1080
ttttttacac agctgtcggt gtcggtgggt gttacgccgg taagaagggtt gttatcggtta 1140
aaccacatga tgaagggttc aagtctcacc catttggtca cgctttgggt gccggtattg 1200
aaagataccc attgaaggtc accaagaagc acgggtgccaa gaagggttgct aagagaacca 1260
agatcaagcc tttcatcaag gtcgtcaact acaaccattt attgccaacc agatacactt 1320
tagatgttga agctttcaaa tccgttggtt ctactgaaac tttcgaacaa ccttcccaac 1380
gtgaagaagc taagaaagtc gtcaagaagg ctttcgaaga aagacaccaa gctggttaaga 1440
accaatgggt cttctctaag ttgagatttt aa 1472

<210> 126
<211> 136
<212> PRT
<213> Candida albicans

<400> 126
Met Ala Lys Phe Leu Lys Ala Gly Lys Val Ala Val Val Val Arg Gly
1 5 10 15

Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly

	20		25		30
Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg	35	40	45		
Tyr Pro Leu Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys	50	55	60		
Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu	65	70	75	80	
Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val	85	90	95		
Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys	100	105	110		
Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln	115	120	125		
Trp Phe Phe Ser Lys Leu Arg Phe	130	135			

<210> 127

<211> 1299

<212> DNA

<213> Candida albicans

<400> 127

```

ttacttacgt ctattataac cttccgcgta aaaaagaaat attgacatcc tttcttgtat 60
ttagcccata cattttcacc catgcacccat tggattataa agaaaaaaat ttaataaaaa 120
tctgccgggg aaatttcaga agaaaaaagg aagggtgtgt cgcatttaac acggggccacc 180
ataaaactttt gtttgccacc catctagacg gga'tccgccc cgcccaaggc tctcttcctc 240
tagctaggca atgtggctct cggaaaggaa actcccacca ggacgtggtg ggaaatgcag 300
caattccccct ctgcttcccg ctgacctttc ttgggcccag tttagtaagt atgctctcat 360
ctttcatgtg tgctgtaact tgcaagtcac taacactatc tataattgat attagacgtt 420
aaaagtctta tatagcattt gcttttattt agagaatacg aaaacacacc agataattag 480
tgcatatata ttagatcaat atggatatgt aaagagatat taaacataag atgtgaaggga 540
aacagaagag aacaatatatt gaggaatgaa ttcggatgaa attctagtag aagaaaaaag 600
cctaaaataa aaagaaagaa aggaaaataa agcagtaatc aacctctgac atttgatagg 660
agtatgctgt tccgcaaaat caacaaatca tgcattaaac tggtaacgga gactttaaaag 720
acgtgcaaag aaagcaatta attttttagat aggggaattga aaggctctgt atagcagaaa 780
atlttgagatc tactgtggag ataagcatat ggtgttgagt tatgggtaat ctaacaataa 840
tagaaactta tagcagttga agatggcgga tcatgatgcc ggatactgct gggtaatgat 900
ttatccttct ttttttggag cacaaatgct cactttttcc tgtctcctct aacttttctg 960
atgtatccta cccaacccta cagttttcaa attactaaca tcaatttttt tgtgaaacga 1020
ctttcgtttt cgtttctatt tatttcatta caggtttttag ttcaagattt gttgcaccca 1080
actgctgctt ctgaagccag aaagcacaag ttaaagactt tggttcaagg cccaagatcc 1140
tacttcttgg atgtcaaagt cccagggttg ttgaacatca ccactgtttt ttctcatgct 1200
caaactgctg tcaattgtga atcatgctct actgtcttat gtactccaac cgggtggtgaag 1260
gccaaattat ctgaaggtac ttctttcaga agaaagtaa 1299

```

<210> 128

<211> 82

127

Met Ser Leu Arg Pro Cys Leu Thr Pro Ser Ser Met Gln Tyr Ser Asp
 1 5 10 15
 Ile Tyr Ile His Thr Pro His Pro His Pro His Pro His Pro His Thr
 20 25 30
 Pro Thr His Thr His Pro His Thr Pro Thr Pro Thr Pro His Pro His
 35 40 45
 Pro His Thr Pro His Pro His Thr Thr Pro Thr Pro Thr Pro His His
 50 55 60
 Thr His Thr Pro His Thr Thr Leu Ser Asn Leu Ser Leu Asn Leu Pro
 65 70 75 80
 Ser His Tyr Pro Thr Ser Pro Leu Val Thr Leu Pro His Ser Thr Ile
 85 90 95
 Pro Leu Pro Thr Thr Ile His Leu Ser Thr Tyr Tyr Tyr His Pro Pro
 100 105 110
 Pro Ile Ile Thr Val Thr Leu Gln Leu Pro Ile Ser Asn Ser Thr Thr
 115 120 125
 Ile Thr Leu Leu Leu Pro Tyr His Pro Pro Cys Pro Thr His Cys Thr
 130 135 140
 Val Val Leu Pro Ser Ile Leu Lys Arg
 145 150

<210> 133
 <211> 3752
 <212> DNA
 <213> Candida albicans

<400> 133
 ttccataggg cttattttcc agttgatgga atgggaggtt gctcttaacg cgaagactaa 60
 cgtgcaagcc aacagttata gaaaagtacc gtgagagaga aaaaaaaaaa agatatagca 120
 ttcaatgagg ctttattgag gggcacgatg ctcttttttt cttctgtact ttataaataa 180
 ttccgtatatt cttcgctttg tttcatgctc tgttctgagc ttttagtttc tcttattgag 240
 agccttttcc aaatcaaggc tcaggaagtg actcgtcctt agaagaacaa ggtttgatt 300
 tggtaggggt cttgtacgaa gttctcaata taatttgccg atttactgta cggttcatac 360
 tagtttatte cgggtaacaa gttttcttgt gatgctaaat caatgtgtat attgagaaaa 420
 ctatgtagta agttacacaa agcaacaaag gatattatta tatgtgacag agaagaattg 480
 ctgtagagat tcatgacaat atgaatgaga ctactacaaa acagccgcta aagaaaagg 540
 ccctgagcag ctatctttca aacgtgagca cgagacggga ggagctggaa aagatttcta 600
 aacaagaaac atccgaagag gaagatactg ccggcaagca tgaacaaagg gaaacactgt 660
 cggagaagt aagtgataag tttccagaaa atgttgcatc gtttcgctca cagactacaa 720
 gcgtcatca agccacccaa aataacctga atgcaaagga atccgaagac ctggcccata 780
 agaattgatc gagttcacac gaaggagagg ttaatgggga cagccgtccg gacgatgttc 840
 ctgaaacgaa tgaaaaata agccaagcaa taccgacgaa aatttcgtca tcatcatcat 900
 caccatgt acgtaattgt gatataccaa accatcaacc tttttcgaga gaccaacttc 960
 gagcgtgtt gaaagaacca aaaaggaaaa ctgttgatga tttcatagaa gaagagggtt 1020
 tgggagctgt tgaagaagag gatttaagt atgaggtact tgaaaaaat acaacagaac 1080
 cagaaaatgt ggaaaaagat atagagtata gcgactcaga taaggacaca gacgatgtgg 1140

```

gaagcgatga tcccacggca cccaactcac caataaaaact tggctcgtcgc aaactgggta 1200
gaggtgacca acttgatgca acaacaagtt ccatgtttta taacgaatca gattctgaat 1260
tatcagatat cgatgatagc aagaatattg ctttatccag tagcctattt agaggcggtt 1320
cttcacctgt gaaagagaca aacaacaacc tttcaaatat gaattcttca ccagcacaaa 1380
atccaaaaag gggttctgtc tccaggagta atgatagtaa caagagttct catatagctg 1440
tttccaagcg ccccaaacag aagaagggca tatatagga ttctgggtgg 1500
tacagattgc ctgtgacaag ggcaaatatg atgtagtcaa aaagatgatt gaagaaggag 1560
gttacgatat taatgaccaa gacaatgctg gtaatacagc attgcatgaa gcggcggttg 1620
aaggtcatat tgagattgtg gaactgttga tagaaaatgg tgcagatgta aatatcaagt 1680
ctattgaaat gttcggcgat actcccttga tcatgtcttc cgccaatgga cacttggatg 1740
ttgtcaagta tcttcttaaa aacgggtgagg acccaactat acgtaacgct aaagggttaa 1800
ctgcgtttga atctgtcgat gatgaatctg aatttgatga tgaagaagac caaaagattt 1860
tgcgtgaaat aaaaaaaagg ttgagtatag ccgctaaaaa atggactaac agagcaggaa 1920
ttcataatga caaatctaaa aatggcaata atgctcacac aatagatcag ccaccttttg 1980
ataataccac aaaagccaaa aacgaaaagg ccgctgactc accttcaatg gcttccaata 2040
ttgatgagaa agctccggaa gaggaattct attggacaga tgttacttct agagcgggaa 2100
aagaaaaact gtttaaagct tcgaaggagg gacatttacc atacgttggg acgtatgtag 2160
aaaaatgggtg taagatagac ttaaggtcat ttttcgaag cgtaaagtgt ggccatgaag 2220
atattacaag tatctttttg gcattcggat ttcccgtaaa tcaaacttca agggataata 2280
aaacatccgc tttaatggta gctgtaggtc gtggccatct tggaaactgt aaactgctat 2340
tagaggcagg tgcagatcca accaaaagag ataaaaaggg tcgtaccgct ttgtactatg 2400
ccaaaaacag cataatggga ataacaaaac gtgaagaaat tcaattgatt gaaaatgcta 2460
taaataacta tttgaagaag cactctgaag ataataatga tgatgatgat gatgatgata 2520
ataataatga aacatataaa catgaaaaaa agagagagaa aacgcaatca cccatattag 2580
caagccgaag aagtgccact cctagaattg aagacgaaga ggacgatacg aggatgctca 2640
atctggcaga cgatgacttt aataacgata gtgatgtcaa ggaatctaca acttcggatt 2700
cgcgcaagag attggatgac aatgaaaatg ttgggtactca atactcattg gactggaaaa 2760
aacgtaaaac aaatgccttg caagatgaag aaaaattaaa aagtatctca ccactctcta 2820
tggaacctca ttctccaaaag aaggcaaaat ctgtagagat aagtaaaata catgaagaaa 2880
cggctgctga aagagaagca agactcaagg aagaggaaga atacagaaag aaaagattag 2940
aaaagaaaag aaaaaaagaa caggaactac taaaaaagct ggccgaagat gagaaaaaaa 3000
ggatcgaaga acaggagaag cagaaagtct tagaaatgga aagattggaa aaagctactt 3060
tagagaaagc aagaaaaaatg gaaagggaaa aagaaatgga agaaatctct tatagaaggg 3120
cagtaaggga cttatatccg ttaggactga agattattaa cttcaacgat aaacttgatt 3180
acaaaagatt tttgccgcta tattattttg tagacgaaaa aaacgataaa tttgtgctcg 3240
acttgcaagt aatgatattg ttgaaggata tcgacttgct ctcaaaggac aaccaacca 3300
cttctgagaa gattcccgtc gatccctcgc acctgactcc attgtggaat atgttgaaat 3360
tcattttcct gtatggagggt agttatgatg ataaaaagaa caacatggaa aataaaagat 3420
atgttgtaaa ctttgatggg gttgatttgg acacaaagat tgggtatgag cttttggagt 3480
acaaaaaatt tgtagtttg cccatggcgt ggattaaatg ggataacgtt gttattgaaa 3540
accacgcaaa aagaaaagaa attgaaggaa atatgattca aatatcaata aacgaatttg 3600
cacgatggag aaacgataag ctgaacaaag cgcagcagcc gacgcgcaaa cagcgttctc 3660
taaaaaatcc tcgagagtta ccggttaaat ttcaacaccg tatgagcata tcctccgtcc 3720
tccagcagac atccaaagaa ccatttttgg aa 3752

```

<210> 134

<211> 1083

<212> PRT

<213> Candida albicans

<400> 134

```

Met Asn Glu Thr Thr Thr Lys Gln Pro Leu Lys Lys Arg Ser Leu Ser
  1                               5                10                15

```

```

Ser Tyr Leu Ser Asn Val Ser Thr Arg Arg Glu Glu Leu Glu Lys Ile
      20                25                30

```

Ser Lys Gln Glu Thr Ser Glu Glu Glu Asp Thr Ala Gly Lys His Glu
 35 40 45
 Gln Arg Glu Thr Leu Ser Glu Glu Val Ser Asp Lys Phe Pro Glu Asn
 50 55 60
 Val Ala Ser Phe Arg Ser Gln Thr Thr Ser Val His Gln Ala Thr Gln
 65 70 75 80
 Asn Asn Leu Asn Ala Lys Glu Ser Glu Asp Leu Ala His Lys Asn Asp
 85 90 95
 Ala Ser Ser His Glu Gly Glu Val Asn Gly Asp Ser Arg Pro Asp Asp
 100 105 110
 Val Pro Glu Thr Asn Glu Lys Ile Ser Gln Ala Ile Arg Ala Lys Ile
 115 120 125
 Ser Ser Ser Ser Ser Ser Pro Asn Val Arg Asn Val Asp Ile Gln Asn
 130 135 140
 His Gln Pro Phe Ser Arg Asp Gln Leu Arg Ala Met Leu Lys Glu Pro
 145 150 155 160
 Lys Arg Lys Thr Val Asp Asp Phe Ile Glu Glu Glu Gly Leu Gly Ala
 165 170 175
 Val Glu Glu Glu Asp Leu Ser Asp Glu Val Leu Glu Lys Asn Thr Thr
 180 185 190
 Glu Pro Glu Asn Val Glu Lys Asp Ile Glu Tyr Ser Asp Ser Asp Lys
 195 200 205
 Asp Thr Asp Asp Val Gly Ser Asp Asp Pro Thr Ala Pro Asn Ser Pro
 210 215 220
 Ile Lys Leu Gly Arg Arg Lys Leu Val Arg Gly Asp Gln Leu Asp Ala
 225 230 235 240
 Thr Thr Ser Ser Met Phe Asn Asn Glu Ser Asp Ser Glu Leu Ser Asp
 245 250 255
 Ile Asp Asp Ser Lys Asn Ile Ala Leu Ser Ser Ser Leu Phe Arg Gly
 260 265 270
 Gly Ser Ser Pro Val Lys Glu Thr Asn Asn Asn Leu Ser Asn Met Asn
 275 280 285
 Ser Ser Pro Ala Gln Asn Pro Lys Arg Gly Ser Val Ser Arg Ser Asn
 290 295 300
 Asp Ser Asn Lys Ser Ser His Ile Ala Val Ser Lys Arg Pro Lys Gln
 305 310 315 320
 Lys Lys Gly Ile Tyr Arg Asp Ser Gly Gly Arg Thr Arg Leu Gln Ile
 325 330 335

Ala Cys Asp Lys Gly Lys Tyr Asp Val Val Lys Lys Met Ile Glu Glu
 340 345 350
 Gly Gly Tyr Asp Ile Asn Asp Gln Asp Asn Ala Gly Asn Thr Ala Leu
 355 360 365
 His Glu Ala Ala Leu Gln Gly His Ile Glu Ile Val Glu Leu Leu Ile
 370 375 380
 Glu Asn Gly Ala Asp Val Asn Ile Lys Ser Ile Glu Met Phe Gly Asp
 385 390 395 400
 Thr Pro Leu Ile Asp Ala Ser Ala Asn Gly His Leu Asp Val Val Lys
 405 410 415
 Tyr Leu Leu Lys Asn Gly Ala Asp Pro Thr Ile Arg Asn Ala Lys Gly
 420 425 430
 Leu Thr Ala Phe Glu Ser Val Asp Asp Glu Ser Glu Phe Asp Asp Glu
 435 440 445
 Glu Asp Gln Lys Ile Leu Arg Glu Ile Lys Lys Arg Leu Ser Ile Ala
 450 455 460
 Ala Lys Lys Trp Thr Asn Arg Ala Gly Ile His Asn Asp Lys Ser Lys
 465 470 475 480
 Asn Gly Asn Asn Ala His Thr Ile Asp Gln Pro Pro Phe Asp Asn Thr
 485 490 495
 Thr Lys Ala Lys Asn Glu Lys Ala Ala Asp Ser Pro Ser Met Ala Ser
 500 505 510
 Asn Ile Asp Glu Lys Ala Pro Glu Glu Glu Phe Tyr Trp Thr Asp Val
 515 520 525
 Thr Ser Arg Ala Gly Lys Glu Lys Leu Phe Lys Ala Ser Lys Glu Gly
 530 535 540
 His Leu Pro Tyr Val Gly Thr Tyr Val Glu Asn Gly Gly Lys Ile Asp
 545 550 555 560
 Leu Arg Ser Phe Phe Glu Ser Val Lys Cys Gly His Glu Asp Ile Thr
 565 570 575
 Ser Ile Phe Leu Ala Phe Gly Phe Pro Val Asn Gln Thr Ser Arg Asp
 580 585 590
 Asn Lys Thr Ser Ala Leu Met Val Ala Val Gly Arg Gly His Leu Gly
 595 600 605
 Thr Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Pro Thr Lys Arg Asp
 610 615 620
 Lys Lys Gly Arg Thr Ala Leu Tyr Tyr Ala Lys Asn Ser Ile Met Gly
 625 630 635 640

Ile Thr Asn Ser Glu Glu Ile Gln Leu Ile Glu Asn Ala Ile Asn Asn
645 650 655

Tyr Leu Lys Lys His Ser Glu Asp Asn Asn Asp Asp Asp Asp Asp Asp
660 665 670

Asp Asn Asn Asn Glu Thr Tyr Lys His Glu Lys Lys Arg Glu Lys Thr
675 680 685

Gln Ser Pro Ile Leu Ala Ser Arg Arg Ser Ala Thr Pro Arg Ile Glu
690 695 700

Asp Glu Glu Asp Asp Thr Arg Met Leu Asn Leu Ala Asp Asp Asp Phe
705 710 715 720

Asn Asn Asp Arg Asp Val Lys Glu Ser Thr Thr Ser Asp Ser Arg Lys
725 730 735

Arg Leu Asp Asp Asn Glu Asn Val Gly Thr Gln Tyr Ser Leu Asp Trp
740 745 750

Lys Lys Arg Lys Thr Asn Ala Leu Gln Asp Glu Glu Lys Leu Lys Ser
755 760 765

Ile Ser Pro Leu Ser Met Glu Pro His Ser Pro Lys Lys Ala Lys Ser
770 775 780

Val Glu Ile Ser Lys Ile His Glu Glu Thr Ala Ala Glu Arg Glu Ala
785 790 795 800

Arg Leu Lys Glu Glu Glu Tyr Arg Lys Lys Arg Leu Glu Lys Lys
805 810 815

Arg Lys Lys Glu Gln Glu Leu Leu Gln Lys Leu Ala Glu Asp Glu Lys
820 825 830

Lys Arg Ile Glu Glu Gln Glu Lys Gln Lys Val Leu Glu Met Glu Arg
835 840 845

Leu Glu Lys Ala Thr Leu Glu Lys Ala Arg Lys Met Glu Arg Glu Lys
850 855 860

Glu Met Glu Glu Ile Ser Tyr Arg Arg Ala Val Arg Asp Leu Tyr Pro
865 870 875 880

Leu Gly Leu Lys Ile Ile Asn Phe Asn Asp Lys Leu Asp Tyr Lys Arg
885 890 895

Phe Leu Pro Leu Tyr Tyr Phe Val Asp Glu Lys Asn Asp Lys Phe Val
900 905 910

Leu Asp Leu Gln Val Met Ile Leu Leu Lys Asp Ile Asp Leu Leu Ser
915 920 925

Lys Asp Asn Gln Pro Thr Ser Glu Lys Ile Pro Val Asp Pro Ser His
930 935 940

Leu Thr Pro Leu Trp Asn Met Leu Lys Phe Ile Phe Leu Tyr Gly Gly
 945 950 955 960
 Ser Tyr Asp Asp Lys Lys Asn Asn Met Glu Asn Lys Arg Tyr Val Val
 965 970 975
 Asn Phe Asp Gly Val Asp Leu Asp Thr Lys Ile Gly Tyr Glu Leu Leu
 980 985 990
 Glu Tyr Lys Lys Phe Val Ser Leu Pro Met Ala Trp Ile Lys Trp Asp
 995 1000 1005
 Asn Val Val Ile Glu Asn His Ala Lys Arg Lys Glu Ile Glu Gly Asn
 1010 1015 1020
 Met Ile Gln Ile Ser Ile Asn Glu Phe Ala Arg Trp Arg Asn Asp Lys
 1025 1030 1035 1040
 Leu Asn Lys Ala Gln Gln Pro Thr Arg Lys Gln Arg Ser Leu Lys Ile
 1045 1050 1055
 Pro Arg Glu Leu Pro Val Lys Phe Gln His Arg Met Ser Ile Ser Ser
 1060 1065 1070
 Val Leu Gln Gln Thr Ser Lys Glu Pro Phe Trp
 1075 1080

<210> 135
 <211> 4883
 <212> .DNA
 <213> Candida albicans

<400> 135
 tttcaatgcg ctacaactga ctgaaccagt ccacaaatth ggctgggtctc tctcgtttctc 60
 gccctgagag attttatttt cttataaatt ttactaaata aggatttgta cttttgatag 120
 agtttttttt ttttctgacg tttgtttagt taatattata taatagtatt taggaaacta 180
 ggtgggaggg gacatcgcaa cttttatcgt gacctacgac cagtgttttt tcaattgttt 240
 gatcaaaaaga gaaaaaaaga caaaggaccg aaggatagtt gcacgcataa actggagaaa 300
 aaattgtggt tgacatcggc gtttaggctt gtttgttctg tcacacatac gctgcttcac 360
 accaattcat atttctcagg ttaatttgtc tcctctccaa cttcaataac gattttgcgt 420
 gaaggtttaa tttcattatt gcaatttttag cagagaaacg cacataaata tatatatatt 480
 gattacagaa ccattataac atgtcttctt tgaaggatga agtaccact gagacttccg 540
 aagacttcgg ttttaagttt ttaggtcaaa aacaaattct accttccttc aatgaaaaac 600
 tgccatttgc atctctacaa aatctcgata tttcaaacag taagtcttta ttcgttgctg 660
 cctctggtag taaggcgggtg gtcggcgaat tacaattact gagagatcat atcacctccg 720
 actctactcc gttaacgttc aagtgaggaga aagaaatccc agatgtaata tttgtgtgct 780
 ttcattggtga tcagggttttg gtttcaacca gaaatgcatt atattcggtta gacttggagg 840
 aattgagtga atttcgaacg gtcacttctt ttgagaagcc agttttccaa ttgaagaacg 900
 ttaataacac ttttagtaatt ttaaattcag tcaatgattt atcagcactg gatttaagaa 960
 caaaatcgac taagcaactg gcacaaaacg ttacctcttt tgatgtcaca aattcgcagt 1020
 tagcagttct actaaaagat agaagttttt aaagtttttg atggcgaaat ggcgaaatgg 1080
 aaaaacaatt tgagttctct ctaccgtcag aattagaaga gcttccagta gaagaatatt 1140
 cccctttgag tgttaccatt ctctctccac aggatttttt ggcggttttc ggtaatgtta 1200
 tatcagagac cgatgacgaa gtttcatacg atcaaaaaat gtacattata aagcacatag 1260

acggcagcgc ctcatttcaa gaaacttttg atattacacc tccattcggg caaatagtaa 1320
 gggtcccata tatgtacaaa gttaccttgt ctggtttaat tgaacctgat gcaaacgtaa 1380
 atgtgctagc atcatcatgt tcaagtgaag taagtatatg ggactcgaag caagttattg 1440
 aaccttccca ggattctgaa cgagcagtat tgcccatcag tgaggaaaca gataaggaca 1500
 caaatccaat aggtgtggca gttgacgtcg ttacttcagg cactattcta gaaccttggt 1560
 ccggtgttga tacgatagag cgattgccgc tcgtttacat attgaataac gaaggtagct 1620
 tacagatagt cgggttggtt catgtggcag caatcaaaag cggccattat agcataaatc 1680
 tggaatcttt agaacatgag aaatctctct ctctacatc agaaaaaatt cctattgctg 1740
 gacaggagca ggaagaaaaa aagaaaaata atgaatcaag taaggcttta tcagagaatc 1800
 ctttcacatc agcaaatata tcaggcttca cttttcttaa aacacaacca gccgctgcca 1860
 atagcctgca gtctcaaagt tcttcaacct ttggtgctcc ctcatctgga tcatccgcat 1920
 ttaaaattga cttgccatca gtctcatcta ccagtactgg tgtagcgtcc agtgaacaag 1980
 acgcaacaga tcctgcttct gctaagccag tattcggcaa acccgcgttc ggagctattg 2040
 ccaaagaacc gtcaacatca gaatatgcct ttggcaagcc atcttttggg gctccctcct 2100
 ttggctctgg aaagtcatct gttgaatcgc ctgcctccgg atctgccttt ggtaagccct 2160
 cttttggtac tccttccttt ggctctggaa attcatctgt tgagccgcct gcctccggat 2220
 ctgcatttgg taagccctct tttggtactc ctctcttgg ctctggaaat tcatctgctg 2280
 agccgcctgc ttccggatct gcctttggta agccctcttt tggtagatct gcattcggaa 2340
 ctgcatcaag taacgaaact aactctggat ccatatttgg aaaggctgca tttggttcat 2400
 catcttttgc acccgccaac aatgaacttt tcggatcaaa ctttactatt tcaaaacct 2460
 cagttgacag cccaaaggag gtagattcaa cgtcaccttt cccatcttct ggcgatcaaa 2520
 gtgaagatga gtctaagagt gatgtagact cttcttcgac accttttggg acgaaacct 2580
 acacctctac gaaaccaaag accaatgcct ttgattttgg gagttcttcc tttggatctg 2640
 gattttcaaa ggctctggaa tctgttgggt ccgatacaac ttttaaattc ggtactcagg 2700
 cttcaccttt ctcttcacag ttaggaaaca aatcaccatt cagttccttc acaaaagatg 2760
 atactgaaaa tggatcttta agtaagggtc ctaccagtga aatcaatgac gataatgaag 2820
 aacacgaaag caatggctcc aacgtaagcg gtaatgattt gacagattct acggttgagc 2880
 aaacatcttc tactagatta ccggaacttc cctcgatga agatggtgaa gttgtcgagg 2940
 aggaagcgca aaaatcccc ataggcaagc taactgaaac tataaaaaaa agtgccaata 3000
 ttgacatggc tggtttaaaa aatcctgtat ttggaatca tgtcaaagca aaatccgaat 3060
 cgccgttttc agcatttgca acaaatatta ccaaaccaag ctctacaaca cctgcttttt 3120
 cgtttggtaa ctccacaatg aataaaaagta atacatctac ggtttcacca atggaagaag 3180
 ctgatactaa gaaaagtagt gaaaagggcc ccataacctt gaagagtgtg gagaatccgt 3240
 ttctaccagc gaaagaagaa agaactggag aaagttctaa aaaggatcat aacgatgacc 3300
 caaaagatgg ttatgtatca ggaagtgaat tatctgtaag gacttctgaa agtgcctttg 3360
 ataccacagc aaacgaagaa attccaaagt cacaggacgt gaacaatcat gaaaaagcg 3420
 aaacagaccc aaaatatagt caacatgctg tggttgatca cgataacaag tctaaagaaa 3480
 tgaatgaaac ttcgaagaat aatgaaagga gcggtcaacc aaatcatggg gtccaaggag 3540
 atggaatagc attgaaaaaa gacaatgaaa aagagaattt tgattcaaat atggcaata 3600
 agcaattcga agaccaccaa tcttcagaag aggacgcgag cgaaaaagac agtagacaaa 3660
 gcagtgaagt taaagaatca gatgataaca tgtcactcaa cagtgaccgg gatgaaagta 3720
 tatctgagtc ctacgataaa ctggaagata ttaatactga tgagctacct catggtggag 3780
 aagcttttaa agcacgtgaa gtgagcgctt ccgctgattt tgatgtacaa acttcattag 3840
 aagacaatta tgctgaatct ggcatacaga cagaccttcc agaaagttcc aaggaaaaatg 3900
 aagttcaaac ggatgccata cccgtgaaac acacagtagc acaaactgtt aagaaggag 3960
 cagtcgacaa tggctctgcaa actgagcctg ttgaaacatg taatttttct gttcaaact 4020
 ttgaaggatga cgaaaattat ttagcagagc aatgcaatc atattttctc aaagaatatt 4080
 acacaagtgc aaaagtatca aatattcctt tcgtttcaca aaattctacg ttaagggttga 4140
 ttgagagtac atttcagacg gtcgaagctg agtttactgt tctgatggaa aacatccgga 4200
 atatggatac tttttttact gatcaatcga gcaccccttt ggtgaagcgt acagtgcggt 4260
 ctatcaataa tctgtatact tggagaatac cagaggctga aattctatta aatattcaga 4320
 ataatatcaa gtgtgaacaa atgcaaataa caaatgctaa cattcaagac ctgaaggaaa 4380
 aagttacaga ttatgtcagg aaagatattg cacaataaac tgaagatgta gccaatgcaa 4440
 aagaggagta tctgttttta atgcatttg atgatgcttc gagtggatac gttaaagat 4500
 tcagcacgca tcaattttag atgcaaaaga cattacgtca aaagctattc gatgtgtccg 4560
 ccaaaattaa tcatactgaa gagttgctga acatttttaa attgttctact gtaaagaata 4620
 agagatttga cgataatcca ttagtggtgaa aactagctaa agaattctct gcacgtgacg 4680

Val Ser Tyr Asp Gln Lys Met Tyr Ile Ile Lys His Ile Asp Gly Ser
 245 250 255
 Ala Ser Phe Gln Glu Thr Phe Asp Ile Thr Pro Pro Phe Gly Gln Ile
 260 265 270
 Val Arg Phe Pro Tyr Met Tyr Lys Val Thr Leu Ser Gly Leu Ile Glu
 275 280 285
 Pro Asp Ala Asn Val Asn Val Leu Ala Ser Ser Cys Ser Ser Glu Val
 290 295 300
 Ser Ile Trp Asp Ser Lys Gln Val Ile Glu Pro Ser Gln Asp Ser Glu
 305 310 315 320
 Arg Ala Val Leu Pro Ile Ser Glu Glu Thr Asp Lys Asp Thr Asn Pro
 325 330 335
 Ile Gly Val Ala Val Asp Val Val Thr Ser Gly Thr Ile Leu Glu Pro
 340 345 350
 Cys Ser Gly Val Asp Thr Ile Glu Arg Leu Pro Leu Val Tyr Ile Leu
 355 360 365
 Asn Asn Glu Gly Ser Leu Gln Ile Val Gly Leu Phe His Val Ala Ala
 370 375 380
 Ile Lys Ser Gly His Tyr Ser Ile Asn Leu Glu Ser Leu Glu His Glu
 385 390 395 400
 Lys Ser Leu Ser Pro Thr Ser Glu Lys Ile Pro Ile Ala Gly Gln Glu
 405 410 415
 Gln Glu Glu Lys Lys Lys Asn Asn Glu Ser Ser Lys Ala Leu Ser Glu
 420 425 430
 Asn Pro Phe Thr Ser Ala Asn Thr Ser Gly Phe Thr Phe Leu Lys Thr
 435 440 445
 Gln Pro Ala Ala Ala Asn Ser Leu Gln Ser Gln Ser Ser Ser Thr Phe
 450 455 460
 Gly Ala Pro Ser Phe Gly Ser Ser Ala Phe Lys Ile Asp Leu Pro Ser
 465 470 475 480
 Val Ser Ser Thr Ser Thr Gly Val Ala Ser Ser Glu Gln Asp Ala Thr
 485 490 495
 Asp Pro Ala Ser Ala Lys Pro Val Phe Gly Lys Pro Ala Phe Gly Ala
 500 505 510
 Ile Ala Lys Glu Pro Ser Thr Ser Glu Tyr Ala Phe Gly Lys Pro Ser
 515 520 525
 Phe Gly Ala Pro Ser Phe Gly Ser Gly Lys Ser Ser Val Glu Ser Pro
 530 535 540

Lys	Ala	Lys	Ser	Glu	Ser	Pro	Phe	Ser	Ala	Phe	Ala	Thr	Asn	Ile	Thr
850						855									860
Lys	Pro	Ser	Ser	Thr	Thr	Pro	Ala	Phe	Ser	Phe	Gly	Asn	Ser	Thr	Met
865					870					875					880
Asn	Lys	Ser	Asn	Thr	Ser	Thr	Val	Ser	Pro	Met	Glu	Glu	Ala	Asp	Thr
				885					890					895	
Lys	Glu	Thr	Ser	Glu	Lys	Gly	Pro	Ile	Thr	Leu	Lys	Ser	Val	Glu	Asn
			900					905					910		
Pro	Phe	Leu	Pro	Ala	Lys	Glu	Glu	Arg	Thr	Gly	Glu	Ser	Ser	Lys	Lys
		915					920					925			
Asp	His	Asn	Asp	Asp	Pro	Lys	Asp	Gly	Tyr	Val	Ser	Gly	Ser	Glu	Ile
	930					935					940				
Ser	Val	Arg	Thr	Ser	Glu	Ser	Ala	Phe	Asp	Thr	Thr	Ala	Asn	Glu	Glu
945					950					955					960
Ile	Pro	Lys	Ser	Gln	Asp	Val	Asn	Asn	His	Glu	Lys	Ser	Glu	Thr	Asp
				965					970					975	
Pro	Lys	Tyr	Ser	Gln	His	Ala	Val	Val	Asp	His	Asp	Asn	Lys	Ser	Lys
			980					985					990		
Glu	Met	Asn	Glu	Thr	Ser	Lys	Asn	Asn	Glu	Arg	Ser	Gly	Gln	Pro	Asn
		995					1000					1005			
His	Gly	Val	Gln	Gly	Asp	Gly	Ile	Ala	Leu	Lys	Lys	Asp	Asn	Glu	Lys
	1010					1015						1020			
Glu	Asn	Phe	Asp	Ser	Asn	Met	Ala	Ile	Lys	Gln	Phe	Glu	Asp	His	Gln
1025					1030					1035					1040
Ser	Ser	Glu	Glu	Asp	Ala	Ser	Glu	Lys	Asp	Ser	Arg	Gln	Ser	Ser	Glu
				1045					1050					1055	
Val	Lys	Glu	Ser	Asp	Asp	Asn	Met	Ser	Leu	Asn	Ser	Asp	Arg	Asp	Glu
			1060					1065					1070		
Ser	Ile	Ser	Glu	Ser	Tyr	Asp	Lys	Leu	Glu	Asp	Ile	Asn	Thr	Asp	Glu
		1075					1080					1085			
Leu	Pro	His	Gly	Gly	Glu	Ala	Phe	Lys	Ala	Arg	Glu	Val	Ser	Ala	Ser
	1090					1095					1100				
Ala	Asp	Phe	Asp	Val	Gln	Thr	Ser	Leu	Glu	Asp	Asn	Tyr	Ala	Glu	Ser
1105					1110					1115					1120
Gly	Ile	Gln	Thr	Asp	Leu	Ser	Glu	Ser	Ser	Lys	Glu	Asn	Glu	Val	Gln
				1125					1130					1135	
Thr	Asp	Ala	Ile	Pro	Val	Lys	His	Asn	Ser	Thr	Gln	Thr	Val	Lys	Lys
				1140				1145					1150		

Glu Ala Val Asp Asn Gly Leu Gln Thr Glu Pro Val Glu Thr Cys Asn
 1155 1160 1165
 Phe Ser Val Gln Thr Phe Glu Gly Asp Glu Asn Tyr Leu Ala Glu Gln
 1170 1175 1180
 Cys Lys Pro Lys Gln Leu Lys Glu Tyr Tyr Thr Ser Ala Lys Val Ser
 1185 1190 1195 1200
 Asn Ile Pro Phe Val Ser Gln Asn Ser Thr Leu Arg Leu Ile Glu Ser
 1205 1210 1215
 Thr Phe Gln Thr Val Glu Ala Glu Phe Thr Val Leu Met Glu Asn Ile
 1220 1225 1230
 Arg Asn Met Asp Thr Phe Phe Thr Asp Gln Ser Ser Ile Pro Leu Val
 1235 1240 1245
 Lys Arg Thr Val Arg Ser Ile Asn Asn Leu Tyr Thr Trp Arg Ile Pro
 1250 1255 1260
 Glu Ala Glu Ile Leu Leu Asn Ile Gln Asn Asn Ile Lys Cys Glu Gln
 1265 1270 1275 1280
 Met Gln Ile Thr Asn Ala Asn Ile Gln Asp Leu Lys Glu Lys Val Thr
 1285 1290 1295
 Asp Tyr Val Arg Lys Asp Ile Ala Gln Ile Thr Glu Asp Val Ala Asn
 1300 1305 1310
 Ala Lys Glu Glu Tyr Leu Phe Leu Met His Phe Asp Asp Ala Ser Ser
 1315 1320 1325
 Gly Tyr Val Lys Asp Leu Ser Thr His Gln Phe Arg Met Gln Lys Thr
 1330 1335 1340
 Leu Arg Gln Lys Leu Phe Asp Val Ser Ala Lys Ile Asn His Thr Glu
 1345 1350 1355 1360
 Glu Leu Leu Asn Ile Leu Lys Leu Phe Thr Val Lys Asn Lys Arg Leu
 1365 1370 1375
 Asp Asp Asn Pro Leu Val Ala Lys Leu Ala Lys Glu Ser Leu Ala Arg
 1380 1385 1390
 Asp Gly Leu Leu Lys Glu Ile Lys Leu Leu Arg Glu Gln Val Ser Arg
 1395 1400 1405
 Leu Gln Leu Glu Glu Lys Gly Lys Lys Ala Ser Ser Phe Asp Ala Ser
 1410 1415 1420
 Ser Ser Ile Thr Lys Asp Met Lys Gly Phe Lys Val Val Glu Val Gly
 1425 1430 1435 1440
 Leu Ala Met Asn Thr Lys Lys Gln Ile Gly Asp Phe Phe Lys Asn Leu
 1445 1450 1455

Asn Met Ala Lys
1460

<210> 137
<211> 1321
<212> DNA
<213> *Candida albicans*

<400> 137
tcgatcaact ctatccaaca attctataat atccactgtt cattaacgaa tattgggtcct 60
tttcccttat ggtgaagtaa attttccatg caatatcccg gtaagctatc gacaagttta 120
ttgactgcaa tttgagttta ttacatccgt acattactaa gatgtatggg ttttctatatt 180
ttgtgctccg tgtcgatatt tcgtggagca aaccagaaaa gatgcggaac ctcttagcac 240
tccgcctgga cataggcgga gcatattcct cctatgggat gggttttgtt gtactctttt 300
ctctctagac aggacctccg attgcctccc tgagggtgag atggtttccg gcctcaggac 360
ggccttctcc agtttctagc gaggcataca ttccaaccaa aggtgtatca agaatatctg 420
aaattaaagg tagttgaatc tctatttggt gttgttatta ccgcttatta tcccatagtt 480
gagacgacca agattcaaac atgcaaatgt atgcaccata tccattctaa acatagtttt 540
tcgaacgttc agagcttaaa gggacaatta ttttagaaac tgaattttta cccagtggaa 600
taacatcgta tctgtaaagt ctacaaaatt ttttatccat caaaaattaa aacaaagaaa 660
actgccaaac tgaatatgag gaactttcct ctctaggaat gacttagtga atgtacagtg 720
acttgtggaa aatatgatta gattttgagc ggggtgatgcg acttaacagt ctcatgtcgt 780
aagaaatatc caaatttggt gttcatgctc tccccaaaga tatgacgatg agagctcgtt 840
taaaattttg tcttcttccg aacagttatg aaaaaactat tacgtgtttt tatgatattc 900
ttactaactt gtcatttttt tataaaatta tttttttaac agttttgtca agactttgac 960
tggttaagacc atcacttttg aagttgaatc ttctgacact attgacaatg tcaagtcaaa 1020
gattcaagac aaggaaggta tcccacctga ccaacaaaga ttgatctttg ctggtaagca 1080
attggaagac ggtagaacct tgtctgacta caacattcaa aaagaatcca ctttgcaactt 1140
agtcttgaga ttgagagggt gtatcattga accatctttg aaagcttttg cttccaagta 1200
caactgtgac aaatctgttt gccgtaagtg ttatgctaga ttgccaccaa gagctaccaa 1260
ctgtagaaaag agaaagtgtg gtcacaccaa ccaattgctt ccaaagaaga agttaaaatg 1320
a 1321

<210> 138
<211> 128
<212> PRT
<213> *Candida albicans*

<400> 138
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro
65 70 75 80

Ser	Leu	Lys	Ala	Leu	Ala	Ser	Lys	Tyr	Asn	Cys	Asp	Lys	Ser	Val	Cys
				85					90					95	
Arg	Lys	Cys	Tyr	Ala	Arg	Leu	Pro	Pro	Arg	Ala	Thr	Asn	Cys	Arg	Lys
			100					105					110		
Arg	Lys	Cys	Gly	His	Thr	Asn	Gln	Leu	Arg	Pro	Lys	Lys	Lys	Leu	Lys
			115				120					125			

<210> 139
 <211> 2216
 <212> DNA
 <213> Candida albicans

<400> 139
 aatattcaac ctgaagttgc agtcaaagcg gcgattaact tttccaacgt aaccgatcta 60
 actaacaata gcaccgatgg agcaaaaata acagaaattg gaagtacatc taaacggcca 120
 attgagagcg gtacatcttc tgatccagac accaaaaagg ttaaagagag tccagcaaat 180
 gatcaagctt ccaacgagtg atgtaatat aaacaatgta attatataaa tatgaaacat 240
 ctacatatatt taaatgtcac taatgtcatt acagaggaca taaagtgatt tatgacacat 300
 ccgtactagt agttaagtat gaacaaattt tgggtttatt tgccattttt tttcacgcgg 360
 gtttcttggg tgcgcaaacc cactttttct aacaccacta agaaatatca actttatagg 420
 ccatcgaaga taaaggaacg taagtttgtc aattcaacct cacattttca acgcacatta 480
 agcacttggt tcgtggagaa atgaatgatc ctctgaaat tttagcgggt gatccgtaca 540
 ataattattac ttctgatgaa gaggatgagc aagccatcgc gagagaactt gaatttatgg 600
 aacgaaagag gcaggcctta gtggaacgat taaaaagaaa gcaagaattt aagaacccc 660
 aggatcctaa ttttgaagcc atcgaggtag ctcaatctcc taccaaaaac cgtgtgaaag 720
 tgggggtctca taatgctaca caacaaggca caaaattcga aggttcgaat attaataag 780
 taaggttatc tcaattacag cagcaaccaa aaccaccagc tagtacaacc acatacttta 840
 tggagaaatt tcaaaacgca aagaagaacg aagataaaca aattgccaag tttgaaagca 900
 tgatgaatgc aagagtacat acgttcagta ccgatgagaa gaaatatgtg ccgataatca 960
 caaacgaatt agaaagcttt tcaaattctt ggggttaaaaa gaggtacata cctgaagatg 1020
 acttaaaacg ggctttgcat gagatcaaaa tccttcgggt gggcaaaact tttgctaaaa 1080
 ttcgcccacc taaatttcaa gagcctgaat acgccaactg ggccaccgta ggcctcatta 1140
 gccacaaatc ggacatcaaa tttacatcat ctgaaaagcc agtcaaattc ttcattgttc 1200
 ccataacgga ctttcagcat acactagatg tttatatctt cgggaaaaag ggtgtagaaa 1260
 gatattataa tcttcgcctg ggtgatgtga tagcaatatt aaaccagaa gtactaccat 1320
 ggagaccctc agggcgagga aattttatca aatccttcaa ccttcgaatt agtcatgact 1380
 tcaaattgat cctggagata ggttcaagta gagatttagg ttggtgtccc atagtgaata 1440
 aaaagactca caaaaaatgt ggctctccca ttaacatatc tcttcataag tgttgcgatt 1500
 accatagaga agtgcaattt cgtggaacaa gtgctaaaag aattgaatta aatgggtggg 1560
 acgccttggg cgcgcctacg aaagtggact ctcaaccaag cctatataag gccaaagggg 1620
 aaaacgggtt taatataatc aaaggtagc gtaagcgct gtcagaagag gaggaaagac 1680
 ttaaaaagag ctctcacaat tttacgaata gtaattctgc caaagcattt ttcgacgaga 1740
 aatttcagaa tccagatatg ctggcaaaact tagacaataa aagaaggaaa ataatagaaa 1800
 ctaagaaatc gacagcactg agccgcgaac taggcaaaat tatgagaagg agggaaatcca 1860
 gcggattaga agataagagc gtcggagagc gacagaaaat gaaacgaacc acagaaagtg 1920
 ccctccagac agggcttata caacgcctag gattcgatcc cactcatgga aaaatttccc 1980
 aagtactcaa gtcttctgta tcagggagcg aacctaaaga caacttactc ggtaaaaaaa 2040
 aaactgttat aaacgatctc ttgcattaca agaaggaaaa agtcattctc gcaccttcaa 2100
 agaacgaatg gttcaagaaa agaagccatc gcgaagaagt ttggcaaaaa catttcggat 2160
 ccaaggaaaac taaagaaact tctgacggta gtgccagcga tcttgagata atataa 2216

141

<210> 140

<211> 571

<212> PRT

<213> Candida albicans

<400> 140

Met Asn Asp Pro Arg Glu Ile Leu Ala Val Asp Pro Tyr Asn Asn Ile
 1 5 10 15

Thr Ser Asp Glu Glu Asp Glu Gln Ala Ile Ala Arg Glu Leu Glu Phe
 20 25 30

Met Glu Arg Lys Arg Gln Ala Leu Val Glu Arg Leu Lys Arg Lys Gln
 35 40 45

Glu Phe Lys Lys Pro Gln Asp Pro Asn Phe Glu Ala Ile Glu Val Pro
 50 55 60

Gln Ser Pro Thr Lys Asn Arg Val Lys Val Gly Ser His Asn Ala Thr
 65 70 75 80

Gln Gln Gly Thr Lys Phe Glu Gly Ser Asn Ile Asn Glu Val Arg Leu
 85 90 95

Ser Gln Leu Gln Gln Gln Pro Lys Pro Pro Ala Ser Thr Thr Thr Tyr
 100 105 110

Phe Met Glu Lys Phe Gln Asn Ala Lys Lys Asn Glu Asp Lys Gln Ile
 115 120 125

Ala Lys Phe Glu Ser Met Met Asn Ala Arg Val His Thr Phe Ser Thr
 130 135 140

Asp Glu Lys Lys Tyr Val Pro Ile Ile Thr Asn Glu Leu Glu Ser Phe
 145 150 155 160

Ser Asn Leu Trp Val Lys Lys Arg Tyr Ile Pro Glu Asp Asp Leu Lys
 165 170 175

Arg Ala Leu His Glu Ile Lys Ile Leu Arg Leu Gly Lys Leu Phe Ala
 180 185 190

Lys Ile Arg Pro Pro Lys Phe Gln Glu Pro Glu Tyr Ala Asn Trp Ala
 195 200 205

Thr Val Gly Leu Ile Ser His Lys Ser Asp Ile Lys Phe Thr Ser Ser
 210 215 220

Glu Lys Pro Val Lys Phe Phe Met Phe Thr Ile Thr Asp Phe Gln His
 225 230 235 240

Thr Leu Asp Val Tyr Ile Phe Gly Lys Lys Gly Val Glu Arg Tyr Tyr
 245 250 255

Asn Leu Arg Leu Gly Asp Val Ile Ala Ile Leu Asn Pro Glu Val Leu

260					265					270					
Pro	Trp	Arg	Pro	Ser	Gly	Arg	Gly	Asn	Phe	Ile	Lys	Ser	Phe	Asn	Leu
		275					280					285			
Arg	Ile	Ser	His	Asp	Phe	Lys	Cys	Ile	Leu	Glu	Ile	Gly	Ser	Ser	Arg
	290					295					300				
Asp	Leu	Gly	Trp	Cys	Pro	Ile	Val	Asn	Lys	Lys	Thr	His	Lys	Lys	Cys
305					310					315					320
Gly	Ser	Pro	Ile	Asn	Ile	Ser	Leu	His	Lys	Cys	Cys	Asp	Tyr	His	Arg
				325					330					335	
Glu	Val	Gln	Phe	Arg	Gly	Thr	Ser	Ala	Lys	Arg	Ile	Glu	Leu	Asn	Gly
			340					345					350		
Gly	Tyr	Ala	Leu	Gly	Ala	Pro	Thr	Lys	Val	Asp	Ser	Gln	Pro	Ser	Leu
		355					360					365			
Tyr	Lys	Ala	Lys	Gly	Glu	Asn	Gly	Phe	Asn	Ile	Ile	Lys	Gly	Thr	Arg
	370					375					380				
Lys	Arg	Leu	Ser	Glu	Glu	Glu	Glu	Arg	Leu	Lys	Lys	Ser	Ser	His	Asn
385						390					395				400
Phe	Thr	Asn	Ser	Asn	Ser	Ala	Lys	Ala	Phe	Phe	Asp	Glu	Lys	Phe	Gln
				405					410					415	
Asn	Pro	Asp	Met	Leu	Ala	Asn	Leu	Asp	Asn	Lys	Arg	Arg	Lys	Ile	Ile
			420					425					430		
Glu	Thr	Lys	Lys	Ser	Thr	Ala	Leu	Ser	Arg	Glu	Leu	Gly	Lys	Ile	Met
		435					440					445			
Arg	Arg	Arg	Glu	Ser	Ser	Gly	Leu	Glu	Asp	Lys	Ser	Val	Gly	Glu	Arg
			450			455					460				
Gln	Lys	Met	Lys	Arg	Thr	Thr	Glu	Ser	Ala	Leu	Gln	Thr	Gly	Leu	Ile
465						470					475				480
Gln	Arg	Leu	Gly	Phe	Asp	Pro	Thr	His	Gly	Lys	Ile	Ser	Gln	Val	Leu
				485					490					495	
Lys	Ser	Ser	Val	Ser	Gly	Ser	Glu	Pro	Lys	Asn	Asn	Leu	Leu	Gly	Lys
			500					505					510		
Lys	Lys	Thr	Val	Ile	Asn	Asp	Leu	Leu	His	Tyr	Lys	Lys	Glu	Lys	Val
			515				520					525			
Ile	Leu	Ala	Pro	Ser	Lys	Asn	Glu	Trp	Phe	Lys	Lys	Arg	Ser	His	Arg
						535					540				
Glu	Glu	Val	Trp	Gln	Lys	His	Phe	Gly	Ser	Lys	Glu	Thr	Lys	Glu	Thr
545						550					555				560
Ser	Asp	Gly	Ser	Ala	Ser	Asp	Leu	Glu	Ile	Ile					

565

570

<210> 141
 <211> 1133
 <212> DNA
 <213> Candida albicans

<400> 141
 gacattttga aaaaattaca tttatagaag tttattataa cgtaacagtt aacaacaaag 60
 gctcatagtc cgagatcaat ataataaatt attcaagggt taaggaagaa gttaccatgg 120
 aaatgactta ctatgaaaag acacctttga ttcgtcaatt tttgaacaat ggtaagacaa 180
 attcgtgggt ttacgttaag catgagatgt tacaaccagg tggaagtttc aaatcgagag 240
 gaatcgggca tttgataagg aagagtaatg aagaagcgct aagcgagggg tctgggaagc 300
 ttgctgtatt ttctagctct gggggaaatg ctggtttagc agcagcaact gcctgcagat 360
 cgatggcact taattgcagt gtagtggttc ctaaaactac aaaacctaga atggtaaaga 420
 aaattcaaag tgcaggagcc aaagtcatta tccatgggtga tcattggggg gaagcagatg 480
 aatacttgag gcacgaatga atggcgcaag aaagccaaca tggttcgaag acactatatg 540
 tgcacccgtt tgataacgag acaatttggg aaggtcattc tacgattgtg gatgaaatca 600
 tagaacaatt gaaggaaaat gatatatcct tacctagggt gaaagctttg gtttgtagtg 660
 ttggtgggtg tgggctatatt agtggcataa ttaaaggcct agataggaat cagcttgctg 720
 aaaaaattcc ggtcgttgct gtagaaaactg ccggttggtga cgtattgaat aagtctctca 780
 aaaaaggtag tccagttact cttgaaaaat tgacaagtgt tgcaacttct ttggcctccc 840
 catacatagc atcattcgcg tttgagagtt ttaacaagta tggatgtaag tctgtagttt 900
 tatcagatca agacgttctg gcaacatgct tgagatatgc cgatgactac aattttatag 960
 tggaaccagc ctgtggagca tccttacatt tatgttatca tccagagatt cttgaagaca 1020
 ttctggaaca aaaaatatat gaggatgata tcgttattat aatcgcatgc ggtggatcat 1080
 gtatgacgta tgaagacttg gtgaaagcgt cgagcacatt aaacgtatca taa 1133

<210> 142
 <211> 210
 <212> PRT
 <213> Candida albicans

<400> 142
 Met Ala Gln Glu Ser Gln His Gly Ser Lys Thr Leu Tyr Val His Pro
 1 5 10 15
 Phe Asp Asn Glu Thr Ile Trp Glu Gly His Ser Thr Ile Val Asp Glu
 20 25 30
 Ile Ile Glu Gln Leu Lys Glu Asn Asp Ile Ser Leu Pro Arg Val Lys
 35 40 45
 Ala Leu Val Cys Ser Val Gly Gly Gly Gly Leu Phe Ser Gly Ile Ile
 50 55 60
 Lys Gly Leu Asp Arg Asn Gln Leu Ala Glu Lys Ile Pro Val Val Ala
 65 70 75 80
 Val Glu Thr Ala Gly Cys Asp Val Leu Asn Lys Ser Leu Lys Lys Gly
 85 90 95
 Ser Pro Val Thr Leu Glu Lys Leu Thr Ser Val Ala Thr Ser Leu Ala
 100 105 110

Ser Pro Tyr Ile Ala Ser Phe Ala Phe Glu Ser Phe Asn Lys Tyr Gly
 115 120 125

Cys Lys Ser Val Val Leu Ser Asp Gln Asp Val Leu Ala Thr Cys Leu
 130 135 140

Arg Tyr Ala Asp Asp Tyr Asn Phe Ile Val Glu Pro Ala Cys Gly Ala
 145 150 155 160

Ser Leu His Leu Cys Tyr His Pro Glu Ile Leu Glu Asp Ile Leu Glu
 165 170 175

Gln Lys Ile Tyr Glu Asp Asp Ile Val Ile Ile Ile Ala Cys Gly Gly
 180 185 190

Ser Cys Met Thr Tyr Glu Asp Leu Val Lys Ala Ser Ser Thr Leu Asn
 195 200 205

Val Ser
 210

<210> 143
 <211> 2549
 <212> DNA
 <213> Candida albicans

<400> 143
 ccatgaactc agcatgtgct actccagtta atgacttggt cgtatcggtc atgccataag 60
 ccatcacctg gccagttggc gtatgtacaa agatgcaagc taccggtgtc tcatcgtggt 120
 caagagcgta tctagccaaa cggacagctg tcctcatatg tttaatatgc tgcatagtgt 180
 gaggctccta gtttttaccg cagccaccag ccgcttctcg agcaaagtgt agatccatt 240
 aggactcatc attcatctaa ttttgctatg ttagctgcaa ctttctattt taatagaacc 300
 ttctggaaat ttcacccggc gcggcacccg aggaactgga cagcgtgtcg aaaaagttgc 360
 ttttttatat aaaggacacg aaaaggggtc tctggaagat ataaatatgg ctatgtaatt 420
 cttaaagatta acgtgttact gttttacttt tttaaagtcc ccaagagtag tctcaaggga 480
 aaaagcgat caaacatacc atgtttttca acagactaag cgctggcaag ctgctgggtac 540
 cactctccgt ggtcctgtac gcccttttcg tggtaatat acctttacag aattctttcc 600
 actcctcaa tgttttagtt agaggtgccg atgatgtaga aaactacgga actgttatcg 660
 gtattgactt aggtactact tattcctgtg ttgctgtgat gaaaaatggt aagactgaaa 720
 ttcttgctaa tgagcaagggt aacagaatca ccccatctta cgtggcatc accgatgatg 780
 aaagattgat tggatgatgt gcaaagaacc aagttgctgc caatcctcaa aacaccatct 840
 tcgacattaa gagattgac ggtttgaaat ataacgacag atctgttcag aaggatatca 900
 agcacttgcc atttaattgt gtttaataaag atgggaagcc cgctgtagaa gtaagtgtca 960
 aaggagaaaa gaagggtttt actccagaag aaatttctgg tatgatcttg ggtaagatga 1020
 aacaaattgc cgaagattat ttaggcacta aggttaccca tgctgtcgtt actgttctcg 1080
 ctattttcaa tgacgcgcaa agacaagcca ccaaggatgc tggtagcatc gctgggttga 1140
 acgttttgag aattgttaat gaaccaaccg cagccgccat tgacctacgg ttggataaat 1200
 ctgataagga acatcaaatt attgtttatg atttgggtgg tggactttc gatgtctctc 1260
 tattgtctat tgaaaacggg gttttcgaag tccaagccac ttctgggtgat actcatttag 1320
 gtgggtgaaga ttttgactat aagatcggtc gtcaattgat aaaagcttc aagaagaagc 1380
 atggtattga tgtgtctgac aacaacaagg ccctagctaa attgaagaga gaagctgaaa 1440
 aggctaaaac tgccttgccc agccaaatgt ccaccggtat tgaaattgac tccttcgttg 1500
 atggtatcga cttaagtga accttgacca gagctaagtt tgaggaatta aacctagatc 1560
 tattcaagaa gaccttgaag cctgtcgaga aggttttgca agattctggt ttggaaaaga 1620

Ala Glu Asp Tyr Leu Gly Thr Lys Val Thr His Ala Val Val Thr Val
 180 185 190
 Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly
 195 200 205
 Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr Ala
 210 215 220
 Ala Ala Ile Ala Tyr Gly Leu Asp Lys Ser Asp Lys Glu His Gln Ile
 225 230 235 240
 Ile Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Ser
 245 250 255
 Ile Glu Asn Gly Val Phe Glu Val Gln Ala Thr Ser Gly Asp Thr His
 260 265 270
 Leu Gly Gly Glu Asp Phe Asp Tyr Lys Ile Val Arg Gln Leu Ile Lys
 275 280 285
 Ala Phe Lys Lys Lys His Gly Ile Asp Val Ser Asp Asn Asn Lys Ala
 290 295 300
 Leu Ala Lys Leu Lys Arg Glu Ala Glu Lys Ala Lys Arg Ala Leu Ser
 305 310 315 320
 Ser Gln Met Ser Thr Arg Ile Glu Ile Asp Ser Phe Val Asp Gly Ile
 325 330 335
 Asp Leu Ser Glu Thr Leu Thr Arg Ala Lys Phe Glu Glu Leu Asn Leu
 340 345 350
 Asp Leu Phe Lys Lys Thr Leu Lys Pro Val Glu Lys Val Leu Gln Asp
 355 360 365
 Ser Gly Leu Glu Lys Lys Asp Val Asp Asp Ile Val Leu Val Gly Gly
 370 375 380
 Ser Thr Arg Ile Pro Lys Val Gln Gln Leu Leu Glu Ser Tyr Phe Asp
 385 390 395 400
 Gly Lys Lys Ala Ser Lys Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr
 405 410 415
 Gly Ala Ala Val Gln Ala Gly Val Leu Ser Gly Glu Glu Gly Val Glu
 420 425 430
 Asp Ile Val Leu Leu Asp Val Asn Ala Leu Thr Leu Gly Ile Glu Thr
 435 440 445
 Thr Gly Gly Val Met Thr Pro Leu Ile Lys Arg Asn Thr Ala Ile Pro
 450 455 460
 Thr Lys Lys Ser Gln Ile Phe Ser Thr Ala Val Asp Asn Gln Pro Thr
 465 470 475 480

Val Met Ile Lys Val Tyr Glu Gly Glu Arg Ala Met Ser Lys Asp Asn
485 490 495

Asn Leu Leu Gly Lys Phe Glu Leu Thr Gly Ile Pro Pro Ala Pro Arg
500 505 510

Gly Val Pro Gln Ile Glu Val Thr Phe Ala Leu Asp Ala Asn Gly Ile
515 520 525

Leu Lys Val Ser Ala Thr Asp Lys Gly Thr Gly Lys Ser Glu Ser Ile
530 535 540

Thr Ile Thr Asn Asp Lys Gly Arg Leu Thr Gln Glu Glu Ile Asp Arg
545 550 555 560

Met Val Glu Glu Ala Glu Lys Phe Ala Ser Glu Asp Ala Ser Ile Lys
565 570 575

Ala Lys Val Glu Ser Arg Asn Lys Leu Glu Asn Tyr Ala His Ser Leu
580 585 590

Lys Asn Gln Val Asn Gly Asp Leu Gly Glu Lys Leu Glu Glu Glu Asp
595 600 605

Lys Glu Thr Leu Leu Asp Ala Ala Asn Asp Val Leu Glu Trp Leu Asp
610 615 620

Asp Asn Phe Glu Thr Ala Ile Ala Glu Asp Phe Asp Glu Lys Phe Glu
625 630 635 640

Ser Leu Ser Lys Val Ala Tyr Pro Ile Thr Ser Lys Leu Tyr Gly Gly
645 650 655

Ala Asp Gly Ser Gly Ala Ala Asp Tyr Asp Asp Glu Asp Glu Asp Asp
660 665 670

Asp Gly Asp Tyr Phe Glu His Asp Glu Leu
675 680

<210> 145

<211> 1253

<212> DNA

<213> Candida albicans

<400> 145

tacctaagtc aataccgata acagttccgt agttttctac atcatcggca cctctaacta 60
aaacattgga ggagtgga aaattctgta aaggtaatat taccacgaaa agggcggtaca 120
ggaccacgga gagtggtacc agcagcttgc cagcgcttag tctgttgaaa aacatgggtat 180
gtttgatacg ctttttccct tgagactact cttggggact ttaaaaaagt aaaacagtaa 240
cacgttaatc tttagaatta catagccata tttatatctt ccagagaacc cttttcgtgt 300
cctttatata aaaaagcaac tttttcgaca cgctgtccag ttcctcgggt gccgcgccgg 360
gtgaaatttc cagaagggtc tattaaaata gaaagttgca gctaacaatag caaaattaga 420
tgaatgatga gtcctaattg gatctacact ttgctcgaga agcggctggt ggctgcggta 480
aaaactagag gactcacact atgcagcata ttaaacatat gaggacagct gtccggttgg 540
ctagatacgc tcttgaccac gatgagacac cggtagcttg catctttgta catacgccaa 600

ctggccaggt gatggcttat ggcataaacg atacgaacaa gtcattaact ggagtagcac 660
 atgctgagtt catggggatc gatcagatca aggcgatgtt gggctcccga ggagttgttg 720
 acgtgttcaa agacattact ctatatgtta ctgtagaacc gtgtataatg tgtgcatctg 780
 ctctcaagca attagacatt ggaaagggtg tgttcgggtg tggcaacgag agatttgagg 840
 gcaacggtag tgtcttgtca gtaaatcatg atacgtgtac attagtgcc aagaacaata 900
 gtgcggcagg gtacgagagt ataccgggga tcttgaggaa agaagcaata atgctgctga 960
 gatactttta tgtaagacaa aatgaaaggg cgccaaagcc acggtccaag agtgacagag 1020
 tgttggataa aaacacgttt ccgcctatgg aatgggtcaaa gtatcttaat gaagaagcat 1080
 tcattgagac ttttggtgat gattacagga cttgttttgc gaataaagtt gacttgtcca 1140
 gtaatagcgt cgattgggat ttgattgact cccaccaaga taatataatc caagaactgg 1200
 aagaacaatg caaaatgttt aagtttaatg tacataagaa atctaagggt tga 1253

<210> 146

<211> 250

<212> PRT

<213> *Candida albicans*

<400> 146

Met Gln His Ile Lys His Met Arg Thr Ala Val Arg Leu Ala Arg Tyr
 1 5 10 15

Ala Leu Asp His Asp Glu Thr Pro Val Ala Cys Ile Phe Val His Thr
 20 25 30

Pro Thr Gly Gln Val Met Ala Tyr Gly Met Asn Asp Thr Asn Lys Ser
 35 40 45

Leu Thr Gly Val Ala His Ala Glu Phe Met Gly Ile Asp Gln Ile Lys
 50 55 60

Ala Met Leu Gly Ser Arg Gly Val Val Asp Val Phe Lys Asp Ile Thr
 65 70 75 80

Leu Tyr Val Thr Val Glu Pro Cys Ile Met Cys Ala Ser Ala Leu Lys
 85 90 95

Gln Leu Asp Ile Gly Lys Val Val Phe Gly Cys Gly Asn Glu Arg Phe
 100 105 110

Gly Gly Asn Gly Thr Val Leu Ser Val Asn His Asp Thr Cys Thr Leu
 115 120 125

Val Pro Lys Asn Asn Ser Ala Ala Gly Tyr Glu Ser Ile Pro Gly Ile
 130 135 140

Leu Arg Lys Glu Ala Ile Met Leu Leu Arg Tyr Phe Tyr Val Arg Gln
 145 150 155 160

Asn Glu Arg Ala Pro Lys Pro Arg Ser Lys Ser Asp Arg Val Leu Asp
 165 170 175

Lys Asn Thr Phe Pro Pro Met Glu Trp Ser Lys Tyr Leu Asn Glu Glu
 180 185 190

Ala Phe Ile Glu Thr Phe Gly Asp Asp Tyr Arg Thr Cys Phe Ala Asn
 195 200 205

Lys Val Asp Leu Ser Ser Asn Ser Val Asp Trp Asp Leu Ile Asp Ser
 210 215 220

His Gln Asp Asn Ile Ile Gln Glu Leu Glu Glu Gln Cys Lys Met Phe
 225 230 235 240

Lys Phe Asn Val His Lys Lys Ser Lys Val
 245 250

<210> 147

<211> 3167

<212> DNA

<213> Candida albicans

<400> 147

```

tcccctgatg gtcaaatact gtgcatggca tcccgtgcag tcaaggatgc tttgagacta 60
gttcatctgc cttctttagt cgtgttcagc aactggccta ccagcgggac gcctttgggt 120
aaagttacca gtgtcgcat ttcgccatct ggtgggctac tggccgtggg taacgaacaa 180
ggtaaaagtga ggctctggaa attaaaccac tactaaattt ccattttatag acaaacttag 240
atattaaaag caatgtacaa atacatacac aaaatatcac tgtaaaaaaa ttgcgaagaa 300
acttgaaatt gaatatgatt ctgcccactt ttttcttgct gtcatttata gtcagaaatg 360
aaaaattgtc cgagaaatta aatataatat atggaaaaaa aggggacatt gagtttaaag 420
aatttgatta aaatgtcttc tcaatatect ctgtaagagt tatctaaatc tcactttact 480
tattcatctc gctgggaatt atgcaggcgg tagagagaag gccctcgtaa ctctttgacg 540
aatatcaaaa ttctgttact aagcctaata agacgaagaa taaagaagcc agggctctgt 600
cagagaatga cggtgatgtc tccccatctg ttttgaaaca gaaggaaata tcagtcgatg 660
atatggatat gatttctttg ccacaggaa ttgacaggca aatggtttta ggttcaccta 720
tgtttttoga tcttgaagac gaagaaaaca aaattgatcc acttccttca gtttcccatc 780
attatggaaa gacagctttg tctcatcgta caccgctca aatctgaaaa 840
cgggtgaaga aactaaagat cttttcatta atccgtttga attggtttct caaatgagaa 900
aaagatacat tgctgcttcc aaacaagatg gcatttcaaa cataaaaaat gacactgaaa 960
agtggttttt atacccaaaa ccactgccaa agttttggag atttgaagac gataaacgat 1020
tccaagatcc ctctgactct gacttaaatg acgatggaga cagtactggg accggagccg 1080
ctacaccgca ccgccatggc tactattacc caagttactt taccgatcac tactactact 1140
acacaaaatc tgggttgaaa ggaaaaggaa atataaaagt accatacacc ggtgaatat 1200
tcgatttaga ggattacaaa aaacaatata ttaccattt aagtaatcag gaaaatacgc 1260
aaaaccactt ttacacttat tctagtaagg aggagtcact agaggaagaa tttttaacag 1320
atgtgcctac gtttcaagaa tttagggatg attttgcata cataatagag ttaatccaat 1380
ctcataaatt caacgaggtt tcacgaaagc gattatctta tttattagat aaatttgaat 1440
tgtttcagta cctaaactct aagaaagaaa ttttagctaa taaaaatgtt ccctacagag 1500
atttttataa ttctcgtaag gtagatcgag acttgtcttt aagtggttgt atttctcaac 1560
gtcaattgag tgaatatata tgggagaaaa taaatttaga acctgaaagg atagtttatc 1620
aagaccggga aacgtcaagg aaactcagtt tgagagacat ttttcagttt gggtgttctt 1680
ctaattgacca acccattgctg attgggttga aattgattga tgatgaattc ttggattggg 1740
atagaaatat ttacctata gattaccatc taactcctaa caaagtagca aagttggctg 1800
gcaaagaaat gaggttttac ctattagcca aagtgtttct ggagtttgat aatttcattg 1860
aagggtgagta cctagcagaa attttcataa aatacgttat tcatatcctc gaaaaatcaa 1920
agtaccaatt ggcccaagta tcagttaatt ttcaattcta ttccagtggg gaagactggg 1980
acaagaaatt ttctcaatgg ttgctacgat ggaagctagt atcgtataat atccgctgga 2040
atatacaaat tgcaggatt tttcccaaac tattcaagga aaatgtcgtg tcaaatttcc 2100
aggagttttt ggatcttata ttcaatcctt tattcactct ggaaaaggag cagttaccaa 2160
tagattcatc tgtaaaatact gatatacttg gtctgcagtt ttttttatca aatgtgtgtt 2220
ctatggatct ggtcattaaa gagtcggatg aatattactg gaaagaattt actgatatga 2280
attgtaagcc aaaatttttg acagcacagg gtgacaatcc aactgttgcg cattacatgt 2340

```


Ala	Ala	Thr	Pro	His	Arg	His	Gly	Tyr	Tyr	Tyr	Pro	Ser	Tyr	Phe	Thr
	195						200					205			
Asp	His	Tyr	Tyr	Tyr	Tyr	Thr	Lys	Ser	Gly	Leu	Lys	Gly	Lys	Gly	Asn
	210					215					220				
Ile	Lys	Val	Pro	Tyr	Thr	Gly	Glu	Tyr	Phe	Asp	Leu	Glu	Asp	Tyr	Lys
225					230					235					240
Lys	Gln	Tyr	Ile	Tyr	His	Leu	Ser	Asn	Gln	Glu	Asn	Thr	Gln	Asn	Pro
			245						250					255	
Leu	Ser	Pro	Tyr	Ser	Ser	Lys	Glu	Glu	Ser	Leu	Glu	Glu	Glu	Phe	Leu
		260					265						270		
Thr	Asp	Val	Pro	Thr	Phe	Gln	Glu	Phe	Arg	Asp	Asp	Phe	Ala	Tyr	Ile
	275					280						285			
Ile	Glu	Leu	Ile	Gln	Ser	His	Lys	Phe	Asn	Glu	Val	Ser	Arg	Lys	Arg
	290					295					300				
Leu	Ser	Tyr	Leu	Leu	Asp	Lys	Phe	Glu	Leu	Phe	Gln	Tyr	Leu	Asn	Ser
305					310					315					320
Lys	Lys	Glu	Ile	Leu	Ala	Asn	Lys	Asn	Val	Pro	Tyr	Arg	Asp	Phe	Tyr
			325						330					335	
Asn	Ser	Arg	Lys	Val	Asp	Arg	Asp	Leu	Ser	Leu	Ser	Gly	Cys	Ile	Ser
		340						345					350		
Gln	Arg	Gln	Leu	Ser	Glu	Tyr	Ile	Trp	Glu	Lys	Ile	Asn	Leu	Glu	Pro
	355						360					365			
Glu	Arg	Ile	Val	Tyr	Gln	Asp	Pro	Glu	Thr	Ser	Arg	Lys	Leu	Ser	Leu
	370					375					380				
Arg	Asp	Ile	Phe	Gln	Phe	Gly	Cys	Ser	Ser	Asn	Asp	Gln	Pro	Ile	Ala
385				390						395					400
Ile	Gly	Leu	Lys	Leu	Ile	Asp	Asp	Glu	Phe	Leu	Asp	Trp	Tyr	Arg	Asn
		405						410					415		
Ile	Tyr	Leu	Ile	Asp	Tyr	His	Leu	Thr	Pro	Asn	Lys	Val	Ala	Lys	Leu
		420						425					430		
Val	Gly	Lys	Glu	Met	Arg	Phe	Tyr	Leu	Leu	Ala	Lys	Val	Phe	Leu	Glu
	435						440					445			
Phe	Asp	Asn	Phe	Ile	Glu	Gly	Glu	Tyr	Leu	Ala	Glu	Ile	Phe	Ile	Lys
	450					455					460				
Tyr	Val	Ile	His	Ile	Leu	Glu	Lys	Ser	Lys	Tyr	Gln	Leu	Ala	Gln	Val
465					470					475					480
Ser	Val	Asn	Phe	Gln	Phe	Tyr	Ser	Ser	Gly	Glu	Asp	Trp	Tyr	Lys	Lys
			485						490					495	

Phe	Ser	Gln	Trp	Leu	Leu	Arg	Trp	Lys	Leu	Val	Ser	Tyr	Asn	Ile	Arg
			500					505					510		
Trp	Asn	Ile	Gln	Ile	Ala	Arg	Ile	Phe	Pro	Lys	Leu	Phe	Lys	Glu	Asn
		515					520					525			
Val	Val	Ser	Asn	Phe	Gln	Glu	Phe	Leu	Asp	Leu	Ile	Phe	Asn	Pro	Leu
	530					535					540				
Phe	Thr	Leu	Glu	Lys	Glu	Gln	Leu	Pro	Ile	Asp	Ser	Ser	Val	Asn	Thr
545					550					555					560
Asp	Ile	Ile	Gly	Leu	Gln	Phe	Phe	Leu	Ser	Asn	Val	Cys	Ser	Met	Asp
			565						570					575	
Leu	Val	Ile	Lys	Glu	Ser	Asp	Glu	Tyr	Tyr	Trp	Lys	Glu	Phe	Thr	Asp
			580					585					590		
Met	Asn	Cys	Lys	Pro	Lys	Phe	Trp	Thr	Ala	Gln	Gly	Asp	Asn	Pro	Thr
		595					600					605			
Val	Ala	His	Tyr	Met	Tyr	Tyr	Ile	Tyr	Lys	Ser	Leu	Ala	Lys	Val	Asn
	610						615				620				
Phe	Leu	Arg	Ser	Gln	Asn	Leu	Gln	Asn	Thr	Ile	Thr	Leu	Arg	Asn	Tyr
625					630					635					640
Cys	Ser	Pro	Leu	Ser	Ser	Arg	Thr	Ser	Gln	Phe	Gly	Val	Asp	Leu	Tyr
			645						650					655	
Phe	Thr	Asp	Gln	Val	Glu	Ser	Leu	Val	Cys	Asn	Leu	Leu	Leu	Cys	Asn
			660					665						670	
Gly	Gly	Leu	Leu	Gln	Val	Glu	Pro	Leu	Trp	Asp	Thr	Ala	Thr	Met	Ile
		675					680					685			
Gln	Tyr	Leu	Phe	Tyr	Leu	Phe	Gln	Ile	Pro	Ile	Leu	Ala	Ala	Pro	Leu
	690					695					700				
Ser	Ser	Val	Ser	Leu	Leu	Asn	Ser	Gln	Lys	Ser	Thr	Phe	Leu	Lys	Asn
705					710					715					720
Lys	Asn	Val	Leu	Leu	Glu	His	Asp	Tyr	Leu	Lys	Asp	Gln	Glu	Thr	Ala
			725						730					735	
Lys	Ile	Asn	Pro	Ser	Arg	Asp	Ile	Thr	Val	Gly	Glu	Gln	Arg	Ser	Tyr
			740					745					750		
Glu	Thr	Asn	Pro	Phe	Met	Lys	Met	Phe	Lys	Met	Gly	Leu	Lys	Ile	Ser
		755					760					765			
Leu	Ser	Ser	Lys	Ser	Ile	Leu	Tyr	Asn	Ser	Ser	Tyr	Thr	Leu	Glu	Pro
	770					775					780				
Leu	Ile	Glu	Glu	Tyr	Ser	Val	Ala	Ala	Ser	Ile	Tyr	Leu	Leu	Asn	Pro
785					790					795					800

Thr Asp Leu Cys Glu Leu Ser Arg Thr Ser Val Leu Ser Ser Gly Tyr
 805 810 815
 Glu Gly Trp Tyr Lys Ala His Trp Ile Gly Val Gly Val Lys Lys Ala
 820 825 830
 Pro Tyr Phe Glu Glu Asn Val Gly Gly Ile Asp Asn Trp Tyr Asp Thr
 835 840 845
 Ala Lys Asp Thr Ser Ile Lys His Asn Val Pro Met Ile Arg Arg Arg
 850 855 860
 Tyr Arg Lys Glu Thr Leu Asp Gln Glu Trp Asn Phe Val Arg Asp His
 865 870 875 880
 Phe Gly Val Ile Asn Ser Ile Trp
 885

<210> 149

<211> 3146

<212> DNA

<213> Candida albicans

<400> 149

```

tttttcttcg cacatggctg gttctgctgg aggcggctgg gtgtttatag ttaccgcaat 60
gcaggctcgt tcgtttactt ttctctgcgt gctcgagaac tgataaatac tggtttagga 120
aaaccgtcca cttatggatt taacaaggag gtgaaaggta ggtaccatgg caatatagct 180
agcaacgcta cgcactagct gtgtgtgctt gctctcttgt gttcgtcttt cgtatatattgc 240
gggttccgcg gggttaattca acaacaaata tggatatctag gcagggaccc agcaacggaa 300
ggatgtaatt gctatatagg gccgatgaaa cagttctcat gtttcaactc ggtcgaagaa 360
ttctctaaaa catattctat acttcaaagt ttttagcttc ttgcttttcg gtagttgcca 420
aaccaatatc ggcataaaat tataattgct gcacccctgc aactccaaac aacttaaaac 480
aacttaaaac gaaaacgctt atgctggagt ttccaatatc agttctgcta ggatgcctag 540
tagccgtcaa ggcacaaaacc acgtttccaa acttcgagag cgatgtgctg aacgagcata 600
acaagttcag agcgctacat gttgacacag cgccgctcac ctgggtccgac actctggcca 660
cctatgcgca gaactacgcc gaccaatatg attgttcggg tgtcttaacg cattccgatg 720
gcccataatg tgagaacctt gcccttggtt acacagacac gggagcggtg gacgcctggg 780
acggggagat aagcaagtat aattattcaa atcccggatt ttctgaatcc acgggtcact 840
tcacacaggt ggttttgaag tcaaccgcg agattggatg tggttataaa tattgtggta 900
cgacatggaa caattatatt gtgtgctcct acaaccctcc tggaaactac ctgggtgagt 960
ttgcagagga agtggaacca cttataagca ctgtttcctc gtcctcatcc tcgtcctctt 1020
ctacctcaac tacatcagac acagtctcca ccactcctac cagtattatg cccgctgtag 1080
cgcaagggta tacaacaacg gtatcgtctg cggctagcag cagttcttta aaatcgacga 1140
ccataaaccg tgccaagacc gctaccctca ctgcgtcctc ttctaccgta attactagta 1200
gcacagaatc agttggatcc tccactgtct catcagcctc aagctcttct gtcactactt 1260
cctatgctac ctctcgagt accgtcgtct ctagtgatgc tacttcatcc actaccacca 1320
cctcatcggt tgctacatcg tccagtagca cttcttccga ccctacctcg agcactgctg 1380
ctgcttcttc ttctgatcct gccatgaagt ccgctgccgc ttcctccagc gcgagtaccg 1440
agaacgccgc ttctcttagc agcgccatct cgagctcttc atcaatggtt tctgctcctt 1500
tgagttagta tcttactact tccaccgcaa gctccagaag tgtaacttcc aattcagtta 1560
attctgttaa gtttgcaaac acaactgtgt tttctgctca aacaacctct tctgtaagcg 1620
cctcattatc atcatctgta gctgctgacg atattcaggg tagcacttcc aaggaggcca 1680
caagctcagt ttccgaacat actagtatag taactagtgc aactaatgct gcccaatatg 1740
caacgagact tgggtcatct tccagaagtt cttccggggc cgtctcttcc tcagctgtgt 1800

```


Ser Val Thr Ser Val Ser Ser Thr Ala His Thr Thr Lys Asp Thr Ala
 450 455 460
 Thr Thr Ser Val Thr Ala Ser Glu Ser Ile Thr Ser Glu Thr Ala Gln
 465 470 475 480
 Ala Ser Ser Ser Thr Glu Lys Asn Ile Ser Asn Ser Ala Ala Thr Ser
 485 490 495
 Ser Ser Ile Tyr Ser Asn Ser Ala Ser Val Ser Gly His Gly Val Thr
 500 505 510
 Tyr Ala Ala Glu Tyr Ala Ile Thr Ser Glu Gln Ser Ser Ala Leu Ala
 515 520 525
 Thr Ser Val Pro Ala Thr Asn Cys Ser Ser Ile Val Lys Thr Thr Thr
 530 535 540
 Leu Glu Asn Ser Ser Thr Thr Thr Ile Thr Ala Ile Thr Lys Ser Thr
 545 550 555 560
 Thr Thr Leu Ala Thr Thr Ala Asn Asn Ser Thr Arg Ala Ala Thr Ala
 565 570 575
 Val Thr Ile Asp Pro Thr Leu Asp Pro Thr Asp Asn Ser Ala Ser Pro
 580 585 590
 Thr Asp Asn Ala Lys His Thr Ser Thr Tyr Gly Ser Ser Ser Thr Gly
 595 600 605
 Ala Ser Leu Asp Ser Leu Arg Thr Thr Thr Ser Ile Ser Val Ser Ser
 610 615 620
 Asn Thr Thr Gln Leu Val Ser Thr Cys Thr Ser Glu Ser Asp Tyr Ser
 625 630 635 640
 Asp Ser Pro Ser Phe Ala Ile Ser Thr Ala Thr Thr Thr Glu Ser Asn
 645 650 655
 Leu Ile Thr Asn Thr Ile Thr Ala Ser Cys Ser Thr Asp Ser Asn Phe
 660 665 670
 Pro Thr Ser Ala Ala Ser Ser Thr Asp Glu Thr Ala Phe Thr Arg Thr
 675 680 685
 Ile Ser Thr Ser Cys Ser Thr Leu Asn Gly Ala Ser Thr Gln Thr Ser
 690 695 700
 Glu Leu Thr Thr Ser Pro Met Lys Thr Asn Thr Val Val Pro Ala Ser
 705 710 715 720
 Ser Phe Pro Ser Thr Thr Thr Thr Cys Leu Glu Asn Asp Asp Thr Ala
 725 730 735
 Phe Ser Ser Ile Tyr Thr Glu Val Asn Ala Ala Thr Ile Ile Asn Pro
 740 745 750

Gly Glu Thr Ser Ser Leu Ala Ser Asp Phe Ala Thr Ser Glu Lys Pro
 755 760 765
 Asn Glu Pro Thr Ser Val Lys Ser Thr Ser Asn Glu Gly Thr Ser Ser
 770 775 780
 Thr Thr Thr Thr Tyr Gln Gln Thr Val Ala Thr Leu Tyr Ala Lys Pro
 785 790 795 800
 Ser Ser Thr Ser Leu Gly Ala Arg Thr Thr Thr Gly Ser Asn Gly Arg
 805 810 815
 Ser Thr Thr Ser Gln Gln Asp Gly Ser Ala Met His Gln Pro Thr Ser
 820 825 830
 Ser Ile Tyr Thr Gln Leu Lys Glu Gly Thr Ser Thr Thr Ala Lys Leu
 835 840 845
 Ser Ala Tyr Glu Gly Ala Ala Thr Pro Leu Ser Ile Phe Gln Cys Asn
 850 855 860
 Ser Leu Ala Gly Thr Ile Ala Ala Phe Val Val Ala Val Leu Phe Ala
 865 870 875 880
 Phe

<210> 151
 <211> 830
 <212> DNA
 <213> Candida albicans

<400> 151
 ttgcattatc aactataatt ccatttccta gaggagtttt tatagtctctg ccattctaatt 60
 gtagagcaat ctttcctttc tcaacatccc tatttagtga caccttttcc caaaacttct 120
 gtgaagtgtt gctcaatcta tttgtttccg taggagtgtt attctcaatc gtgttgtctg 180
 tccccagtgg ctgggcattt aatgagtaga atcggggcag tttcaatctt atggaattca 240
 caatgaagca tcccttcctt aatgatggca gcattccgta ttctcttttg tagggtttcg 300
 tttgccttca agtggtttgt tcttatttag ctttttcctt taccttaatt tttttctttt 360
 ctctgaagaa aatgaatgag tttaaagata tagcaattaa aaagtaacag tgaagaaatt 420
 tctcagatga gcagatggga attaaagaac tatctacaga gctctttact aaattgaatc 480
 aataatacat acttacaac atgtcacaga tagcacaaga aatgacagt agcttaagaa 540
 acgccaggac acaattggat atggtcaatc agcagctagc atatttggac agacaagaaa 600
 agcttgctga attgacaaag aaagaactag agtcttatcc aacggacaaa gtatggagat 660
 cttgcggtaa atcgtttatc ttacaggata aatccaaata cgtaaatgat ttatcacatg 720
 ccgaaactgt tcttctggat caaagaaaaa cattaaagat aaagaagaac tatttagaaa 780
 ctactgttga aaaaacaata gacaatctaa aggcatgtat gaagaattaa 830

<210> 152
 <211> 109
 <212> PRT
 <213> Candida albicans

158

<400> 152

Met Ser Gln Ile Ala Gln Glu Met Thr Val Ser Leu Arg Asn Ala Arg
 1 5 10 15

Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln
 20 25 30

Glu Lys Leu Ala Glu Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr
 35 40 45

Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys
 50 55 60

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Glu Thr Val Leu Leu Asp
 65 70 75 80

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val
 85 90 95

Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn
 100 105

<210> 153

<211> 1478

<212> DNA

<213> Candida albicans

<400> 153

aatagttcct ctttatcttt aatgtttttc tttgatccag aagaacagtt tcggcatgtg 60
 ataaatcatt aacgtatttg gattttatcct gtaagataaa cgattttaccg caagatctcc 120
 atactttgtc cgttgataaa gactctagtt ctttctttgt caattcagca agcttttctt 180
 gtctgtccaa atatgctagc tgctgattga ccatatccaa ttgtgtcctg gcgtttctta 240
 agctcactgt catttcttgt gctatctgtg acatgtttgt aagtatgtat tattgattca 300
 atttagtaaa gagctctgta gatagttctt taattcccat ctgctcatct gagaaaatttc 360
 ttcactgtta ctttttaatt gctatatctt taaactcatt cattttcttc agagaaaaga 420
 aaaaaattaa ggtaaaggaa aaggctaaat aagaacaaaa cacttgaagg caaacgaaac 480
 cctacaaaag agaatacggg atgctgccat cattaaggaa gggatgcttc attgtgaatt 540
 ccataagatt gaaactgcc cgattctact cattaatgc ccagccactg gggacagaca 600
 acacgattga gaataacact cctacggaaa caaatagatt gagcaaaact tcacagaagt 660
 tttgggaaaa ggtgtcacta aatagggatg ttgagaaagg aaagattgct ctacaattag 720
 atggcaggac tataaaaact cctctaggaa atggaattat agttgataat gcaaagtctc 780
 tcttagcata cctattaaaa ctggagtggg cgctccctatc cagtctttcc atcaaaactc 840
 actctttgcc actaacttca ttagtggaag gatgcataga tttacaaatg acaaatgagc 900
 ctggctgtga cctcaatta gttgcaaaga ttggaggcaa cagtgatgtt ataaaaaatc 960
 agttgttaag atatttagat accgatactt tattggctctt ttccccctatg aatgagtttg 1020
 aaggaagatt acgcaatgcg caaatagagt tatatatacc catcatcaaa ggaatggaag 1080
 agtttttacg caacttttca tccgagtcta atattcgact acaaatttta gatgccgaca 1140
 tccatgggtt acgaggcaat cagcagtcgg atatcggttaa gaatgcagca aaaaaatata 1200
 tgagcagctt atcaccatgg gatcttgcaa ttcttgaaaa aactgtatta accacaaagt 1260
 ccttcatttg cggcgtgcta ttattagaaa ataaaaaaga tactgcgaac ttaattcccg 1320
 ccttgaaaaa tgatattggat aatattgtac gtgccgccac ctagaaaca atcttccaag 1380
 ttgaaaagtg gggagaggtt gaagatactc atgacgttga caaaagagac atcagaagaa 1440
 aaattcatac tgctgcgatt gctgctttta agcaataa 1478

<210> 154

<211> 325

<212> PRT

<213> Candida albicans

<400> 154

Met	Leu	Pro	Ser	Leu	Arg	Lys	Gly	Cys	Phe	Ile	Val	Asn	Ser	Ile	Arg
1				5					10					15	

Leu	Lys	Leu	Pro	Arg	Phe	Tyr	Ser	Leu	Asn	Ala	Gln	Pro	Leu	Gly	Thr
			20					25					30		

Asp	Asn	Thr	Ile	Glu	Asn	Asn	Thr	Pro	Thr	Glu	Thr	Asn	Arg	Leu	Ser
		35					40					45			

Lys	Thr	Ser	Gln	Lys	Phe	Trp	Glu	Lys	Val	Ser	Leu	Asn	Arg	Asp	Val
	50					55					60				

Glu	Lys	Gly	Lys	Ile	Ala	Leu	Gln	Leu	Asp	Gly	Arg	Thr	Ile	Lys	Thr
65					70					75					80

Pro	Leu	Gly	Asn	Gly	Ile	Ile	Val	Asp	Asn	Ala	Lys	Ser	Leu	Leu	Ala
				85					90					95	

Tyr	Leu	Leu	Lys	Leu	Glu	Trp	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile	Lys
			100					105						110	

Thr	His	Ser	Leu	Pro	Leu	Thr	Ser	Leu	Val	Ala	Arg	Cys	Ile	Asp	Leu
		115					120					125			

Gln	Met	Thr	Asn	Glu	Pro	Gly	Cys	Asp	Pro	Gln	Leu	Val	Ala	Lys	Ile
	130					135					140				

Gly	Gly	Asn	Ser	Asp	Val	Ile	Lys	Asn	Gln	Leu	Leu	Arg	Tyr	Leu	Asp
145					150					155					160

Thr	Asp	Thr	Leu	Leu	Val	Phe	Ser	Pro	Met	Asn	Glu	Phe	Glu	Gly	Arg
			165						170					175	

Leu	Arg	Asn	Ala	Gln	Asn	Glu	Leu	Tyr	Ile	Pro	Ile	Ile	Lys	Gly	Met
			180					185					190		

Glu	Glu	Phe	Leu	Arg	Asn	Phe	Ser	Ser	Glu	Ser	Asn	Ile	Arg	Leu	Gln
		195					200					205			

Ile	Leu	Asp	Ala	Asp	Ile	His	Gly	Leu	Arg	Gly	Asn	Gln	Gln	Ser	Asp
	210					215					220				

Ile	Val	Lys	Asn	Ala	Ala	Lys	Lys	Tyr	Met	Ser	Ser	Leu	Ser	Pro	Trp
225					230					235					240

Asp	Leu	Ala	Ile	Leu	Glu	Lys	Thr	Val	Leu	Thr	Thr	Lys	Ser	Phe	Ile
			245						250					255	

Cys	Gly	Val	Leu	Leu	Leu	Glu	Asn	Lys	Lys	Asp	Thr	Ala	Asn	Leu	Ile
		260						265						270	

Pro Ala Leu Lys Thr Asp Met Asp Asn Ile Val Arg Ala Ala Thr Leu
 275 280 285

Glu Thr Ile Phe Gln Val Glu Lys Trp Gly Glu Val Glu Asp Thr His
 290 295 300

Asp Val Asp Lys Arg Asp Ile Arg Arg Lys Ile His Thr Ala Ala Ile
 305 310 315 320

Ala Ala Phe Lys Gln
 325

<210> 155

<211> 2336

<212> DNA

<213> Candida albicans

<400> 155

```

gcaagtcagt acgatgcac cttggatcaa gaaggtgagt ctggaaacgg tgcttcta 60
ggcgatgttt accattataa tgaaggggac ttggctgcct ccttcaaggg atgtagatca 120
agaggtacgt gtgctagtga aataggtcac atgtaccaga aaatcaagaa atcttagatg 180
tgtgtaatct tgcaatttag tttcaaacia gattccttgta tttatataaa caaagatata 240
atttttaaaa aaaaattaga aaaagcaaat ataattcagg tcccacttgg aataatggca 300
ctgtattgat gcattttcct tatgcttagt gacgcgtttt cgcgcgtcag tttcaagttt 360
ttcttggett tttttttttt attttcgtaa agggctctta aaggattaaa aaatgcagta 420
ttgaaataaa gaacaattac gaacggtgaa gctgctatct tggttattat acccttccag 480
gacagtacgc gcaaaactatt atggagatat tcaaggaaga agaagaagaa gctttttcgg 540
cgatagaagg tataatatat gcctgtgagg tgtatgacct tgtaccccgat catttacata 600
aaagcaaaac aaagatcatc aatgctgcta aattaattat agaaacgcac ctttcatatt 660
atacaatact caataacatt tcagatatac aagcctatct ttctacttgg cttagggatc 720
ttggaacgac aggtccatac caaacaattc tttcagaaag tatttctctc atgtttgacc 780
gcactgtatc tatcttcagg aaatgtacga tagagggagg ttttccacat ttgatcgac 840
gtctttatct cagattgaaa agctaccaga agctcttaaa cgatgcagga ttaaagaatt 900
ttttttcaag ctacgattat gctttcgggg ttgcatacaa ccttgtaaat tgctctgaat 960
acaggtatga cgaagttcat tacatatcga acggcactta ctcatagtt gcacgatga 1020
agatagatcc tgctgaagtc attaaaaggg aacatttttag gcttacaatt ccgaaattta 1080
acatatctaa tatatttaatt gaaatttttc atttgctcga tggattagca ttttttaagg 1140
tgaacctga tagtttatct atatctacag cttcagcaga aacaatcttt cgcagtatct 1200
ccgaaggtaa tcacaggtc ctagaattgg ggagaagttt aatgtttcca ttgttgagga 1260
ctggagattt tgaatctgt cgtattgacg acgcgggagc tgtcataaca tttacagaag 1320
cgaaggatgt aaaactagaa ataatcagtc tggatgaagt ttcttgggta atgcagtgga 1380
aatcttgtct tcaaaattat gagagaaggg cagcaaata cagttcattt atcaaaacac 1440
acctacaatt taagaaggcc aacaatttca atgaagataa taatgggcta ggactaattg 1500
tagacagaaa tattccaaca gatgatttta cgctagcttc tacaaccgt caaagtcccc 1560
cgctttcaaa tactggttgt tcattacaca ggtctaaacc cttgcatatc cctttatcat 1620
ctgttattcg tgaagacttt tatgatagct ctctaaatga gcgtatatct aaagacggag 1680
atagcagttg tgaatccttc agtggcgccg aaagtatctt atcagactac gattttcatg 1740
ataatgaatt ttttaacaac cagtcacctc attatttttc agaacacata gacaataact 1800
cgagagaggt ggtaataaca gatgaaaata cgataatatc tttggaaaat acccaagtaa 1860
gtcgggtggtc aaattactca tggcaaaaaa tttcaccgca tcaattacag gtctctatta 1920
tccaactgcg catgggaaac ttcatgtgtg cttatgatgc tgattataac cttcatcagt 1980
tcaaaattcg tttgtgtgac gatataaaat gtatacaatc cacagagcaa gacatacaaa 2040
tacgtgtccc gtcggcgca ataattgtgca gcgtcactgg tatcttgaat attaggacga 2100
aggacgctga caagtgtctt cgggtattaa gcttttatac cactgaccac acggaagctg 2160
tategcactc aaacaatcaa gatgctactg caagtcactc ttcgtcagtt tcatcagcaa 2220

```

tggatctcaa gcattcatta cagaaatgtt cctctacaat aatgccccaa gagttgacgc 2280
aggacgtcat cggttcaaaa tcagacctaa tcagtaatat tcgtcaaaaa atataa 2336

<210> 156
<211> 611
<212> PRT
<213> Candida albicans

<400> 156
Met Glu Ile Phe Lys Glu Glu Glu Glu Glu Ala Phe Ser Ala Ile Glu
1 5 10 15
Gly Ile Ile Tyr Ala Cys Glu Val Tyr Asp Pro Val Pro Arg His Leu
20 25 30
His Lys Ser Lys Thr Lys Ile Ile Asn Ala Ala Lys Leu Ile Ile Glu
35 40 45
Thr His Leu Ser Tyr Tyr Thr Ile Leu Asn Asn Ile Ser Asp Ile Gln
50 55 60
Ala Tyr Leu Ser Thr Trp Leu Arg Asp Leu Gly Thr Thr Gly Pro Tyr
65 70 75 80
Gln Thr Ile Leu Ser Glu Ser Ile Ser Leu Met Phe Asp Arg Thr Val
85 90 95
Ser Ile Phe Arg Lys Cys Thr Ile Glu Gly Gly Phe Pro His Leu Ile
100 105 110
Ala Arg Leu Tyr Leu Arg Leu Lys Ser Tyr Gln Lys Leu Leu Asn Asp
115 120 125
Ala Gly Leu Lys Asn Phe Phe Ser Ser Tyr Asp Tyr Ala Phe Gly Val
130 135 140
Ala Tyr Asn Leu Val Asn Cys Ser Glu Tyr Arg Tyr Asp Glu Val His
145 150 155 160
Tyr Ile Ser Asn Gly Thr Tyr Ser Leu Val Ala Ser Met Lys Ile Asp
165 170 175
Pro Ala Glu Val Ile Lys Arg Glu His Phe Arg Leu Thr Ile Pro Lys
180 185 190
Phe Asn Ile Ser Asn Ile Leu Ile Glu Ile Phe His Leu Leu Asp Gly
195 200 205
Leu Ala Phe Phe Lys Val Asn Pro Asp Ser Leu Ser Ile Ser Thr Ala
210 215 220
Ser Ala Glu Thr Ile Phe Arg Ser Ile Ser Glu Gly Asn His Gln Val
225 230 235 240
Leu Glu Leu Gly Arg Ser Leu Met Phe Pro Leu Leu Arg Thr Gly Asp
245 250 255

Phe	Glu	Ile	Cys	Arg	Ile	Asp	Asp	Ala	Gly	Ala	Val	Ile	Thr	Phe	Thr	260	265	270
Glu	Ala	Lys	Asp	Val	Lys	Leu	Glu	Ile	Ile	Ser	Leu	Asp	Glu	Val	Ser	275	280	285
Trp	Val	Met	Gln	Trp	Lys	Ser	Cys	Leu	Gln	Asn	Tyr	Glu	Arg	Arg	Ala	290	295	300
Ala	Asn	Asp	Ser	Ser	Phe	Ile	Lys	Thr	His	Leu	Gln	Phe	Lys	Lys	Ala	305	310	315
Asn	Asn	Phe	Asn	Glu	Asp	Asn	Asn	Gly	Leu	Gly	Leu	Ile	Val	Asp	Arg	325	330	335
Asn	Ile	Pro	Thr	Asp	Asp	Phe	Thr	Leu	Ala	Ser	Thr	Asn	Arg	Gln	Ser	340	345	350
Pro	Pro	Pro	Ser	Asn	Thr	Gly	Cys	Ser	Leu	His	Arg	Ser	Lys	Pro	Leu	355	360	365
His	Ile	Pro	Leu	Ser	Ser	Val	Ile	Arg	Glu	Asp	Phe	Tyr	Asp	Ser	Ser	370	375	380
Leu	Asn	Glu	Arg	Ile	Ser	Lys	Asp	Gly	Asp	Ser	Ser	Cys	Glu	Ser	Phe	385	390	395
Ser	Gly	Ala	Glu	Ser	Ile	Leu	Ser	Asp	Tyr	Asp	Phe	His	Asp	Asn	Glu	405	410	415
Phe	Phe	Asn	Asn	Gln	Ser	Pro	His	Tyr	Phe	Ser	Glu	His	Ile	Asp	Asn	420	425	430
Asn	Ser	Arg	Glu	Val	Val	Ile	Thr	Asp	Glu	Asn	Thr	Ile	Ile	Ser	Leu	435	440	445
Glu	Asn	Thr	Gln	Val	Ser	Arg	Trp	Ser	Asn	Tyr	Ser	Trp	Gln	Lys	Ile	450	455	460
Ser	Pro	His	Gln	Leu	Gln	Val	Ser	Ile	Ile	Gln	Leu	Arg	Met	Gly	Asn	465	470	475
Phe	Ile	Val	Ala	Tyr	Asp	Ser	Asp	Tyr	Asn	Leu	His	Gln	Phe	Lys	Ile	485	490	495
Arg	Leu	Cys	Asp	Asp	Ile	Lys	Cys	Ile	Gln	Ser	Thr	Glu	Gln	Asp	Ile	500	505	510
Gln	Ile	Arg	Val	Pro	Leu	Gly	Ala	Ile	Met	Cys	Ser	Val	Thr	Gly	Ile	515	520	525
Leu	Asn	Ile	Arg	Thr	Lys	Asp	Ala	Asp	Lys	Leu	Leu	Arg	Val	Leu	Ser	530	535	540
Phe	Tyr	Thr	Thr	Asp	His	Thr	Glu	Ala	Val	Ser	His	Ser	Asn	Asn	Gln	545	550	555

Asp Ala Thr Ala Ser Pro Leu Ser Ser Val Ser Ser Ala Met Asp Leu
565 570 575

Lys His Ser Leu Gln Lys Cys Ser Ser Thr Ile Met Pro Gln Glu Leu
580 585 590

Thr Gln Asp Val Ile Gly Ser Lys Ser Asp Leu Ile Ser Asn Ile Arg
595 600 605

Gln Lys Ile
610

<210> 157

<211> 2960

<212> DNA

<213> *Candida albicans*

<400> 157

tcttgcaacc	atcgctcctct	aaggaaagaa	atgtggcacc	tttaaataagg	ttccacctca	60
cagatgccaa	catgtgggag	atagggggct	attcgcaatt	tattaacgtc	tctagtactg	120
gtaagccttt	ctaacattct	tgtgggcacg	tgatgtgtat	gtttcttttt	tttattcctc	180
cgggtgataa	cgacgcgaaa	aataattttt	catttttctt	ttaaccatca	caatttgcga	240
cgcgacgcga	aaaaaatgca	gagaagtaaa	agaatgctgg	ataagaaatc	aacaacacag	300
ttgaacattg	gcgtgcccct	gtgtattaag	taaaggttgt	ccaagaggct	cttttttgta	360
tgtatgcgtg	tgtaaactat	cctgcacatc	atcttgcgca	gttagtccaa	taaaaaagga	420
ttactactga	acaggtctta	ctatttttga	ttgcgtagt	ctggggaaaa	gtaaacacac	480
acaggcgcac	acgagaacag	atgagttctt	tggacgagga	tgaagaggac	ttcgaaatgc	540
tggacacgga	gaacctccag	tttatgggga	agaagatggt	tggcaaacag	gccggcgaag	600
acgagagtga	tgatttttgc	atagggggta	gcaccccgac	caataaactg	aaattttatc	660
catattcgaa	caacaaattg	acaagaagta	cggggacctt	gaacctgtca	ttaagtaata	720
cagctttgtc	agaggctaac	tccaaatttc	ttgggaaaat	tgaagaagag	gaagaagagg	780
aggaagaagg	caaggatgag	gaaagcgtgg	attctcgtat	taaaagggtg	tctccgttcc	840
atgaaaatga	aagtgttact	actcctatta	caaaaagatc	tgcggaaaaa	acgaacagtc	900
ctattttctc	caaacaatgg	aaccagcgat	ggtttccgaa	aaatgatgct	cgcactgaaa	960
atacatcctc	atcctcttca	tatagcgctg	ctaaacctaa	ccaatcagcc	tttacgtctt	1020
cgggcctcgt	atctaaaatg	tctatggaca	cttcgttata	ccctgcgaaa	ttgaggatac	1080
cagaaacacc	agtgaaaaaa	tcacccttag	tggaggggaag	agaccataag	catgtccacc	1140
tttcgagttc	gaaaaaatgca	tcgctcttct	taagtgtttc	ccctttaaat	tttgttgaag	1200
acaataatth	acaagaagac	cttttattht	cagattctcc	gtcttcgaaa	gctttacctt	1260
ccatccatgt	accaaccata	gactcatccc	cactgagcga	ggcaaaatat	catgcacatg	1320
atcgtcacaa	taaccagaca	aacatcctgt	ctcccactaa	tagcttggtt	accaacagct	1380
ctccacaaac	attgcattct	aacaagttca	aaaaaatcaa	aagagcaagg	aattcggtta	1440
ttttgaaaaa	tagagagcta	acaaacagtt	tacaacaatt	caaagatgat	ttatacggca	1500
cggacgagaa	tttcccacct	ccaatcataa	tatcaagtca	tcattcaact	agaaagaacc	1560
ctcaacctta	tcaatttcgt	ggacgctatg	acaatgacac	tgacgaagag	atctccactc	1620
caacaagacg	aaaatctatt	attggggcaa	catctcaaac	acatagagaa	agcagaccat	1680
tgtcactctc	ctctgccatc	gtgacaaaac	caacaagtgc	agagacgcat	tccatatctt	1740
ccaccgatth	ttcgccgtta	aattccaaaa	ggcgtctaatt	ctcttcaaat	aagttatcag	1800
caaatccaga	ttcccatctt	ttcgaaaaat	ttacgaatgt	gcattccatt	ggtaaaggcc	1860
agttttccac	ggtctaccag	gttacgtht	cccaaacaaa	caaaaagtat	gcaatcaaag	1920
ccattaaacc	aaacaaaatt	aattccttga	aacgcataatt	actggaaatt	aaaatactaa	1980
acgaggtaac	aaaccaaatt	acaatggatc	aagaagggaa	ggaatacatc	atcgattaca	2040
tcagttcctg	gaagtttcaa	aattcatact	atattatgac	agaattgtgc	gaaaatggta	2100
atttgatggt	atttttacaa	gagcaagtta	tcgcaaagaa	aaaaaggtht	gaagattgga	2160

<400> 158																
Met	Ser	Ser	Leu	Asp	Glu	Asp	Glu	Glu	Asp	Phe	Glu	Met	Leu	Asp	Thr	
1				5					10					15		
Glu	Asn	Leu	Gln	Phe	Met	Gly	Lys	Lys	Met	Phe	Gly	Lys	Gln	Ala	Gly	
			20					25					30			
Glu	Asp	Glu	Ser	Asp	Asp	Phe	Ala	Ile	Gly	Gly	Ser	Thr	Pro	Thr	Asn	
		35					40					45				
Lys	Leu	Lys	Phe	Tyr	Pro	Tyr	Ser	Asn	Asn	Lys	Leu	Thr	Arg	Ser	Thr	
	50					55					60					
Gly	Thr	Leu	Asn	Leu	Ser	Leu	Ser	Asn	Thr	Ala	Leu	Ser	Glu	Ala	Asn	
65					70					75					80	
Ser	Lys	Phe	Leu	Gly	Lys	Ile	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
				85					90					95		
Gly	Lys	Asp	Glu	Glu	Ser	Val	Asp	Ser	Arg	Ile	Lys	Arg	Trp	Ser	Pro	
			100					105					110			
Phe	His	Glu	Asn	Glu	Ser	Val	Thr	Thr	Pro	Ile	Thr	Lys	Arg	Ser	Ala	
		115					120					125				
Glu	Lys	Thr	Asn	Ser	Pro	Ile	Ser	Leu	Lys	Gln	Trp	Asn	Gln	Arg	Trp	
	130					135					140					
Phe	Pro	Lys	Asn	Asp	Ala	Arg	Thr	Glu	Asn	Thr	Ser	Ser	Ser	Ser	Ser	
145					150					155					160	
Tyr	Ser	Val	Ala	Lys	Pro	Asn	Gln	Ser	Ala	Phe	Thr	Ser	Ser	Gly	Leu	
				165					170					175		
Val	Ser	Lys	Met	Ser	Met	Asp	Thr	Ser	Leu	Tyr	Pro	Ala	Lys	Leu	Arg	
			180					185					190			

Ile Pro Glu Thr Pro Val Lys Lys Ser Pro Leu Val Glu Gly Arg Asp
 195 200 205
 His Lys His Val His Leu Ser Ser Ser Lys Asn Ala Ser Ser Ser Leu
 210 215 220
 Ser Val Ser Pro Leu Asn Phe Val Glu Asp Asn Asn Leu Gln Glu Asp
 225 230 235 240
 Leu Leu Phe Ser Asp Ser Pro Ser Ser Lys Ala Leu Pro Ser Ile His
 245 250 255
 Val Pro Thr Ile Asp Ser Ser Pro Leu Ser Glu Ala Lys Tyr His Ala
 260 265 270
 His Asp Arg His Asn Asn Gln Thr Asn Ile Leu Ser Pro Thr Asn Ser
 275 280 285
 Leu Val Thr Asn Ser Ser Pro Gln Thr Leu His Ser Asn Lys Phe Lys
 290 295 300
 Lys Ile Lys Arg Ala Arg Asn Ser Val Ile Leu Lys Asn Arg Glu Leu
 305 310 315 320
 Thr Asn Ser Leu Gln Gln Phe Lys Asp Asp Leu Tyr Gly Thr Asp Glu
 325 330 335
 Asn Phe Pro Pro Pro Ile Ile Ile Ser Ser His His Ser Thr Arg Lys
 340 345 350
 Asn Pro Gln Pro Tyr Gln Phe Arg Gly Arg Tyr Asp Asn Asp Thr Asp
 355 360 365
 Glu Glu Ile Ser Thr Pro Thr Arg Arg Lys Ser Ile Ile Gly Ala Thr
 370 375 380
 Ser Gln Thr His Arg Glu Ser Arg Pro Leu Ser Leu Ser Ser Ala Ile
 385 390 395 400
 Val Thr Asn Thr Thr Ser Ala Glu Thr His Ser Ile Ser Ser Thr Asp
 405 410 415
 Ser Ser Pro Leu Asn Ser Lys Arg Arg Leu Ile Ser Ser Asn Lys Leu
 420 425 430
 Ser Ala Asn Pro Asp Ser His Leu Phe Glu Lys Phe Thr Asn Val His
 435 440 445
 Ser Ile Gly Lys Gly Gln Phe Ser Thr Val Tyr Gln Val Thr Phe Ala
 450 455 460
 Gln Thr Asn Lys Lys Tyr Ala Ile Lys Ala Ile Lys Pro Asn Lys Tyr
 465 470 475 480
 Asn Ser Leu Lys Arg Ile Leu Leu Glu Ile Lys Ile Leu Asn Glu Val
 485 490 495

Phe Phe Ile

<400>	159					
aattcccgca	tgggtaccga	aattttcttat	tgatggtgaa	tcacttgaga	gaatagtagc	60
atggatgata	gagcccaatt	atgagagaag	gccacgga	aatcaaactc	tacaaactga	120
ggaatgcctg	tatgtagaaa	tgacacgcaa	tgagggtgct	attatccagg	aagacgactt	180
tggacctaa	ccaaaatttt	ttatatgata	aatggaacaa	aaaaccttgt	tttattttaca	240
tacttttttc	ccacacgtgc	ttatgggccc	cattgtataa	ataatccaat	aacgaaaaag	300
agtgttaatt	cagtcgggta	gtaataccat	gtaaaacctt	agatgagttt	atttttaagta	360
cagcgcgttc	aagcattttt	attttttatt	tacagatgta	gcagataaca	accgttaaata	420
tatatattat	atatatatat	atatatatca	aatacgacgt	attacatata	tattgagaat	480
aagggaagga	tggaagacaa	atgacaaaaa	gtttgaagca	taaatatggt	cttcgcttag	540
atgttcatct	tggttcttct	ccagtttctt	ctcttagcgt	tgtaacggat	agtgttggtg	600
gtttcacaat	tgatccattg	tggcaatggg	ctgttttgct	tcttagcctt	agccattttt	660
tgcttgattc	tgaagaactt	ttgagccta	ttaaaaggga	aacatatact	gcacatacga	720
agtgataaat	tgtaaaaaat	gttagataca	atgttcaaac	tcatcaatat	gatgcattca	780
cgtatccaag	gcaataccac	ctgcataata				809

```
<210> 160
<211> 102
<212> PRT
<213> Candida albicans
```

[illegible]

<400> 163
tctcgacagc ccaaaagccg aattgcgtta gttagcccac gcgcgagcgt aaacgcaagg 60
accattgagc ttggaacaga aggaatcgct tcgcgcgtccc cgccaaggcg tactgtttgc 120

170

```

ctaccaaaaca aatacaactt tggaatacac cagatattct gctaattcac cttaaaaggt 3540
ttgaaagtca aaggtctttt agcgataaaa ttgatgccac gggttaatttc cccattacag 3600
atttggatct gtcgaggtac gttgtctata aagatgatcc cagagggtta atctatgacc 3660
tgtatgcagt agataaccac tatgggtggtt tgggtggtgg gcactatacc gcgtacgtaa 3720
agaatthttgc cgacaataaa tgggtactatt ttgatgattc tcgagtaact gaaactgcgc 3780
cagaaaatag tatagctgga tcggcttatt tgctatthta cattcgccgt cataaagatg 3840
gcaatggatt aggcagctct aaactacagg aaataatcca aaagtcacgc cacggatatg 3900
atgagcgtat caaaaagata tacgatgaac agatgaagtt gtatgaattt aataagactg 3960
acgaggagga agatgtttct gatgatatga tagaatgtaa tgaagatgtg caggcccctg 4020
aatatagtaa tcgtagtttg gaggttgggc atattgaaac tcaggactgc aacgacgaag 4080
atgacaatga tgatggtgag aggacaaatt caggtaggag aaagttaaga ttggtgaaaa 4140
aagtctacaa gaataattca ggcttggggt catcgagtac gtctgaaata tctgagggat 4200
gcccagaaaa cgaagtcgct gatttgaatt taaaaaatgg tgtgacacta gaatcgccag 4260
aataa 4265

```

<210> 166

<211> 1254

<212> PRT

<213> Candida albicans

<400> 166

```

Met Gly Ser Ser Asp Val Ser Ser Arg Glu Cys Ser Leu Val Tyr Asn
  1              5              10              15

```

```

Glu Asp Pro Asp Phe Thr Asp Gly Thr Thr Pro Cys Asp Arg Leu Gly
      20              25              30

```

```

Val Asp Leu Met Asn Val Leu Asp Lys Asp Glu Ile Lys Gln Glu
      35              40              45

```

```

Ser Val Pro Val Ser Asp Arg Glu Ile Glu Asp Thr Glu Ser Asp Ala
      50              55              60

```

```

Ser Ala Val Ser Ser Phe Ala Ser Ala Asn Glu Leu Ile Ala Glu Pro
      65              70              75              80

```

```

His Ala Ala Ser Glu Thr Asn Leu Gly Thr Asn Gly Gln Asp Gly Arg
      85              90              95

```

```

Asn Val Leu Glu Gln Gln Arg Asp Val Val Ala Arg Leu Ile Glu Glu
      100             105             110

```

```

Asn Lys Glu Thr Gln Lys Glu Gly Asp Lys Val Cys Ile Val Pro Lys
      115             120             125

```

```

Val Trp Tyr Asp Lys Phe Phe Asp Pro Asp Val Thr Asp Pro Glu Asp
      130             135             140

```

```

Ile Gly Pro Ile Asn Thr Arg Met Ile Cys Arg Asp Phe Glu Asn Phe
      145             150             155             160

```

```

Val Leu Glu Asp Tyr Asn Arg Cys Pro Tyr Leu Ser Ile Ala Glu Pro
      165             170             175

```

```

Val Phe Asn Phe Leu Ser Glu Ile Tyr Gly Met Thr Ser Gly Ser Tyr
      180             185             190

```

Pro Val Val Thr Asn Leu Val Ile Asn Gln Thr Thr Gly Glu Leu Glu
 195 200 205
 Thr Glu Tyr Asn Lys Trp Phe Phe Arg Leu His Tyr Leu Thr Glu Lys
 210 215 220
 Gln Asp Gly Arg Lys Arg Arg His Gly Gln Asp Asp Ser Ile Met Tyr
 225 230 235 240
 Leu Ser Met Ser Ala Leu Asn Leu Val Arg Asp Leu Val Glu Lys Ser
 245 250 255
 Met Asn Leu Phe Phe Glu Lys Ala Asp His Leu Asp Val Asn Ala Val
 260 265 270
 Asp Phe Lys Ile Trp Phe Val Ser Glu Gly Ser Asp Ile Ala Thr Asp
 275 280 285
 Ser Asn Val Ser Thr Phe Leu Asn Ser Ser Tyr Glu Ile Thr Pro Leu
 290 295 300
 Gln Phe Leu Glu Leu Pro Ile Lys Lys Leu Leu Ile Pro Asp Met Phe
 305 310 315 320
 Glu Asn Arg Leu Asp Lys Ile Thr Ser Asn Pro Ser Asp Leu Val Ile
 325 330 335
 Glu Ile Lys Pro Ile Glu Gly Asn His His Trp Pro Ser Asn Tyr Phe
 340 345 350
 Ala Tyr Asn Lys Leu Glu Pro Ala Ser Gly Thr Thr Gly Leu Val Asn
 355 360 365
 Leu Gly Asn Thr Cys Tyr Met Asn Ser Ala Leu Gln Cys Leu Val His
 370 375 380
 Ile Pro Gln Leu Arg Asp Tyr Phe Leu Tyr Asp Gly Tyr Glu Asp Glu
 385 390 395 400
 Ile Asn Glu Glu Asn Pro Leu Gly Tyr His Gly Tyr Val Ala Arg Ala
 405 410 415
 Phe Ser Asp Leu Val Gln Lys Leu Phe Gln Asn Arg Met Ser Ile Met
 420 425 430
 Gln Arg Asn Ala Ala Phe Pro Pro Ser Met Phe Lys Ser Thr Ile Gly
 435 440 445
 His Phe Asn Ser Met Phe Ser Gly Tyr Met Gln Gln Asp Ser Gln Glu
 450 455 460
 Phe Leu Ala Phe Leu Leu Asp Ser Leu His Glu Asp Leu Asn Arg Ile
 465 470 475 480
 Ile Lys Lys Glu Tyr Thr Glu Lys Pro Ser Leu Ser Pro Gly Asp Asp
 485 490 495


```

gcacaaatga cgaagttccc ccactagact tggatgatga cgaagacgac gacgaatttt 1140
acgatgatca atctaattatt gaagataata ctgctttgct gcatcattcg cagtataaca 1200
ttaagtctca gaaaaaatcg ctgttgaaga agtcgatcgt aaacctatat atcgatcttt 1260
gccagttgaa gtcgttcacg gaattgaacc gcattggggtt tgcaaaaatt acaaagaaat 1320
cagacaaagt tcttcacttg aatacaagaa ccgaactgat cgaatcggag cagtttttca 1380
aagacacata tgcattccag gcagaaacga tcgaattgct aaattccaaa atttcccagc 1440
tagtcacatt ttatgcgcgc atcactgacc ggctcctataa tatctcgcat agcaagcaag 1500
agttgaaatc ctacctgcat gaccacattg tttgggaaag aagtaacact tggaaagaca 1560
tgttgggact gctatcgcaa gctgacgagt tgacaccaa ggaaacagaa tataatgcaa 1620
ataagctggg aggcaagtta gatttggaa actacagatg gccactaccc agaccgataa 1680
acttaaaatt cactagtata aacaacgttg cactaccgaa attatttttc accaagaaag 1740
catacaagat ttacttttatt attctagtca ctggactcct gtttaggaata aagaccttca 1800
acgacgctgc tcagcaccgc tgcattggccc ttgtcgagtg tgtcgccctt ttgtgggcta 1860
gtgaggccat cccattacac attacagcat tccttgtacc actacttgta gtccttttca 1920
aagtcctaaa aacctccgac ggggctataa tgagtgtgc aagcgcttca tcagaaattt 1980
tgggccgcat gtggtcttct acaattatga ttctgctggc aggttttact ttgggtgaag 2040
tacttgcaca atataacatc gccaaagttc ttgcctcgtg gttgttggcc ttcgctgggt 2100
gtaaaaccag aaacgttctt ttaatggcaa tgtgtgtcgt gttcttctca tcaatgtgga 2160
tttccaatgt cgcagcacct gttctaacat attcggtgtt atctccccta ttggatgcca 2220
tggtatgcaga tagccattt gcgcaagcat tgggtgttagg tgtagcgttg gctgcaaata 2280
tcggtggtat gtcttcacca atctcttcac ctcaaaacat catttccatg tcgtacttga 2340
aaccctatgg tattggctgg ggccaattct ttgctgttgc attgccatct ggtatcctgg 2400
ccatgctttt ggtttgatt ttattgttca ctactttcaa gatgaataag accaaattgg 2460
aaaaatttaa gcctattaag acgaaattca cagttaagca gtattatata attactgtca 2520
ctgtggccac tattttgttg tgggtgtgtg aaagccagat tgaaggtgct tttgggtcat 2580
caggtcaaat tgcaatcatt cccatcgttt tgttttttgg taccggatta ctatcaacac 2640
aagattttaa tgcctttccg tgggtcaatcg ttattttggc aatgggaggt attgctttgg 2700
ggaaggccgt ctcatcctcg ggtttgctat caaccattgc aaaagcatta caaaagaaaa 2760
ttgagaatga tgggtgtttt gccattctat gtattttcgg tatcctgatg ttggttgtgg 2820
gtactttcgt ctgcataca gtatccgcta ttatcatcat tcccttgggt caagaagttg 2880
gtgacaagct tggcaacccc aaagctgctc ctatccttgt tttcggttgt gcattattgt 2940
catcctgtgg tatgggacta gcttcttcgg ggttcccca tgtaactgcc atctctaaag 3000
tagatagaaa gggcgatcgc tatttaagtg tcatgacttt cttaacgaga ggtgttccag 3060
cttctatttt ggctttccta tgtgtcatta ctctaggtta tggatatcat gcatctgttg 3120
tcaagggtaa cgcaacctct gcgtaa 3146

```

<210> 168

<211> 881

<212> PRT

<213> Candida albicans

<400> 168

```

Met Arg Phe Ser His Phe Leu Lys Tyr Asn Ala Val Pro Glu Trp Gln
  1             5             10             15

```

```

Asn His Tyr Met Asp Tyr Ser Glu Leu Lys Asn Leu Ile Tyr Thr Leu
          20             25             30

```

```

Gln Thr Asp Glu Leu Gln Val Gly Asp Asn Glu Glu Gly Phe Gly Ala
      35             40             45

```

```

Gly Lys Ser Ser Asn Ile Thr Asp Arg Phe Lys Asn Lys Phe Ser Phe
      50             55             60

```

```

Lys Asn Ala Lys Glu Asp Thr Ser Ser Gly Met Asn Lys Asp Ala Gly
      65             70             75             80

```


Tyr	Arg	Trp	Pro	Leu	Pro	Arg	Pro	Ile	Asn	Leu	Lys	Phe	Thr	Ser	Ile	385	390	395	400
Asn	Asn	Val	Ala	Leu	Pro	Lys	Leu	Phe	Phe	Thr	Lys	Lys	Ala	Tyr	Lys	405	410	415	
Ile	Tyr	Phe	Ile	Ile	Leu	Val	Thr	Gly	Leu	Leu	Leu	Gly	Ile	Lys	Thr	420	425	430	
Phe	Asn	Asp	Ala	Ala	Gln	His	Arg	Cys	Met	Ala	Leu	Val	Glu	Cys	Val	435	440	445	
Ala	Phe	Leu	Trp	Ala	Ser	Glu	Ala	Ile	Pro	Leu	His	Ile	Thr	Ala	Phe	450	455	460	
Leu	Val	Pro	Leu	Leu	Val	Val	Leu	Phe	Lys	Val	Leu	Lys	Thr	Ser	Asp	465	470	475	480
Gly	Ala	Ile	Met	Ser	Ala	Ala	Ser	Ala	Ser	Ser	Glu	Ile	Leu	Ala	Ala	485	490	495	
Met	Trp	Ser	Ser	Thr	Ile	Met	Ile	Leu	Leu	Ala	Gly	Phe	Thr	Leu	Gly	500	505	510	
Glu	Val	Leu	Ala	Gln	Tyr	Asn	Ile	Ala	Lys	Val	Leu	Ala	Ser	Trp	Leu	515	520	525	
Leu	Ala	Phe	Ala	Gly	Cys	Lys	Pro	Arg	Asn	Val	Leu	Leu	Met	Ala	Met	530	535	540	
Cys	Val	Val	Phe	Phe	Leu	Ser	Met	Trp	Ile	Ser	Asn	Val	Ala	Ala	Pro	545	550	555	560
Val	Leu	Thr	Tyr	Ser	Leu	Leu	Ser	Pro	Leu	Leu	Asp	Ala	Met	Asp	Ala	565	570	575	
Asp	Ser	Pro	Phe	Ala	Gln	Ala	Leu	Val	Leu	Gly	Val	Ala	Leu	Ala	Ala	580	585	590	
Asn	Ile	Gly	Gly	Met	Ser	Ser	Pro	Ile	Ser	Ser	Pro	Gln	Asn	Ile	Ile	595	600	605	
Ser	Met	Ser	Tyr	Leu	Lys	Pro	Tyr	Gly	Ile	Gly	Trp	Gly	Gln	Phe	Phe	610	615	620	
Ala	Val	Ala	Leu	Pro	Ser	Gly	Ile	Leu	Ala	Met	Leu	Leu	Val	Trp	Ile	625	630	635	640
Leu	Leu	Phe	Thr	Thr	Phe	Lys	Met	Asn	Lys	Thr	Lys	Leu	Glu	Lys	Phe	645	650	655	
Lys	Pro	Ile	Lys	Thr	Lys	Phe	Thr	Val	Lys	Gln	Tyr	Tyr	Ile	Ile	Thr	660	665	670	
Val	Thr	Val	Ala	Thr	Ile	Leu	Leu	Trp	Cys	Val	Glu	Ser	Gln	Ile	Glu	675	680	685	


```

taaatgagga agatgggtcga aatgatcatc ataacaacaa taataacttg atgaagaagg 600
ccatgatgaa caatgagcaa attgatagaa ctcaggatat cgacaacgcc aaagaaatgt 660
tgaggaaaaat atcaagtgaag agcagctcgc gcagaagctc cctgttgaat aaagattcat 720
ctctcgtgaa cggcaatgca aacagtggcg gtggtacgag cattaacgga acaagaggaa 780
gttctaagag tagtaataca cactttcagt atgcctccac ggcgtatggg gtaagaatgt 840
tgagtaaaga tatatctaata accaaagtgg aactggatgt ggaaaatttg atgattgtta 900
cgaaactcaa cgatgtctca ctgtatttct taacaagaga gttggtagaa tgggttttgg 960
tacattttcc acgtgtgact gtttatgtgg attccgaatt gaaaaacagc aaaaaatttg 1020
ccgctggcga gttatgtgaa gatagtaaata gtagagaatc aaggatcaag tattggacaa 1080
aggatttcat cagggaacat gatgttttct tctgatttgg agtgactttg ggtggcgacg 1140
gtactgttct ttttgtaagt tccatttttc agagacatgt accaccgtt atgtcgtttt 1200
cattaggggtc tctaggattt ttaacaaatt ttaagtttga acatttcagg gaggatttac 1260
ctcggattat gaatcataaa atcaagacaa atttacgggt gaggttggag tgcacaattt 1320
atcgtagaca ccgccctgaa gtagacccaa acacggggaa gaaaatatgt gtggtggaaa 1380
aactaagcac acaccacatt ttgaacgaag tgaccatcga tctgtgtcca agtccttttc 1440
tatccatggt agaattgtat ggtgacggct cattaatgac cgttgcgacg gcggacggac 1500
tgattgctgc tactccgact ggggtccacgg cctattcttt gagtgcaggt gggtcattgg 1560
tatgcccac cgtcaatgca atcgctttta caccatttg tccacatgca ttgagtttca 1620
gacccatcat cttaccagaa agtataaatt taaaagtga agtctcgatg aagtcaaggg 1680
ctccagcatg ggcggtttt gatgggaaag atagaattga attgcaaaaa ggtgatttta 1740
taaccatatg cgccagccca tatgcttttc caaccgtgga agcctcgccc gatgagtta 1800
ttaacagtat cagtcgacaa ctaaactgga atgtgaggga acaacaaaag tcctttacgc 1860
atattttgtc ccaaaagaac caagaaaaat atgcacatga ggccaacaaa gtcagaaatc 1920
aagcagaacc tttagaggta ataagagata aatactctct ggaagcagac gctactaagg 1980
aaaacaacaa cggaagcgat gatgagagcg acgatgagag tgtaaaactgc gaagcttgca 2040
aattaaagcc ttcgagcgtc ccaaaacctt ctcaagcaag gttttcagta taa 2093

```

<210> 170

<211> 530

<212> PRT

<213> Candida albicans

<400> 170

```

Met Lys Glu Asn Asp Met Asn Asn Gly Val Asp Lys Trp Val Asn Glu
  1              5              10              15

Glu Asp Gly Arg Asn Asp His His Asn Asn Asn Asn Asn Leu Met Lys
      20              25              30

Lys Ala Met Met Asn Asn Glu Gln Ile Asp Arg Thr Gln Asp Ile Asp
      35              40              45

Asn Ala Lys Glu Met Leu Arg Lys Ile Ser Ser Glu Ser Ser Ser Arg
      50              55              60

Arg Ser Ser Leu Leu Asn Lys Asp Ser Ser Leu Val Asn Gly Asn Ala
      65              70              75              80

Asn Ser Gly Gly Gly Thr Ser Ile Asn Gly Thr Arg Gly Ser Ser Lys
      85              90              95

Ser Ser Asn Thr His Phe Gln Tyr Ala Ser Thr Ala Tyr Gly Val Arg
      100              105              110

Met Leu Ser Lys Asp Ile Ser Asn Thr Lys Val Glu Leu Asp Val Glu
      115              120              125

```


Asn Leu Met Ile Val Thr Lys Leu Asn Asp Val Ser Leu Tyr Phe Leu
 130 135 140
 Thr Arg Glu Leu Val Glu Trp Val Leu Val His Phe Pro Arg Val Thr
 145 150 155 160
 Val Tyr Val Asp Ser Glu Leu Lys Asn Ser Lys Lys Phe Ala Ala Gly
 165 170 175
 Glu Leu Cys Glu Asp Ser Lys Cys Arg Glu Ser Arg Ile Lys Tyr Trp
 180 185 190
 Thr Lys Asp Phe Ile Arg Glu His Asp Val Phe Phe Asp Leu Val Val
 195 200 205
 Thr Leu Gly Gly Asp Gly Thr Val Leu Phe Val Ser Ser Ile Phe Gln
 210 215 220
 Arg His Val Pro Pro Val Met Ser Phe Ser Leu Gly Ser Leu Gly Phe
 225 230 235 240
 Leu Thr Asn Phe Lys Phe Glu His Phe Arg Glu Asp Leu Pro Arg Ile
 245 250 255
 Met Asn His Lys Ile Lys Thr Asn Leu Arg Leu Arg Leu Glu Cys Thr
 260 265 270
 Ile Tyr Arg Arg His Arg Pro Glu Val Asp Pro Asn Thr Gly Lys Lys
 275 280 285
 Ile Cys Val Val Glu Lys Leu Ser Thr His His Ile Leu Asn Glu Val
 290 295 300
 Thr Ile Asp Arg Gly Pro Ser Pro Phe Leu Ser Met Leu Glu Leu Tyr
 305 310 315 320
 Gly Asp Gly Ser Leu Met Thr Val Ala Gln Ala Asp Gly Leu Ile Ala
 325 330 335
 Ala Thr Pro Thr Gly Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser
 340 345 350
 Leu Val Cys Pro Thr Val Asn Ala Ile Ala Leu Thr Pro Ile Cys Pro
 355 360 365
 His Ala Leu Ser Phe Arg Pro Ile Ile Leu Pro Glu Ser Ile Asn Leu
 370 375 380
 Lys Val Lys Val Ser Met Lys Ser Arg Ala Pro Ala Trp Ala Ala Phe
 385 390 395 400
 Asp Gly Lys Asp Arg Ile Glu Leu Gln Lys Gly Asp Phe Ile Thr Ile
 405 410 415
 Cys Ala Ser Pro Tyr Ala Phe Pro Thr Val Glu Ala Ser Pro Asp Glu
 420 425 430

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro
65 70 75 80

Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Asp Lys Ser Val Cys
85 90 95

Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr Asn Cys Arg Lys
100 105 110

Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys Lys Lys Leu Lys
115 120 125

<213> *Candida albicans*

agctctcaaa	caactaatatc	tataagttca	agtacaagca	caggaggtgt	aggttcagtc	60
aagccatgtc	tttacttcgt	tttaatgtta	gaaacaatcg	cttatttggt	ttcttaaaca	120
aatatattag	gttcaaggtc	ttcgcagggtg	taagaaaacc	cgtggctcc	atattcttaa	180
gtatgataaa	taaaaaaaaa	cttaataaat	tattaattgc	ttcaaacctt	tttctttttt	240
tagtttttaa	tatttcaaac	gttatcttca	ttgaacgcc	aaatagggaa	aaatcctggc	300
aaatttttta	ttgctgtcat	ccaaggctat	gctagaaaa	tcaagagctt	ggatgatatt	360
aaaagacact	ctcaatcgag	aaagtttatt	ctttgttatt	ctgctttacc	tgatcatatt	420
ccggcgtatt	gtttctaate	aagtgatttc	gatateccagt	tacgaacct	ttacaacatt	480
cctgaaaaata	tttcgctatca	atgatatttg	ctctcttttt	ctccctcatt	aaaaatatct	540
tctgtgtaag	ctttctaate	agccacagtt	ttgctgccaa	aactttaacg	tctagttcca	600
atgacgatac	acttgccagg	tccgcagctg	cagatgcaga	catggcattc	ttcatggagt	660
ttttaaacga	tttcgacacc	gcttttccac	agtataacct	atacatgatg	caaaaccatt	720
taaccctacc	tcaacctgtt	gctgactact	actatcacat	ggttgatttg	gcctcaacag	780
cagattttaca	atctgatatt	gctcagagtt	ttccggtcac	tcaattccaa	acattcatta	840
cggcctttcc	atgggtatacc	tcttttgctaa	acaaagcctc	cgccaccacc	atataccttc	900
cccaacactt	cataacaggt	gagacagaag	ctaccatgac	taactcatct	tatggccagc	960
aaaaaaactc	cgttttccaa	tctgttcctt	tctcgacag	gaacgcaggc	cagtcctatga	1020
tttccatggc	taatgaagaa	aacagtaaca	cagcacttat	atccgcata	aactcttctt	1080
caacatccag	aactagtcaa	tcacagaatg	gtgcccatgc	caaaaagctta	tattttcccca	1140
tqqcqttqtt	cqgaatcttt	gcagttgccc	tttaa			1175

```
<210> 174
<211> 224
<212> PRT
<213> Candida albicans
```

<210>	175
<211>	1618

<213> Candida albicans

gcacccctttt	tcttttttcaa	taacaaaaaaa	gagcttgggc	attacgtttt	caacactttt	60
aatatattccc	ttttttacatc	cgtacatata	aaatgtaaac	ccatgcattc	atgacaattt	120
tacctatttc	ttaaaggcct	ttgtcacttc	tttatgggaa	tggcgctact	ttaattttcc	180
gcctactttg	aaaaattttac	caaggcgaaa	ttgagtgcgc	taggcggaag	ttccaggggca	240
cggtcaccga	acctttgtgc	tgtttcgaac	gagggtcccc	ctggaggttg	acggagcgcg	300
gaggagctgg	aaagatggaa	tggaaaggact	gcaacactca	gtaagaagg	tcgtggtagg	360
gaacatcacc	ttctctagtt	cctgtataaaa	taatatgata	aagtttgaat	cctcgtattg	420
aaaaatcgcg	agttattaag	tgtgtaattt	agaataccga	aatagcacaa	gaagagataa	480
gataagatac	tgataggata	atgtctttac	cagctacttt	tgatttgact	ccagaggatg	540
cccaactttt	gttggccgct	aacacccatt	taggtgctag	aaacgttcaa	gtatgtacac	600
atatcccata	cgattatgtt	ctatagatga	taataggtct	cgaaaagaat	atgtccccga	660
tttaatcata	tttggaggtc	agaggaccaa	aggtaathtt	agaggaattt	tgaacacgcc	720
gggttttagaa	gagttagaat	ttcacttctt	agtgaaggga	aggagaaggaa	actcaataag	780
aaatatacatc	ctcgactgtg	tcaaagatta	tgaactccga	tgaacagta	aaacgtcaaa	840
aaattccacg	ggatataatt	cggtacttta	ttggatatgg	aagaaaacat	tatatatgca	900
caaatgaacg	ctcttactaa	cataatttat	ctttcctctc	tttttttagg	tccaccaaga	960
accatacgtt	ttcaatgcta	gaccagatgg	tgttcacggt	atcaatggtg	gtaagacctg	1020
ggaaaagttg	gttttggctg	ctagaattat	tgctgccatt	ccaaacccag	aagatgttgt	1080
tgccattctc	tcgacaacct	acggtcaaag	agctgtcttg	aaatttgcgt	ctcacactgg	1140
tgtctactcca	atcgccggta	gattcactcc	aggttctttc	actaattaca	tcacccggtc	1200
tttcaaggaa	ccaagatttg	ttattgttac	cgacccaaga	ttagacgctc	aggccattaa	1260
ggaagcttct	tacgttaaca	ttccagtcac	tgctttgact	gatttggact	ccccatctga	1320
atttgttgat	gtcgccatcc	catgtaacaa	cagaggtaag	cactccatcg	gtttaatctg	1380
gtacttgttg	gctagagaag	ttttgagact	aagaggtgct	ttggtcgaca	gaactcaacc	1440
atggtcacat	atgccgatt	tgtactttcta	cagaaaacca	gaagaagttg	agcaagttgc	1500
tgaaggaact	gctgcgctg	aagaaggtga	agagaagaa	gttaaggaa	aagtcactga	1560
aggtcaagct	gaagctactg	aatgggctga	agaaaaatga	gacacgcttg	aatggtaa	1618

<213> Candida albicans

Met	Ser	Leu	Pro	Ala	Thr	Phe	Asp	Leu	Thr	Pro	Glu	Asp	Ala	Gln	Leu
1				5					10					15	
Leu	Leu	Ala	Ala	Asn	Thr	His	Leu	Gly	Ala	Arg	Asn	Val	Gln	Val	His
			20					25					30		
Gln	Glu	Pro	Tyr	Val	Phe	Asn	Ala	Arg	Pro	Asp	Gly	Val	His	Val	Ile
		35					40					45			
Asn	Val	Gly	Lys	Thr	Trp	Glu	Lys	Leu	Val	Leu	Ala	Ala	Arg	Ile	Ile
	50					55					60				
Ala	Ala	Ile	Pro	Asn	Pro	Glu	Asp	Val	Val	Ala	Ile	Ser	Ser	Arg	Thr
65					70					75					80
Tyr	Gly	Gln	Arg	Ala	Val	Leu	Lys	Phe	Ala	Ala	His	Thr	Gly	Ala	Thr
				85					90					95	

<400>	177						
cttcccatgt	agaatatcat	tgtcaaacat	actactaccg	tgagaatcca	atctactaaa	60	
aagaccagc	taaagtcctt	ttgggtgtgtc	aatggaacac	cacgtaattg	tgaaatagct	120	
tccatgcttg	ctaactttatt	accgtcaata	gaagacttga	gtcaggtggc	tttaatgagt	180	
actattcttt	ttttttttcc	aaagagcact	atggttgataa	taccgcagta	atTTTTTTTg	240	
agtatcctgt	agcctagaaa	ggttgaagct	tataaaaccg	tgccaacagc	tttatagtgg	300	
ggagtttggc	ttccctctat	ttgtatatgt	atcgccattc	ctacgaagtt	attgggaagc	360	
catcgtgaac	ctctcacttt	aatgccagcg	gtgaaaaaaa	aagtcataaa	caatacacgc	420	
cgcgtacact	tagaaaagaa	tgacatttgc	tgtcttataa	aaggacttga	cagaccaaag	480	
acgcgtataa	tacaccaaga	atggccttat	tggagaagtt	gcatcgaagg	attgttgata	540	
tggggccttgt	cccgcgata	atcgcccttat	taccagttat	ttccatgcta	tgcgctctat	600	
ttgggtttat	ttctatagct	attctgccta	tggatggaca	gtacagaaga	acatacattt	660	
ctgagaatgc	attgatgcct	tcacaagcgt	atagttactt	tagagaatct	gaatggaaca	720	
tttgagggg	ctatcgatct	caaattaaag	aaatggtaaa	catgacttct	atggaaagaa	780	
acaatttgat	gggttcttgg	ttacaagaat	ttggtactaa	gactgctatt	tacgaaaatg	840	
aacaatatgg	agaaacattg	tacggtgtaa	tgcacgctcc	taggggtgat	ggaacagaag	900	
cgatggtgct	tgcggttcca	tggtttaatt	cagatgatga	attcaatatt	ggcggcgag	960	
ctttgggtgt	atcttttagca	agatttttct	cacgttggcc	agtatggtcc	agaatatata	1020	
ttgttgtctt	cagcgaaaat	cctcgtgcag	cattaagatc	atgggttgag	gcataccata	1080	
cttccttaga	tttgactggg	ggttccattg	aagctgctgt	tgtgttggat	tattcgagta	1140	

cggaagattt cttcgagtat gtagaaatct catacgacgg tctgaatggt gagctgccca 1200
 atttggatct tgtcaacatc gctatatcca ttacggaaca tgaaggatat aaagtttctt 1260
 tgcacggctc acccagtgat cagttaacta ataataattt ctgggtcaaga ttaaaaaatat 1320
 tatgcctggg aataagggat tgggcggtgt ccggtgttaa aaagcccat ggtaacgagg 1380
 catttagcgg ctggaggatt caatctgtaa cattgaaagc acatggaaac agtgggtcatg 1440
 atattactac atttggacgt ataccggaag caatgtttcg ctctattaat aaccttttgg 1500
 aaaaatttca ccaatcgttc ttcttttatt tgttatttagc accacgtcag ttcgtatcca 1560
 ttagtagtta ttgccaagc gctgtggctt tatctatagc attcgccata agttcattaa 1620
 atgcatttat aaacaatgct tatgcaaata tatccttatt ttccgagtat aatttggttag 1680
 cgttgttggg ttggttcgtg tcattgggtga tatcatttgt tgtttcacaa gcgtttcttc 1740
 taataccttc atcgggatta ttgatgacaa ttagcatggc atcttgtttt ttaccttga 1800
 tactttccag aaaaattcac atctcagaac cactatcata caggttgaaa aatgttgctt 1860
 ttttatattt cagtttgggt tcaacatctt tgctaattgat aaactttgca atggctttac 1920
 tgatcggcac attggcattt cctatgacat ttgtgaagac cattgttgaa agttctagcg 1980
 aacatgaggt gacaactcaa tcctctaacc caataaaaac tgagccgaaa gatgagatag 2040
 agctcgtcga gaatcacatg gatacaacgc cagcaacccc ccaacaacag aaacaaaaac 2100
 taaaaaattt agtactatta attttgacaa atccatttat ttcaataacc ttattcggac 2160
 tatttttga tgatgaattt catggatttg atataataaa caaactgggt tcagcatggt 2220
 tggatttgaa atgttggagt tggttgttac tttgtatagg ttggcttcca tgttggctat 2280
 tgatattagc gtcacgttt gaatctaaat ctgtcgtagt aaggtcgaaa gaaaagcaaa 2340
 gtttag 2345

<210> 178

<211> 614

<212> PRT

<213> Candida albicans

<400> 178

Met Ala Leu Leu Glu Lys Leu His Arg Arg Ile Val Asp Met Gly Leu
 1 5 10 15
 Val Pro Arg Ile Ile Ala Leu Leu Pro Val Ile Ser Met Leu Cys Ala
 20 25 30
 Leu Phe Gly Phe Ile Ser Ile Ala Ile Leu Pro Met Asp Gly Gln Tyr
 35 40 45
 Arg Arg Thr Tyr Ile Ser Glu Asn Ala Leu Met Pro Ser Gln Ala Tyr
 50 55 60
 Ser Tyr Phe Arg Glu Ser Glu Trp Asn Ile Leu Arg Gly Tyr Arg Ser
 65 70 75 80
 Gln Ile Lys Glu Met Val Asn Met Thr Ser Met Glu Arg Asn Asn Leu
 85 90 95
 Met Gly Ser Trp Leu Gln Glu Phe Gly Thr Lys Thr Ala Ile Tyr Glu
 100 105 110
 Asn Glu Gln Tyr Gly Glu Thr Leu Tyr Gly Val Met His Ala Pro Arg
 115 120 125
 Gly Asp Gly Thr Glu Ala Met Val Leu Ala Val Pro Trp Phe Asn Ser
 130 135 140
 Asp Asp Glu Phe Asn Ile Gly Gly Ala Ala Leu Gly Val Ser Leu Ala

145		150		155		160
Arg Phe Phe Ser	Arg Trp Pro Val Trp Ser Lys Asn Ile Ile Val Val					
	165		170		175	
Phe Ser Glu Asn Pro Arg Ala Ala Leu Arg Ser Trp Val Glu Ala Tyr						
	180		185		190	
His Thr Ser Leu Asp Leu Thr Gly Gly Ser Ile Glu Ala Ala Val Val						
	195		200		205	
Leu Asp Tyr Ser Ser Thr Glu Asp Phe Phe Glu Tyr Val Glu Ile Ser						
	210		215		220	
Tyr Asp Gly Leu Asn Gly Glu Leu Pro Asn Leu Asp Leu Val Asn Ile						
	225		230		235	240
Ala Ile Ser Ile Thr Glu His Glu Gly Met Lys Val Ser Leu His Gly						
	245		250		255	
Leu Pro Ser Asp Gln Leu Thr Asn Asn Asn Phe Trp Ser Arg Leu Lys						
	260		265		270	
Ile Leu Cys Leu Gly Ile Arg Asp Trp Ala Leu Ser Gly Val Lys Lys						
	275		280		285	
Pro His Gly Asn Glu Ala Phe Ser Gly Trp Arg Ile Gln Ser Val Thr						
	290		295		300	
Leu Lys Ala His Gly Asn Ser Gly His Asp Ile Thr Thr Phe Gly Arg						
	305		310		315	320
Ile Pro Glu Ala Met Phe Arg Ser Ile Asn Asn Leu Leu Glu Lys Phe						
	325		330		335	
His Gln Ser Phe Phe Phe Tyr Leu Leu Leu Ala Pro Arg Gln Phe Val						
	340		345		350	
Ser Ile Ser Ser Tyr Leu Pro Ser Ala Val Ala Leu Ser Ile Ala Phe						
	355		360		365	
Ala Ile Ser Ser Leu Asn Ala Phe Ile Asn Asn Ala Tyr Ala Asn Ile						
	370		375		380	
Ser Leu Phe Ser Glu Tyr Asn Leu Val Ala Leu Leu Val Trp Phe Val						
	385		390		395	400
Ser Leu Val Ile Ser Phe Val Val Ser Gln Ala Phe Leu Leu Ile Pro						
	405		410		415	
Ser Ser Gly Leu Leu Met Thr Ile Ser Met Ala Ser Cys Phe Leu Pro						
	420		425		430	
Leu Ile Leu Ser Arg Lys Ile His Ile Ser Glu Pro Leu Ser Tyr Arg						
	435		440		445	
Leu Lys Asn Val Ala Phe Leu Tyr Phe Ser Leu Val Ser Thr Ser Leu						

<400>	179						
tccgtcccaa	agatagcttg	atcatcctaa	gcgggtcgca	ttttactatc	cccagttccg	60	
aagaataaca	aggctcaatg	catatgctgt	ttatcgtgct	cacaaggcgg	tatgacgttt	120	
ttagcaatgt	aattatatta	aaaagatctt	cagtcactat	gagtggttga	ttgccccata	180	
gagagctata	agccgacgtg	aaagctgctg	gttccagctt	ggctcatgtc	gtcaccagtc	240	
actagtcact	tggtgcgatt	cattgtctact	catctgcgag	tgagcatatt	tgagacttga	300	
cttgccaagg	gattagaatc	acgtaaagact	cttgatcctt	agaagatatt	tctgacaaag	360	
aaccacctaa	gccatgcaag	tttttttttt	catttggtgg	cgaaacaaag	gtgatgaaag	420	
tttcttcttg	tacaaacgcc	aagcccgata	ggtgagacaa	ttcttgaagt	aatggacctc	480	
tgagtaagca	tatcagtcga	atgaagttcc	aatatgcggt	ggccaaggaa	cagctaggca	540	
gcaactcgcg	cagtggcgtc	aaaaaactaa	taagtaaaca	ccactggctt	ccggaatact	600	
atttctctga	tctctcattt	tctgttgtac	agcagtgggg	cagtagagcc	attgaaaaaa	660	
ctacaatcat	atcttgtatg	cgccccgcaa	accaagagat	ttatcctttg	agacatttgt	720	
agacctccg	ttcgcaaccg	tgctctctgt	tttcatcact	atatgcacgc	tctttccaaa	780	
gctcctgcac	tttgcacgtg	gcggagccat	cgcccggtt	ccatatgtac	ggctgccaca	840	
cctaa						845	

<210> 182

191

<211> 152
 <212> PRT
 <213> *Candida albicans*

<400> 182
 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1 5 10 15
 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
 20 25 30
 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
 35 40 45
 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 50 55 60
 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Gly Lys Lys Arg
 65 70 75 80
 Lys Lys Lys Val Tyr Thr Thr Pro Lys Lys Ile Lys His Lys His Lys
 85 90 95
 Lys Val Lys Leu Ala Val Leu Ser Tyr Tyr Lys Val Asp Ala Glu Gly
 100 105 110
 Lys Val Thr Lys Leu Arg Arg Glu Cys Ser Asn Pro Thr Cys Gly Ala
 115 120 125
 Gly Val Phe Leu Ala Asn His Lys Asp Arg Leu Tyr Cys Gly Lys Cys
 130 135 140
 His Ser Val Tyr Lys Val Asn Ala
 145 150

<210> 183
 <211> 848
 <212> DNA
 <213> *Candida albicans*

<400> 183
 agccaccaat tccaccaggc ccggcattca agtacttgta agaacaccaa caggcaaagt 60
 caacacccca atcatgaagt tgcaatggga cgttccctac agcgtgtgct aaatcccatc 120
 caaccaatat gtcggggaat tgggtgggcaa atgaggatgat tcggccaata tcgaaatatt 180
 gccccgtgta atactgaaca cctgacaaac agaccagcgc caattcatct tgattttacct 240
 ctatggtatc caggatatct tgagttctga tataagtctc tccctcgcgt ggctcgatct 300
 gaataaaaac attctcaggt tccgaaattc catgaatttt gcaactgggtg tagaaagcat 360
 aatagtctga tggaaaggag cccttttcaa aaaggatctt gaatcttttc tcagtagggt 420
 tataaaacgt aattaacaat gaattcaaat ttgcagtgag actattcatt actgcaactt 480
 cattttcttg agcaccacac atggggggcta gtagtggaag aataggtaag tcaatgctga 540
 cccaaggcac ctttccctctg gcttcttcag gatggttgaa atgcgattcc acagcacaat 600
 cgctccacgc cttatgctca gcattaattg aattcctagt tgacttcggc atcaaacct 660
 aagaattccc gcataagtac gtcacaggct tatcgtcgga cgatagtcac atgggatttaa 720
 atgtagggat gttgaattca tccctcagag attccggata ttctccgtct aattccaaag 780
 ctttctccat aattaccagt ttgtttcttt tttccacaga atatttaggc ttaatatgta 840

<400>	185						
gcgcatttttc	cccaccccatg	cgaatcatgg	ctgaaatcaa	tgcttgtag	gtgccctgca	60	
acactagtc	tggtaaccttc	gcagttagcc	ccatttctgg	caaacgggaa	cccactaaac	120	
atgaaatcat	agttctttac	atacatgtag	ccggaatccc	ttgaagttga	tctgcctcct	180	
cctaggatct	gtgaaactgc	cttcgcata	gaatttttct	ctgcgcacac	tagcactttc	240	
attattgtct	ataatacacc	tttacgtagc	tgaagcgagc	gcacagacga	aggcgctttc	300	
aaaagcgatg	ccctctttat	tgacagttac	taattcgcca	aactgctttt	ttttatcaat	360	
gtgatttttcg	cgttcacgcc	attatccaat	gtcaaaaagg	ataatggaaa	tgттаacatg	420	
cctgtatgat	ccgaccgttt	ttagcaaact	tatcagggga	aaaagtatat	tccattaaat	480	
gacacatgcc	accatagata	atggataatg	aagaagttaa	cgaagaatgt	atgagattat	540	
ttttcaagaa	cgctcgtgcg	catctggata	aacatctaac	atcaaggttg	acatgcgatg	600	
aaaatgcata	tatcacgttc	agatgcttcc	tggttggaat	acatcgcaaa	tctactaggt	660	
ttctcgaaga	gctacttttg	aaacaagaaa	atatgtacca	taataacaat	tacgaacgca	720	
taaatgattc	cgtgatacca	ttggttctga	aacttttatg	gcttcaaaat	cacgaacctc	780	
cactccaatg	gtttgagcac	tggtttccat	atatcatcgc	actaagtaac	agaagaaagt	840	
tcagagtttt	tagaattttt	caaaaaaaaa	tgattcaatt	tttcaaaatt	acacacaggt	900	
attactatga	catcatcgaa	cacctatgcg	caaagtacga	tatgaattcc	gttattttcaa	960	

<400> 186																
Met	Asp	Asn	Glu	Glu	Val	Asn	Glu	Glu	Cys	Met	Arg	Leu	Phe	Phe	Lys	
1				5					10						15	
Asn	Ala	Arg	Ala	His	Leu	Asp	Lys	His	Leu	Thr	Ser	Arg	Leu	Thr	Cys	
			20					25						30		
Asp	Glu	Asn	Ala	Tyr	Ile	Thr	Phe	Arg	Cys	Phe	Leu	Asp	Gly	Ile	His	
		35					40					45				
Arg	Lys	Ser	Thr	Arg	Phe	Leu	Glu	Glu	Leu	Leu	Leu	Lys	Gln	Glu	Asn	
	50					55						60				
Met	Tyr	His	Asn	Asn	Asn	Tyr	Glu	Arg	Ile	Asn	Asp	Ser	Val	Ile	Pro	
65					70					75					80	
Leu	Val	Leu	Lys	Leu	Leu	Trp	Leu	Gln	Ile	His	Glu	Pro	Thr	Leu	Gln	
				85					90					95		
Trp	Phe	Glu	His	Trp	Phe	His	Asp	Ile	Met	Arg	Leu	Ser	Asn	Arg	Arg	
			100					105					110			

Lys Phe Arg Val Phe Arg Ile Phe Gln Lys Lys Met Ile Gln Phe Phe
 115 120 125
 Lys Ile Thr His Arg Tyr Tyr Tyr Asp Ile Ile Glu His Leu Cys Ala
 130 135 140
 Lys Tyr Asp Met Asn Ser Val Ile Ser Asn Ala Leu Phe Ala Lys Leu
 145 150 155 160
 Asn Leu Met Gln Tyr Thr Asp Gly Leu Ser Thr His Glu Lys Ile Ile
 165 170 175
 Leu Asn Thr Ser Asn Pro Leu Thr Phe Ser Ile Val Ile Ser Leu Gln
 180 185 190
 Arg Cys Val Ile Asn Leu Gly Ser Thr His Phe Tyr Lys Thr Leu Leu
 195 200 205
 Asn Lys Pro Ser Asn Lys Pro Lys Ser Val Glu Gly Phe Glu Lys Ser
 210 215 220
 Ile Arg Tyr Leu Asn Ile Ala Ser Leu Tyr Leu Pro Ala Val Gly Asp
 225 230 235 240
 Thr Tyr Phe Gln Arg Ala Lys Ile Tyr Leu Ile Thr Gly Lys Phe Ser
 245 250 255
 Leu Tyr Phe Phe Glu Leu Val Arg Gly Ala Leu Val Arg Ile Pro Ser
 260 265 270
 Lys Cys Ala Leu Asn Asn Leu Lys Asp Phe Ile Leu Thr Pro Asp Phe
 275 280 285
 Pro Glu Arg Arg Arg Leu Met Lys Lys Leu Ala Ile Leu Val Ser Lys
 290 295 300
 Asp Leu Lys Gly Glu Lys Ser Phe Phe Glu Gly Gln Ile Val Leu Gln
 305 310 315 320
 Phe Leu Ser Ile Val Glu His Thr Leu Val Pro Gln Ser Trp Asn Ala
 325 330 335
 Ser Arg Ala Ser Asn Cys Trp Leu Leu Lys Glu His Leu Gln Met Ala
 340 345 350
 Ala Leu Lys Tyr His Ser Gly Asn Ile Asn Val Ile Leu Glu Asn Leu
 355 360 365
 Ala Ala Thr Met Gly Ser Phe Asp Leu Met Phe Thr Thr Arg Lys Ser
 370 375 380
 Lys Glu Gln Lys Asn Lys Leu Lys Tyr Ala Asp Leu Ser Glu Arg Gln
 385 390 395 400
 Val Phe Phe Leu Asp Leu Ser Phe Asp Phe Ile Ala Asn Ile Ile Asp
 405 410 415

Val Val Ile Lys Pro Ser Trp Gln Lys Asn Met Glu Asp Phe Arg Tyr
 420 425 430
 Leu Ala Ile Ile Arg Leu Leu Met Cys Trp Ile Lys Ser Tyr Arg Ser
 435 440 445
 Ile Leu Gln Tyr Thr His Arg His Arg Lys Phe Cys Thr Ser Phe Ala
 450 455 460
 Leu Leu Leu Asn Asp Leu Ile Asn Ser Pro Leu Asn Cys Ser Gly Asn
 465 470 475 480
 Ile Tyr Ser His Arg Pro Lys Arg Ser Tyr Leu Phe Arg Glu Asp Ile
 485 490 495
 Ile Phe Arg Glu Phe Ser Cys Ile Asn Phe Ala Leu Thr Asp Phe Asn
 500 505 510
 Asp Asp Tyr Val Tyr Asp Ser Pro Asp Met Ile Asn Asn Ile Ile Gly
 515 520 525
 Cys Pro Thr Leu Thr Lys Val Leu Ser Pro Lys Glu Glu Cys Val Leu
 530 535 540
 Arg Ile Arg Ser Ile Ile Phe Ser Gly Met Lys Phe Leu Glu Lys Asn
 545 550 555 560
 Asp Thr Gly Val Ile Trp Asn Ala Ser Lys Tyr Lys Phe Asp Leu Ile
 565 570 575
 Ser Pro Asn Ile Lys Ile Lys Arg Gln Ile Ala Leu Ser Glu Ile Ser
 580 585 590
 Ser Lys Ile Asn Val Lys Thr Gln Gln Glu Arg Val Val Ser Ser Arg
 595 600 605
 Lys Val Glu Ala Lys Arg Asp Glu Gln Gln Arg Lys Arg Ala Gly Lys
 610 615 620
 Ile Ala Val Thr Glu Leu Glu Lys Gln Phe Ala Asn Val Arg Arg Thr
 625 630 635 640
 Lys Lys Leu Ser Pro Leu Pro Glu Lys Asp Gly Val Ser Ser Glu Leu
 645 650 655
 Val Lys His Ala Ala Ser Arg Gly Arg Lys Thr Ile Thr Gly Pro Leu
 660 665 670
 Ser Ser Asp Phe Leu Ser Tyr Pro Asp Glu Ala Ile Asp Ala Asp Glu
 675 680 685
 Asp Ile Thr Val Gln Val Pro Asp Thr Pro Thr
 690 695

<211> 2471

<212> DNA

<213> *Candida albicans*

<400> 187

```

aatggtatca cggaatcatt tatgcttctg taattgttat tatggtacat attttcttgt 60
ttcaaaagta gctcttcgag aaacctagta gatttgcgat gtattccatc caggaagcat 120
ctgaacgtga tatatgcatt ttcacgcgat gtcaaccttg atgttagatg tttatccaga 180
tgcgcacgag cgttcttgaa aaataatctc atacattctt cgtaaacttc ttcattatcc 240
attatctatg gtggcatgtg tcattttaatg gaatataact tttcccttga taagtttgct 300
aaaaacgggc ggatcataca ggcattgttaa catttccatt atcctttttg acattggata 360
atggcgtgaa cgcgaaaatc acattgataa aaaaaagcag tttggcgaat tagtaactgt 420
caataaagag ggcatcgctt ttgaaagcac cttcgtctgt gcgctcgctt cagctacgta 480
aagggtgtatt atagacaata atgaaagtgc tatgtgtcgc agagaaaaat tctatagcga 540
aggcagtttc acagatccta ggaggaggca gatcaacttc aagggattcc ggctacatgt 600
atgtaaagaa ctatgatttc atgttttagtg ggttcccggt tgccagaaat ggggctaagt 660
cggaagttac catgcatgtg gttgcaggcg acctaacagg cattgatttc agccatgatt 720
cgcattgggtg gggaaaaatgc gccatccaag agttatttga tgcgccactg aacgagatta 780
tgaataacaa ccaaaaaaag atagcaagca acatcaagcg agaagcgagg aatgcagact 840
atctgatgat atggacagat tgcgaccggg aaggagagta catcggttgg gagatatggc 900
aggaggccaa gagagggcaac aggctcatal aaaatgatca agtataccgg gcagtctttt 960
cgcattctcga aagacaacac atattaaatg cagcacgaaa cccaagtcca ttggatatga 1020
agagtgtgca cgctgtaggc acgcggattg aaatcgatct tcgagcaggt gttacattca 1080
ccagactctt acagaaaacg ctacgaaata aactgagaaa ccaagccacc atgaccaagg 1140
atggtgcaaa acaccgcggt ggtaacaaga acgactcaca agtcgtatcg tatggtacat 1200
gccagtttcc aacgctcggc tttgtagtag acaggtttga aagaatacga aattttgttc 1260
ccgaagagtt ctggtatatc caattggtag tcgaaaacaa agacaacggc ggaacaacaa 1320
cgttccagtg ggacaggggc cacttggtcg accggctgag cgtgttaacg ttttacgaga 1380
catgcatcga aaccgcccgc aatgttgctc aagtagtaga cttgaaatca aagccaacaa 1440
cgaaatacag acctttacct ctgaccacag tggagctaca aaaaaactgc gcccgggtacc 1500
tgcgtctgaa cgccaaacaa tcactagacg cagcagaaaa gctataccaa aaggggttca 1560
tatcgtatcc aagaacagag actgatactt tcccacacgc aatggacctt aaatccttgg 1620
tcgaaaagca agctcaattg gaccaactcg ctgcaggcgg cagaaccgcc tgggcatcgt 1680
acgcggcatc gctgctccaa cccgaaaaca caagtaacaa taacaagttc aagtttccac 1740
gaagcggctc ccatgacgac aaagcgcac caccaatcca ccccatcgta agtctggggc 1800
ctgaagcaaa tgtttcgcca gtggaaagaa gagtatacga gtacgtggcd aggcactttt 1860
tggcatgctg ctgagaggac gccaaaggcc aatcgatgac ccttgtgttg gactgggccg 1920
ttgaacgttt ctgagcttca ggtctcgtag tcctagagag aaatttcctc gatgtttacc 1980
cttgggcccc atgggaaacc accaagcagt taccgggct tgaaatgaat gccctcgtag 2040
acatcgcgaa ggccgaaatg aaggcgggca ctacggcgcc gcccaagccg atgactgaga 2100
gtgaactcat tctcctcatg gatacaaac gcattggcac agacgccacc attgcgggagc 2160
acatagacaa gatccaagta cgtaattacg ttaggagcga gaaagtaggc aaggaaacct 2220
acttacaacc cagaccctg ggtgtctcac tagtgacgg cttcgaggcc atcggcctcg 2280
aagactcctt tgcaaagccc ttccagcgca gagaaatgga gcaagacctc aagaaaatct 2340
gcgaaggtca tgcctccaag actgatgttg taaaggacat agtcgagaag tataggaagt 2400
actggcacia gcgaatgcc tgcaagaata ctctcttgca agtttatgac cgtgtcaagg 2460
catccatgta a

```

<210> 188

<211> 656

<212> PRT

<213> *Candida albicans*

<400> 188

Met Lys Val Leu Cys Val Ala Glu Lys Asn Ser Ile Ala Lys Ala Val

1

5

10

15

Ser Gln Ile Leu Gly Gly Gly Arg Ser Thr Ser Arg Asp Ser Gly Tyr
20 25 30

Met Tyr Val Lys Asn Tyr Asp Phe Met Phe Ser Gly Phe Pro Phe Ala
35 40 45

Arg Asn Gly Ala Asn Cys Glu Val Thr Met Thr Ser Val Ala Gly His
50 55 60

Leu Thr Gly Ile Asp Phe Ser His Asp Ser His Gly Trp Gly Lys Cys
65 70 75 80

Ala Ile Gln Glu Leu Phe Asp Ala Pro Leu Asn Glu Ile Met Asn Asn
85 90 95

Asn Gln Lys Lys Ile Ala Ser Asn Ile Lys Arg Glu Ala Arg Asn Ala
100 105 110

Asp Tyr Leu Met Ile Trp Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile
115 120 125

Gly Trp Glu Ile Trp Gln Glu Ala Lys Arg Gly Asn Arg Leu Ile Gln
130 135 140

Asn Asp Gln Val Tyr Arg Ala Val Phe Ser His Leu Glu Arg Gln His
145 150 155 160

Ile Leu Asn Ala Ala Arg Asn Pro Ser Arg Leu Asp Met Lys Ser Val
165 170 175

His Ala Val Gly Thr Arg Ile Glu Ile Asp Leu Arg Ala Gly Val Thr
180 185 190

Phe Thr Arg Leu Leu Thr Glu Thr Leu Arg Asn Lys Leu Arg Asn Gln
195 200 205

Ala Thr Met Thr Lys Asp Gly Ala Lys His Arg Gly Gly Asn Lys Asn
210 215 220

Asp Ser Gln Val Val Ser Tyr Gly Thr Cys Gln Phe Pro Thr Leu Gly
225 230 235 240

Phe Val Val Asp Arg Phe Glu Arg Ile Arg Asn Phe Val Pro Glu Glu
245 250 255

Phe Trp Tyr Ile Gln Leu Val Val Glu Asn Lys Asp Asn Gly Gly Thr
260 265 270

Thr Thr Phe Gln Trp Asp Arg Gly His Leu Phe Asp Arg Leu Ser Val
275 280 285

Leu Thr Phe Tyr Glu Thr Cys Ile Glu Thr Ala Gly Asn Val Ala Gln
290 295 300

Val Val Asp Leu Lys Ser Lys Pro Thr Thr Lys Tyr Arg Pro Leu Pro
305 310 315 320

Leu Thr Thr Val Glu Leu Gln Lys Asn Cys Ala Arg Tyr Leu Arg Leu
 325 330 335
 Asn Ala Lys Gln Ser Leu Asp Ala Ala Glu Lys Leu Tyr Gln Lys Gly
 340 345 350
 Phe Ile Ser Tyr Pro Arg Thr Glu Thr Asp Thr Phe Pro His Ala Met
 355 360 365
 Asp Leu Lys Ser Leu Val Glu Lys Gln Ala Gln Leu Asp Gln Leu Ala
 370 375 380
 Ala Gly Gly Arg Thr Ala Trp Ala Ser Tyr Ala Ala Ser Leu Leu Gln
 385 390 395 400
 Pro Glu Asn Thr Ser Asn Asn Asn Lys Phe Lys Phe Pro Arg Ser Gly
 405 410 415
 Ser His Asp Asp Lys Ala His Pro Pro Ile His Pro Ile Val Ser Leu
 420 425 430
 Gly Pro Glu Ala Asn Val Ser Pro Val Glu Arg Arg Val Tyr Glu Tyr
 435 440 445
 Val Ala Arg His Phe Leu Ala Cys Cys Ser Glu Asp Ala Lys Gly Gln
 450 455 460
 Ser Met Thr Leu Val Leu Asp Trp Ala Val Glu Arg Phe Ser Ala Ser
 465 470 475 480
 Gly Leu Val Val Leu Glu Arg Asn Phe Leu Asp Val Tyr Pro Trp Ala
 485 490 495
 Arg Trp Glu Thr Thr Lys Gln Leu Pro Arg Leu Glu Met Asn Ala Leu
 500 505 510
 Val Asp Ile Ala Lys Ala Glu Met Lys Ala Gly Thr Thr Ala Pro Pro
 515 520 525
 Lys Pro Met Thr Glu Ser Glu Leu Ile Leu Leu Met Asp Thr Asn Gly
 530 535 540
 Ile Gly Thr Asp Ala Thr Ile Ala Glu His Ile Asp Lys Ile Gln Val
 545 550 555 560
 Arg Asn Tyr Val Arg Ser Glu Lys Val Gly Lys Glu Thr Tyr Leu Gln
 565 570 575
 Pro Thr Thr Leu Gly Val Ser Leu Val His Gly Phe Glu Ala Ile Gly
 580 585 590
 Leu Glu Asp Ser Phe Ala Lys Pro Phe Gln Arg Arg Glu Met Glu Gln
 595 600 605
 Asp Leu Lys Lys Ile Cys Glu Gly His Ala Ser Lys Thr Asp Val Val
 610 615 620

Lys Asp Ile Val Glu Lys Tyr Arg Lys Tyr Trp His Lys Thr Asn Ala
625 630 635 640

Cys Lys Asn Thr Leu Leu Gln Val Tyr Asp Arg Val Lys Ala Ser Met
645 650 655

<210> 189

<211> 1937

<212> DNA

<213> Candida albicans

<400> 189

```

cttcgttcac acttaatat aaataacagc tctttcctaa taataacata tacactagat 60
atataatacc aaataaatta aaaaaaaaga aaaacaaaaa ataacgtagc tttgttacag 120
tcgtaaaaaa aagaacaata aaccaatctt attgccagcg tctaactagt cctattatat 180
tccaatatat taaggggtaa ggactactat tattcgccct gaattgaaat cttttagaaa 240
gcacctgttc tctctctggt gttctttttt tctcatctat tatctaattt cttcaacctt 300
cgttatttgt tgttattccg taatcgtggt gctcaacttt tgaaatttca cttgtttacc 360
ataacggaac ataattaaaa atttgttctt gaaagtcaca agcactacgt gaacacaaaa 420
ttaaggcaag agtgacaaag taaccctcac aaggagcctg tcgttggtta tattggaagc 480
tatagatata atcgaatcca atgactgggc ctggacctga aataaataag gaggagcacc 540
ccagttctcc gggcaagaaa cagataacat ataatagtat acccaagaat gcaaactctaa 600
ttgatggatc tacgaattca tcgaagaggc caattgaaaa gtatgacaag agaatagccg 660
acccaacaaa aagctatttt ccacatagca tatcaagaac accaaggaga aaatatactt 720
acattttagt cctcacatca ctaaatggaa cttttgagag caaacatgtg gtgatacttg 780
ttaaaccaga ttggttgaaa ttgggaaggc ctgttgctaa tagtaatagc agctccagtt 840
catcgctcag gggcggtaaa agagtggatt cacacacttt tcccaagta aggtccgata 900
atggtaattt cgattcaaga gtactctcca ggaatcatgc attgttaagt tgcgaccgcg 960
tcacgggtaa ggtatatata cgagacttaa aatccagtaa tggtagcttc attaacgggc 1020
aaagaattgg ctcaaattgac gttagaatca aagttggcga tgtgatagac ttgggaacag 1080
atatagatac gaaaattgag catcgaaaaa taagtgccac agttgaagaa ctatttgtac 1140
aacctttatt agaatcaccg atttttgaaa atgaagatag tgatgattgc catacaatta 1200
cagaaaaaga ggaggtgctt gccataacaa gtcacatata tgggtattcc aacaacctag 1260
aattggaaga agttatcctg ggctctgata cagaaatact gagtgggaatt tttattaata 1320
attgtattgg tacgagcccg actttatcta atatcatcaa aaccctggca atggaaattc 1380
cattttccaa atgcgataat tttaaattac agtcgatgga gaatttctta attaatata 1440
cgacacatct agaatacacg aacaaacttt tagtggaata aatgatcag caactggtaa 1500
agctgcaaaa tggattaaga aggaaactgt cggggaaata cgaaaagatt atcgacaaaa 1560
acagaaatca agtaaaacag ttggaaaggg accatatgtt tttcaaaaag tcatttgaag 1620
tgaagaaaag aagaaataat gaaaagcaaa aaagcatgga aagggaaata gaagacttga 1680
aaactaggtt agaagtggaa cgatataaga attcacaaat gatgaagaag aacaaacaga 1740
aagaacaaga actctcaact gcacttaaaa aaaagactac cgaacatgac actagaggcg 1800
tcccgggcat gaatcctaag ggtactgaca aatttagcat caagaacacg ctatgtaatc 1860
atttcacact attaacattt ggaactattt ccatcgggat tatagctatt gtcttcaaga 1920
tcctttcccc caactag 1937

```

<210> 190

<211> 478

<212> PRT

<213> Candida albicans

200

<400> 190

Met Thr Gly Pro Gly Pro Glu Ile Asn Lys Glu Glu His Pro Ser Ser
 1 5 10 15
 Pro Gly Lys Lys Gln Ile Thr Tyr Asn Ser Ile Pro Lys Asn Ala Asn
 20 25 30
 Leu Ile Asp Gly Ser Thr Asn Ser Ser Lys Arg Pro Ile Glu Lys Tyr
 35 40 45
 Asp Lys Arg Ile Ala Asp Pro Thr Lys Ser Tyr Phe Pro His Ser Ile
 50 55 60
 Ser Arg Thr Pro Arg Arg Lys Tyr Thr Tyr Ile Leu Val Leu Thr Ser
 65 70 75 80
 Leu Asn Gly Thr Phe Glu Ser Lys His Val Val Ile Pro Phe Lys Pro
 85 90 95
 Asp Gly Leu Lys Leu Gly Arg Pro Val Ala Asn Ser Asn Ser Ser Ser
 100 105 110
 Ser Ser Ser Leu Arg Gly Gly Lys Arg Val Asp Ser His Thr Phe Ser
 115 120 125
 Gln Val Arg Ser Asp Asn Gly Asn Phe Asp Ser Arg Val Leu Ser Arg
 130 135 140
 Asn His Ala Leu Leu Ser Cys Asp Pro Leu Thr Gly Lys Val Tyr Ile
 145 150 155 160
 Arg Asp Leu Lys Ser Ser Asn Gly Thr Phe Ile Asn Gly Gln Arg Ile
 165 170 175
 Gly Ser Asn Asp Val Glu Ile Lys Val Gly Asp Val Ile Asp Leu Gly
 180 185 190
 Thr Asp Ile Asp Thr Lys Ile Glu His Arg Lys Ile Ser Ala Thr Val
 195 200 205
 Glu Glu Leu Phe Val Gln Pro Leu Leu Glu Ser Pro Ile Phe Glu Asn
 210 215 220
 Glu Asp Ser Asp Asp Cys His Thr Ile Thr Glu Lys Glu Glu Ala Ala
 225 230 235 240
 Ala Ile Thr Ser His Ile Tyr Gly Asp Ser Asn Asn Leu Glu Leu Glu
 245 250 255
 Glu Val Ile Leu Gly Ser Asp Thr Glu Ile Leu Ser Gly Ile Phe Ile
 260 265 270
 Asn Asn Cys Ile Gly Thr Ser Pro Thr Leu Ser Asn Ile Ile Lys Thr
 275 280 285
 Leu Ala Met Glu Ile Pro Phe Ser Lys Cys Asp Asn Phe Lys Leu Gln

290	295	300
Ser Met Glu Asn Phe Leu Ile Asn Tyr Thr Thr His Leu Glu Tyr Thr		
305	310	315 320
Asn Lys Leu Leu Val Glu Lys Asn Asp Gln Gln Leu Val Lys Leu Gln		
	325	330 335
Asn Gly Leu Arg Arg Lys Leu Ser Gly Lys Tyr Glu Lys Ile Ile Glu		
	340	345 350
Gln Asn Arg Asn Gln Val Lys Gln Leu Glu Arg Asp His Met Phe Phe		
	355	360 365
Lys Lys Ser Phe Glu Val Lys Lys Arg Arg Asn Asn Glu Lys Gln Lys		
	370	375 380
Ser Met Glu Arg Glu Ile Glu Asp Leu Lys Thr Arg Leu Glu Val Glu		
385	390	395 400
Arg Tyr Lys Asn Ser Gln Met Met Lys Lys Asn Lys Gln Lys Glu Gln		
	405	410 415
Glu Leu Ser Thr Ala Ser Lys Lys Lys Thr Thr Glu His Asp Thr Arg		
	420	425 430
Gly Val Pro Gly Met Asn Pro Lys Gly Thr Asp Lys Phe Ser Ile Lys		
	435	440 445
Asn Thr Leu Cys Asn His Phe Thr Leu Leu Thr Phe Gly Thr Ile Ser		
450	455	460
Ile Gly Ile Ile Ala Ile Val Phe Lys Ile Leu Ser Pro Asn		
465	470	475

<210> 191

<211> 2849

<212> DNA

<213> Candida albicans

<400> 191

```

cgaacatacc tgatatcaga atagatccca atggtgctat attacgtgta agagagagat 60
ttaatttgaa tatgtccgaa gaagatgcc aagtgcattt tcagaatcta atcaatgata 120
gtgtaaatgc tttgctgcct atcgtgattg atcattttaca taatctggca caatactggc 180
ggacctgatt ggttgataat tgggtgcttca aaattttaaat ttcgtcactc taattatact 240
taacatataa atggtacctt caatatatct tcttagtaaaa aagtagcatg attttgtgtt 300
aatttgcact ttttttattt aaaaataaaa atcacagtta atttttcatg atcttgcaaaa 360
gacacgcctc cccctaattg ggcataatata acaattgtga atcagaaaaa ctcaacactt 420
taacataatg gcggggcacga aggctaaaca aacaagatta gcattgaatg ccttttttgg 480
gtacaataga acagtactga atgacatcat atatcgaaa gctcaagtgc gcagcatcgt 540
atcttgatac agttccagat gagcatcatg atttcagaaa acccaccgcc aaggttgtaa 600
cgacgcaact gactattgct acttcactag gtatttttgc tttgctttcg ttctcaattc 660
tactaaaaaa gtggcctaga ttatacgcaa gcagacgata taaagatgac gggaaccttc 720
gcttaccgtc ctggaatcag tcaagtttat tcggctgggt aacagtgttg tataagatac 780
gggacgaaca gattctggaa tatgcagggt tagatgcgta tgtgtttttg agttttttca 840

```


Phe Val Thr Met Asp Ser Val Ala Asn Ala Gln Met Ala Ala Gln Ala
 385 390 395 400
 Val Leu Asp Pro Arg Val His Tyr Phe Ile Thr Arg Leu Ala Pro Ala
 405 410 415
 Pro His Asp Ile Lys Trp Asp His Val Cys Leu Ser Arg Lys Asp Arg
 420 425 430
 Leu Thr Lys Val Tyr Ser Thr Thr Val Phe Ile Gly Leu Ser Ser Leu
 435 440 445
 Phe Leu Val Ile Pro Val Ser Tyr Leu Ala Thr Leu Leu Asn Leu Lys
 450 455 460
 Thr Leu Ser Lys Phe Trp Pro Ser Val Gly Gln Leu Leu Lys Asp His
 465 470 475 480
 Gln Trp Ala Ala Asn Ile Val Thr Gly Leu Leu Pro Thr Tyr Leu Phe
 485 490 495
 Thr Leu Leu Asn Phe Gly Ile Pro Tyr Phe Tyr Glu Tyr Leu Thr Ser
 500 505 510
 Tyr Gln Gly Leu Val Ser Tyr Ser Glu Glu Glu Ile Ser Leu Val Ser
 515 520 525
 Lys Asn Phe Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Leu
 530 535 540
 Ala Gly Thr Ala Ser Asn Tyr Trp Ala Tyr Leu Ser Asp Thr Thr Lys
 545 550 555 560
 Ile Ala Tyr Gln Leu Ala Thr Ser Val Lys Glu Phe Ser Leu Phe Tyr
 565 570 575
 Val Asp Leu Ile Ile Leu Gln Gly Ile Gly Met Phe Pro Phe Lys Leu
 580 585 590
 Leu Leu Val Gly Ser Leu Ile Gly Phe Pro Leu Val Lys Ile Lys Ala
 595 600 605
 Lys Thr Pro Arg Gln Arg Asn Glu Leu Tyr Asn Pro Pro Ile Phe Asn
 610 615 620
 Phe Gly Leu Gln Leu Pro Gln Pro Ile Leu Ile Leu Ile Ile Thr Leu
 625 630 635 640
 Ile Tyr Ser Val Met Ser Thr Lys Ile Leu Thr Ser Gly Leu Ala Tyr
 645 650 655
 Phe Ile Ile Gly Phe Tyr Val Tyr Lys Tyr Gln Leu Ile Phe Ala Thr
 660 665 670
 Asp His Leu Pro His Ser Thr Gly Lys Val Trp Pro Leu Ile Phe Arg
 675 680 685

Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln
 275 280 285
 Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser
 290 295 300
 Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Gly Leu
 305 310 315 320
 Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile
 325 330 335
 Leu Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Gln Asp His
 340 345 350
 Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp
 355 360 365
 Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Ile Leu Thr
 370 375 380
 Lys Glu Glu Ile Gln Lys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg
 385 390 395 400
 Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg
 405 410 415
 Leu Asp Asp Leu Glu Thr Thr Met Arg Met
 420 425

<210> 195
 <211> 815
 <212> DNA
 <213> Candida albicans

<400> 195
 gtcatatcaa gatctttaca gtatatagag gcaaattcct ccggagatat ggagtcgtca 60
 ttgtagttcc agagaaactg gtcttttatg gtatgaccca tatgttctat atccaaagta 120
 attggtatca tgattgcctc tccagaattg gcgtttgcct tcgtttcttg atcagtgttg 180
 agtctatatg gagacaccac ttttcggtta atgaaagtat ctcttatttt agggatatctc 240
 aatatgttga aggggttggt gtgttggtct tgcagatccg gtagaacggc gtttccaata 300
 tcctgtgcct gcgctttggt gctcggacca ttgctggcgt tgttattgct attcaaaccg 360
 gataaagatt ccacaaccat gtttgaaccc gcacgtatt tggtgttaga gataataacta 420
 tcagctccat tcatgttctc taggacattg tattcggaac cgtccatggt aacaccattt 480
 gtaagtgccg gagtattttc atgagacact gcattatctt tatagtgtgt atcagcattg 540
 ttgaaattag aaccgttcat attgaattca tcaaagagat cgttgtcata ttccgcatag 600
 ttgaccactt tagccctttt atgctgcctt gtttggttag ccattgtaaa gatggggata 660
 ccacatcttt cgtttgtcaa tctgttatga aagttagaaa tataagcttg tggaataagc 720
 tggttttggt gcgacattgt gtgctgctat gtgcctttct tctttctttt ttcaatgtac 780
 ttcattcaat aatctctatt tgtcgtattt tctaa 815

<210> 196
 <211> 104

208

<212> PRT

<213> Candida albicans

<400> 196

Met Arg His Cys Ile Ile Phe Ile Val Cys Ile Ser Ile Val Glu Ile
 1 5 10 15

Arg Thr Val His Ile Glu Phe Ile Lys Glu Ile Val Val Ile Phe Arg
 20 25 30

Ile Val Asp His Phe Ser Pro Phe Met Leu Pro Cys Leu Leu Ser His
 35 40 45

Cys Lys Asp Gly Asp Thr Ile Ile Phe Val Cys Gln Ser Val Met Lys
 50 55 60

Val Arg Asn Ile Ser Leu Trp Asn Lys Leu Val Leu Val Arg His Cys
 65 70 75 80

Val Leu Leu Cys Ala Phe Leu Leu Ser Phe Phe Asn Val Leu His Ser
 85 90 95

Ile Ile Ser Ile Cys Arg Ile Phe
 100

<210> 197

<211> 737

<212> DNA

<213> Candida albicans

<400> 197

ccacatgtca caactacttt gtgaagttgc aatgcgtgat tagtattata aaacatcata 60
 gccttgccaa ataaactcgc ttcccagaaa agacgccaaa ttaactgccg ctgttatgtg 120
 acaaaacagg gcatctcaca tattcgcgta ctggtgttct tttagctcat tccgatatta 180
 ttccaagacg gaattttcat ctagagaaaa tgcattccgtg cattttcata aaccacaca 240
 attaaaatgc cttgcgaaaa ggaggactcg tccgtgcaac tggtgaaaaa aatagacgga 300
 gcatcatcgc ttcgagtggg aaattatgga gagttttcca agctctatgg catgtagagt 360
 cgtgattgct gctgtacgct tttgcacaat attgaatctt caatctaaag aattaaattt 420
 tctaatttca atgtagaaat atttcaactg ttagtttttt atttcagggt gaatatagta 480
 cgacaaaata tcaaggaaaa atggctagag aaatcaccga catcaaaca tttttggaat 540
 tgaccagaag agctgacggt aagaccgcca ctgttaagat taacaaaaaa ttgaacaagg 600
 ccggttaagcc attcagacaa accaagttca aggttagagg ctcttcttct ttgtacactt 660
 tggttatcaa cgtatgtggt aaggctaaga aattgatcca atctttgcca ccaactttga 720
 aggttaacag attataa 737

<210> 198

<211> 78

<212> PRT

<213> Candida albicans

<400> 198

Met Ala Arg Glu Ile Thr Asp Ile Lys Gln Phe Leu Glu Leu Thr Arg
 1 5 10 15

210

Ala Pro Leu Ser Lys Glu Leu Arg Ala Gln Tyr Gly Ile Lys Ala Leu
 35 40 45
 Pro Ile Arg Arg Asp Asp Glu Val Leu Val Val Arg Gly Ser Lys Lys
 50 55 60
 Gly Gln Glu Gly Lys Ile Ser Ser Val Tyr Arg Leu Lys Phe Ala Val
 65 70 75 80
 Gln Val Asp Lys Val Thr Lys Glu Lys Val Asn Gly Ala Ser Val Pro
 85 90 95
 Ile Asn Leu His Pro Ser Lys Leu Val Ile Thr Lys Leu His Leu Asp
 100 105 110
 Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Leu Glu
 115 120 125

<210> 201
 <211> 1376
 <212> DNA
 <213> Candida albicans

<400> 201
 actttttgtc tgctgctggt cgtttgtcct tcgtttttaa attgcgctag acaagtaaac 60
 agggattgct taagaatcaa agtagcttaa ctctaaagta ttattttcct cagttgtggg 120
 cccatgtgtt ggaggggaagg aatatattga aatgtaaatg ttcttaagtt cggttgaact 180
 tggatattgt tacaagagtt ctagtctttg ataccatttt tacgcaatta caaccgcatt 240
 atttaccttt tcatcttcag ttttacgggt cagttttattc tgttacgaaa gaactatggt 300
 gattcaaagg cgaagtgcgt aggattgtaa ctctatatc tttaggatac ttacaatttt 360
 gtactgtttt caagaccact gtaaccgata ataaaccgga ggacacattt taaccacta 420
 tttttttcag aagatcagat gcgagagctc gaagcataag tataatacta acgtttcaaa 480
 acatagtaat taggtaaaaa atgactcgct ctcccgttt agctgatgct ttgaatgcca 540
 ttaataacgc cgaaaagacc ggtaaacgct aggttctatt gagaccttct tccaagggtta 600
 tcatcaagtt tttacaagtt atgcaaaaagc atgggtatgtt ccaactattt ttcaatattt 660
 tcacatgtgt ttcaatttct gcttattttt aaatgttacc acgagggttg tccaagttca 720
 atgttgcgca actctaacga agaaataatt attgccattg ttttttactc cgggctgata 780
 actagatggt gtgatcgggc agtatactaa tttatactgg acaaagactc gtaaaagatg 840
 ttctttgtgc ttagtcccat actgtttttt aagtgtccgg gatatttaat cccatgtgga 900
 aatgcttctt acacggttat ggattacacc tcatgtgtag ctactatata cattaccggt 960
 tacttttcct caaaatctca ctcttâaaat tttcaatggc aaaattcttc cgcacaactt 1020
 agacaacatt ttcttgtttt ttatgaagta agcaaaaatt tcgaatcaac aacgctccat 1080
 gagattcttc aatactaaca tttactcctt atttagggtta cattggcgaa ttcgaaatata 1140
 ttgacgacca cagatctggt aagattgtcg tccaactgaa cggtagattg aacaaatgtg 1200
 gtgttatttc cccaagattt aacgttaaga ttggtgacat tgaaaaatgg accgccaact 1260
 tattgccagc cagacaattc ggttacgtta ttttgactac ttctgcgggt attatggacc 1320
 atgaggaagc tagaagaaag cacgtttccg gtaaaatctt gggttttgtc tattaa 1376

<210> 202
 <211> 130
 <212> PRT
 <213> Candida albicans

<400> 202

211

Met Thr Arg Ser Ser Val Leu Ala Asp Ala Leu Asn Ala Ile Asn Asn
 1 5 10 15
 Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Leu Arg Pro Ser Ser Lys
 20 25 30
 Val Ile Ile Lys Phe Leu Gln Val Met Gln Lys His Gly Tyr Ile Gly
 35 40 45
 Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln
 50 55 60
 Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asn
 65 70 75 80
 Val Lys Ile Gly Asp Ile Glu Lys Trp Thr Ala Asn Leu Leu Pro Ala
 85 90 95
 Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp
 100 105 110
 His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe
 115 120 125
 Val Tyr
 130

<210> 203

<211> 1340

<212> DNA

<213> Candida albicans

<400> 203

ccctcaaccc gcattttgct gagaattttc accaaggccc taggtgatat tagattccac 60
 ctgactaatt gcattacagc cgacccaagg caatatcagt ttaataaaat atcatgtatc 120
 tcaccctctt cttggtatta gtaaagagac gcctgatctt gtaacagtgg tgaagattgt 180
 actagagcag aatcaagaat ttaaaaagtg taaaggcaag gcagaggcga tgtacataaa 240
 acttcgaagt aagaaatatt taatagttct cgccacatca ctatgcagct atataaaaac 300
 tactataaac gtttgttttg ttctttacgc acaatatcct tgcctagaaa tcgtttttga 360
 aattttaaatt tttattacca tttatttgat tcgccttcag aaaaatatgg aagagtgcac 420
 atttataaaag gactatttca gcatatagta aaagtcaggt tatttggtta tttgcgatat 480
 cagagtaact taaactaact atgcagggca cttttaaaag gttttacat cccacgctta 540
 cgcggatgtc cttcttggat aaattcctca agcctatgat ggcaacggct tccccaaagg 600
 aataccagat caaacaactg gtcaagccaa taggcttaac acaagcacca aggaaaagca 660
 ccaaatactc ccagggggac tctttgaggg atatgtttga ttcggaaaag acaaaccaca 720
 gagttaaaga gttggccgtt gaattcagca aatctggact ttatgacgtg caagtcttcc 780
 aaaagacaaa ggggaaattg tttatagctc cagtttcata ttggaaagaa gataaagctt 840
 tgttttttcc tcatattgata ggaacggcaa tggatggtac gaaacaacag aatatcgagg 900
 atatgttaag gggtaaaacc agtatagtga ggttatttag tacagcatct ggcgataagt 960
 tgagtagttc atacttccaa ggaatcgtag acgataacaa aaaaactgac tacttgactg 1020
 aagctgatgc gcgtttaagt ttaaattgaca gtaacgtcca aatcatcgag gtcaatcttg 1080
 tagaaaacgc tgtgaaaagt gctctagtga aaacgcttgc tcgttgggcc aatcgcgttc 1140
 catcctggcg ccagccattt tatttcgaat gttctagagg ccaatggcca ttttcgctca 1200
 gggaagagct cttttgcaat aatgtctttt ctggatacgt ctttcttgtg gaccagcagt 1260
 taaaaattag gtgggcagct tgcggggagg ctactccatc tgaaaaggaa gcattgtgga 1320

216

<400> 208

Met Ser Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg
 1 5 10 15

Leu Leu Asn Thr Asn Val Asp Gly Asn Ile Lys Ile Val Tyr Ala Leu
 20 25 30

Thr Thr Ile Lys Gly Val Gly Arg Arg Tyr Ser Asn Leu Val Cys Lys
 35 40 45

Lys Ala Asp Val Asp Leu His Lys Arg Ala Gly Glu Leu Thr Gln Glu
 50 55 60

Glu Leu Glu Arg Ile Val Gln Ile Met Gln Asn Pro Thr His Tyr Lys
 65 70 75 80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Asn Asp Ile Thr Asp Gly Lys
 85 90 95

Asp Tyr His Thr Leu Ala Asn Asn Val Glu Ser Lys Leu Arg Asp Asp
 100 105 110

Leu Glu Arg Leu Lys Lys Ile Arg Ala His Arg Gly Ile Arg His Phe
 115 120 125

Trp Gly Leu Arg Val Arg Gly Gln His Thr Lys Thr Thr Gly Arg Arg
 130 135 140

Arg Ala
 145

<210> 209

<211> 1268

<212> DNA

<213> Candida albicans

<400> 209

tatattattt tttcccttct gggttctttt ctctcttttc ttgtttacct tttttgcttt 60
 ttcataaaat aattttctcta gatttgaaga cagcattttt gtacatccat acaccataca 120
 ccatacacca tagcaccagt acactatatt tttatgaatt ttactaagaa ttattcctgc 180
 aggagctcca ctgaaaaaaaa aagagcagca tggatgtccg gtagaagtgc tactgagtaa 240
 atgggaagga cgcggtagat ccagtgtgga atcaagggtg tgccgggtgtg aagccgcctc 300
 ggcgggtctg actctccagg ccggagtgat gattgccacg ctgaacgtaa cacagtttca 360
 caataccagt gtectcatta gtgagttcca atgtatagtt agtagtggtta ttttgatata 420
 tgtgagtggg agcagatttg aacttagtta gttgtattcg cctttgagga aaccaagcaa 480
 aaaaccgata tagactaatc atggctgttg gtaagaataa gagactatcc agaggtaaga 540
 agggtttgaa gaagaaggtc gttgacccat ttaccagaaa ggaatgggtc gatattaaag 600
 ccccatccac ttttgaaaac agaaatgttg gtaagacttt agttaacaag tccactgggt 660
 tgaagaatgc ttccgatgct ttgaagggtta gagttgtcga agtttgtttg gctgacttgc 720
 aaggttctga agaccattct ttcagaaaagg tcaagttgag agtcgatgaa gttcaaggta 780
 agaacttggt gaccaacttc cacggtagtg acttcactac cgacaaattg agatcaatgg 840
 tcagaaaatg gcaaaacttt atcgaagcta atgttaccgt taagacttcc gatgattacg 900
 ttttgagaat ctttgctatt gccttcacca gaagcaagc taaccaagtt aagagacact 960
 cttacgctca atcttcccac atcagagcta tcagaaaagt tatttctgaa atcttgacca 1020
 gagaagttca aaactctact ttggctcaat tgacctccaa attgattcca gaagttatca 1080

Gly Lys Lys Val Ser Gly Phe Lys Asp Glu Val Leu Glu Thr Val
 245 250 255

<210> 211
 <211> 2042
 <212> DNA
 <213> Candida albicans

<400> 211
 ttaataggggt tagccacccat tgtctcgaac atgttcacag gctcggagct tgtggcgggt 60
 gcctcgctta ctggagtacc atttagcgggt gtgtttgaag ctaacgagtt catcttcaat 120
 ctttatttcc acttctttac aagctttctg cttttctcta tgacgtcttt cccaaaacac 180
 tacctcttga cagcacttgt tgttttcggt tttctctaag aatatcacta ttttcaacttt 240
 tttcaccttt tccaccatta cgtcggtaag caacagcatt acgccggcct caccttagag 300
 gggaagaata agggatcttt ggaactgaag gaaaataagg gagagggagg aaacaaggag 360
 gcggtgaaaag gggatcgaca gggattttaa agccactcat ggagtcgtat tcctagcatg 420
 attagattac cggagttagg aagaggatct gcaatagaag aggagacaac taaaaagaa 480
 ctgttaatta agagaagaag atgaagcaat tcaagttggt taatgcggtt tccgcatcat 540
 ttgtgcttat tggcttagtg ttggccaatt cagattcagt gttcgacaag tggacgcagg 600
 aagacctggc cgattattta cgtgataata agaagagctt ggaaaagtac gctacagact 660
 ccattgagga cttgaaaacg gaggcacgc aggtatggga caaacacgcg cagcccaaac 720
 catgggtggca ggtgtggtct agtgacagc gtacgctgag caacagtaac cccggatggt 780
 ttggttatac tggttcttcg gatcaccag tttctgactg gctctttgac acctggtcca 840
 cagacagtct acgtaacttc ttgaagaaaa acggcgtgga tgttgacgac gctaaggctt 900
 ccaaggactc gctggtgaag actgctaagg agaacttcaa caagatttcc aaatctttga 960
 agtcgctcggg atactatcct tctagctctt actttgatag ctggtcaacc aaagatttgc 1020
 aaaactgggt gaatgacaat ggtatcgact acgacaaggc agttcaaaagc aaggacgagc 1080
 tagttcagaa agtcaaggaa aacatctacc gaacttcaga aaaggcagaa cagcagcgtc 1140
 tgggtttgct agaaagcttg gatttggctc accaacaat attagacaca tcgggacaaa 1200
 taaaagacac tgtatttgac aagtggctc gtgatcagtt aaccaattgg ttggagagcc 1260
 acaagggtcaa tattgacaag aacatggcca agaaacacga ctatttgggtt agaatggcca 1320
 aagaaaattc tgccaatttg aaagatgata tctactggta cctggactat atgaaaagag 1380
 agtcttctcc atttttgacc aagaccccag aatacgttgg ttccgtttgg gactcttcta 1440
 aaaatttcct cacaatttg tactccaagt tcagaggttaa gactgacaat gtgatcaatg 1500
 atactttttt gggtggccta gactcttggc caaaggacaa attgaaaatg tttttagatg 1560
 ctcgtggtat taagtactca atgctgtcta ctgaacatca attgagagaa ttagtcaaaa 1620
 aatccagaaa cgaaaaactc aagatcctgc caaaagacta ccaaaaatac tttgacaaca 1680
 gtaactggtc tttggatgac ataaagggtt gggttgctga caaaaaggac gacttccaag 1740
 attctcagac ttactccaca attatgcagg attttgacaa ggtttccaaa aacacaaatg 1800
 atgctaagga ccaaatcgct aagacctggg caaatacctt tcagagctgg tctcaagaag 1860
 acctattgca gtacctaaaa tcattcgggtg ttccggttaa acagacttct acgaaggacg 1920
 acttaataca cttggccaag cagaatacgc aatgggtgtt cggcactggt aaggagcctg 1980
 cttacaagag gtacctacat aacgttaaaa actggtcgaa aagcatatta gggttcaact 2040
 aa 2042

<210> 212
 <211> 513
 <212> PRT
 <213> Candida albicans

<400> 212
 Met Lys Gln Phe Lys Leu Val Asn Ala Val Ser Ala Ser Phe Val Leu
 1 5 10 15

Ile Gly Leu Val Leu Ala Asn Ser Asp Ser Val Phe Asp Lys Trp Thr
 20 25 30
 Gln Glu Asp Leu Ala Asp Tyr Leu Arg Asp Asn Lys Lys Ser Leu Glu
 35 40 45
 Lys Tyr Ala Thr Asp Ser Ile Glu Asp Leu Lys Thr Glu Ala Ser Gln
 50 55 60
 Val Trp Asp Lys His Ala Gln Pro Lys Pro Trp Trp Gln Val Trp Ser
 65 70 75 80
 Ser Asp Ser Ser Ser Val Ser Asn Ser Asn Pro Gly Trp Phe Gly Tyr
 85 90 95
 Thr Gly Ser Ser Asp His Pro Val Ser Asp Trp Leu Phe Asp Thr Trp
 100 105 110
 Ser Thr Asp Ser Leu Arg Asn Phe Leu Lys Lys Asn Gly Val Asp Val
 115 120 125
 Asp Asp Ala Lys Ala Ser Lys Asp Ser Leu Val Lys Thr Ala Lys Glu
 130 135 140
 Asn Phe Asn Lys Ile Ser Lys Ser Leu Lys Ser Ser Gly Tyr Tyr Pro
 145 150 155 160
 Ser Ser Ser Tyr Phe Asp Ser Trp Ser Thr Lys Asp Leu Gln Asn Trp
 165 170 175
 Leu Asn Asp Asn Gly Ile Asp Tyr Asp Lys Ala Val Gln Ser Lys Asp
 180 185 190
 Glu Leu Val Gln Lys Val Lys Glu Asn Ile Tyr Arg Thr Ser Glu Lys
 195 200 205
 Ala Glu Gln Gln Arg Leu Gly Leu Leu Glu Ser Leu Asp Leu Ala His
 210 215 220
 Gln Gln Ile Leu Asp Thr Ser Gly Gln Ile Lys Asp Thr Val Phe Asp
 225 230 235 240
 Lys Trp Ser Ser Asp Gln Leu Thr Asn Trp Leu Glu Ser His Lys Val
 245 250 255
 Asn Ile Asp Lys Asn Met Ala Lys Lys His Asp Tyr Leu Val Arg Met
 260 265 270
 Ala Lys Glu Asn Ser Ala Asn Leu Lys Asp Asp Ile Tyr Trp Tyr Leu
 275 280 285
 Asp Tyr Met Lys Arg Glu Ser Ser Pro Phe Leu Thr Lys Thr Pro Glu
 290 295 300
 Tyr Val Gly Ser Val Trp Asp Ser Ser Lys Asn Phe Leu Thr Asn Leu
 305 310 315 320


```

ttaatgacac tcacttttgt aaggctcgaca ggaatgatca cgttagtccc agttgtaacg 660
taacattcaa tgaattaaat gccataaatg aaaacattag agatgatcct tcggcggttat 720
taaaatctga tttcttcaaa tactttcggc tggatttata caagcaatgt tcattttggg 780
acgccaacga tgggtctgtgc ttaaaccgcg cttgctctgt tgatgtcgta gaggactggg 840
atacactgcc tgagtactgg cagcctgaga tcttgggtag tttcaataat gatacaatga 900
aggaagcgga tgatagcgat gacgaatgta agttcttaga tcaactatgt caaaccagta 960
aaaaacctgt agatatcgaa gacaccatca actactgtga tgtaaatgac tttaacggta 1020
aaaacgcggt tctgattgat ttaacagcaa atccggaacg atttacagggt tatgggtggta 1080
agcaagctgg tcaaatttgg tctactatct accaagacaa ctgttttaca attggcgaaa 1140
ctgggtgaatc attggccaaa gatgcatttt atagacttgt atccggtttc catgcctcta 1200
tcgggtactca cttatcaaag gaatttttga acacgaaaac tggtaaatgg gagcccaatc 1260
tggattttgtt tatggcaaga atcggaact ttcttgatag agtgacaaac atgtatttca 1320
attatgctgt tgtagctaag gctctctgga aaattcaacc atattttacca gaattttcat 1380
tctgtgatct agtcaataaa gaaatcaaaa acaaaatgga taacgttatt tcccagctgg 1440
acacaaaaat ttttaacgaa gacttagttt ttgccaacga cctaagtttg actttgaagg 1500
acgaattcag atctcgcttc aagaatgtca cgaagattat ggattgtgtg caatgtgata 1560
gatgtagatt gtggggcaaa attcaaacta ccggttacgc aactgccttg aaaattttgt 1620
ttgaaatcaa cgacgctgat gaattcacca acaacatat tgttggttaag ttaaccaa 1680
atgagttgat tgcactatta cagactttcg gtagattatc tgaatctatt gaatctgtta 1740
acatgttcga aaaaatgtac gggaaaagggt taaacggttc tgaaaacagg ttaagctcat 1800
tcttccaaaa taacttcttc aacattttga aggaggcagg caaatcgatt cgttacacca 1860
tagagaacat caattccact aaagaaggaa agaaaaagac taacaattct caatcacatg 1920
tatttgatga tttaaaaatg cccaaagcag aaatagttcc aaggccctct aacggtacag 1980
taaataaatg gaagaaagct tggaatactg aagttaacaa cgtttttagaa gcattcagat 2040
ttatttatag aagctatttg gatttaccca ggaacatctg ggaattatct ttgatgaagg 2100
tatacaaat ttggaataaa ttcatecggtg ttgctgatta cgttagttag gagacacgag 2160
agcctatttc ctataagcta gatatacaat aa 2192

```

<210> 214

<211> 563

<212> PRT

<213> Candida albicans

<400> 214

```

Met Arg Leu Arg Thr Ala Ile Ala Thr Leu Cys Leu Thr Ala Phe Thr
  1                      5                      10                      15

```

```

Ser Ala Thr Ser Asn Asn Ser Tyr Ile Ala Thr Asp Gln Thr Gln Asn
      20                      25                      30

```

```

Ala Phe Asn Asp Thr His Phe Cys Lys Val Asp Arg Asn Asp His Val
      35                      40                      45

```

```

Ser Pro Ser Cys Asn Val Thr Phe Asn Glu Leu Asn Ala Ile Asn Glu
      50                      55                      60

```

```

Asn Ile Arg Asp Asp Leu Ser Ala Leu Leu Lys Ser Asp Phe Phe Lys
      65                      70                      75                      80

```

```

Tyr Phe Arg Leu Asp Leu Tyr Lys Gln Cys Ser Phe Trp Asp Ala Asn
      85                      90                      95

```

```

Asp Gly Leu Cys Leu Asn Arg Ala Cys Ser Val Asp Val Val Glu Asp
      100                      105                      110

```

```

Trp Asp Thr Leu Pro Glu Tyr Trp Gln Pro Glu Ile Leu Gly Ser Phe

```

115					120					125					
Asn	Asn	Asp	Thr	Met	Lys	Glu	Ala	Asp	Asp	Ser	Asp	Asp	Glu	Cys	Lys
130					135					140					
Phe	Leu	Asp	Gln	Leu	Cys	Gln	Thr	Ser	Lys	Lys	Pro	Val	Asp	Ile	Glu
145					150					155					160
Asp	Thr	Ile	Asn	Tyr	Cys	Asp	Val	Asn	Asp	Phe	Asn	Gly	Lys	Asn	Ala
				165					170					175	
Val	Leu	Ile	Asp	Leu	Thr	Ala	Asn	Pro	Glu	Arg	Phe	Thr	Gly	Tyr	Gly
			180					185					190		
Gly	Lys	Gln	Ala	Gly	Gln	Ile	Trp	Ser	Thr	Ile	Tyr	Gln	Asp	Asn	Cys
		195					200					205			
Phe	Thr	Ile	Gly	Glu	Thr	Gly	Glu	Ser	Leu	Ala	Lys	Asp	Ala	Phe	Tyr
	210					215					220				
Arg	Leu	Val	Ser	Gly	Phe	His	Ala	Ser	Ile	Gly	Thr	His	Leu	Ser	Lys
225					230					235					240
Glu	Tyr	Leu	Asn	Thr	Lys	Thr	Gly	Lys	Trp	Glu	Pro	Asn	Leu	Asp	Leu
				245					250					255	
Phe	Met	Ala	Arg	Ile	Gly	Asn	Phe	Pro	Asp	Arg	Val	Thr	Asn	Met	Tyr
			260					265					270		
Phe	Asn	Tyr	Ala	Val	Val	Ala	Lys	Ala	Leu	Trp	Lys	Ile	Gln	Pro	Tyr
		275					280					285			
Leu	Pro	Glu	Phe	Ser	Phe	Cys	Asp	Leu	Val	Asn	Lys	Glu	Ile	Lys	Asn
	290					295					300				
Lys	Met	Asp	Asn	Val	Ile	Ser	Gln	Leu	Asp	Thr	Lys	Ile	Phe	Asn	Glu
305					310					315					320
Asp	Leu	Val	Phe	Ala	Asn	Asp	Leu	Ser	Leu	Thr	Leu	Lys	Asp	Glu	Phe
				325					330					335	
Arg	Ser	Arg	Phe	Lys	Asn	Val	Thr	Lys	Ile	Met	Asp	Cys	Val	Gln	Cys
			340					345					350		
Asp	Arg	Cys	Arg	Leu	Trp	Gly	Lys	Ile	Gln	Thr	Thr	Gly	Tyr	Ala	Thr
		355					360					365			
Ala	Leu	Lys	Ile	Leu	Phe	Glu	Ile	Asn	Asp	Ala	Asp	Glu	Phe	Thr	Lys
	370					375					380				
Gln	His	Ile	Val	Gly	Lys	Leu	Thr	Lys	Tyr	Glu	Leu	Ile	Ala	Leu	Leu
385					390					395					400
Gln	Thr	Phe	Gly	Arg	Leu	Ser	Glu	Ser	Ile	Glu	Ser	Val	Asn	Met	Phe
				405					410					415	
Glu	Lys	Met	Tyr	Gly	Lys	Arg	Leu	Asn	Gly	Ser	Glu	Asn	Arg	Leu	Ser

Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg
 130 135 140

<210> 221
 <211> 707
 <212> DNA
 <213> Candida albicans

<400> 221
 gtcccatcat tctttacacc tcgtactgta ttcgatgatca tctatccatt ttacataccg 60
 ctcccttttaa gatacgttta ttcgtaactc ccattttacca atcactatga gccgtccacg 120
 tttccaaaaa aacctaataca tatgatgcaa acctccaatg agactcaacg taacatgcaa 180
 gtaaatacag aagggttaaga gatagttgtc ttaaaggggt accgaaagca tttaggggag 240
 gcttaaggga ggggtgccgat cctatgaagt attaatacgt aatgccaaaa ggaattgttg 300
 aacatctgaa gtggatagat taatcgtaca gtaatcgtac agtactatgt cttactgatg 360
 tcgggaatct caggggcgac cgccccggc tagaattatc tatataacgg taaaaagaat 420
 aaaactctat tctagttctc gccatttacc ttgactttaa tgaaccaata aaagaaattt 480
 ctacaaccaa gacatccaga atgaatacag accaacaaaa agtgagcgaa atatttcaga 540
 gctcaaagga aaaattgcag ggcgatgcaa aggtagttag tgacgctttt aagaaaatgg 600
 ctagtcaaga caaggacggc aagactaccg atgctgatga aagtgaaaaa cacaactatc 660
 aagagcaata caacaagctc aaaggggcgg ggcataagaa ggagtag 707

<210> 222
 <211> 68
 <212> PRT
 <213> Candida albicans

<400> 222
 Met Asn Thr Asp Gln Gln Lys Val Ser Glu Ile Phe Gln Ser Ser Lys
 1 5 10 15
 Glu Lys Leu Gln Gly Asp Ala Lys Val Val Ser Asp Ala Phe Lys Lys
 20 25 30
 Met Ala Ser Gln Asp Lys Asp Gly Lys Thr Thr Asp Ala Asp Glu Ser
 35 40 45
 Glu Lys His Asn Tyr Gln Glu Gln Tyr Asn Lys Leu Lys Gly Ala Gly
 50 55 60
 His Lys Lys Glu
 65

<210> 223
 <211> 1877
 <212> DNA
 <213> Candida albicans

<400> 223
 ggttcgatac aacacttggtg ctggctggta tatcaaccat gggtagctca gcatattgat 60
 tcgatgtggc agtgtacgag agccattctg tatcgttcga caaagtttgc atgacttcat 120
 gttgtttcgt agcagtattc gttgggtccag atgcaggaat gctgggttata aagtttgttg 180

```

ttcctggtcc acattcatct ttggatggcg ttgttggtgg cgaatttgtc ttaggccttt 240
tgttcgcgat gtgcttttgg atagcctgga atacgaaatc tttgtcttcc tgtaaagtcg 300
ccgcttccct taaccatttg tgctcccttc ttaagttatg tgacggcttc gtcaccatta 360
ccgccttggtg tgtacgtgta tgatttttta aatatataca acaataatct gtattttttc 420
ctttcctcta gccaatgact ccaagctggc tgataaaaac aaactaaacg gtaaagccac 480
aaatccgaaa tgtatcacca atgatcaccc agcctgctaa gtgccctcta ttgatccgta 540
tatcagcttt tagatcaggc tcgagtttct tgttatatgt gcattgcaaa agcataaaca 600
aatcctggca gccgaagccg ggcaatccac ttcgaaacgc acggctgaac tatataaata 660
taaaggacat gtggagagaa gcttctcttc cttcacattt cgcatttcat gatctaaagt 720
ggttctttca caatagaaga gcaccaacac gaaatatggc tgcgggtggg aataactgga 780
gcatgtggct gcgaatgtca cgggtccacc tcaggcagat cacgaagtct ctggaccgaa 840
cgctgatcag tttgagccat ggggaattttt cccaccaata taatcgcaat atttttgtca 900
cttgggtggaa gagcctattt gaggcttcta cagcttttag gaggggcaagt ggtttaacgg 960
tatctcctct cagcaggaga ggaatcgcaa ggtttgacca tttcagacct gttcccaatg 1020
tcagtaaatt tgcttctttt cccagagtgc ccaaaggagc cccaaggggc ctttttacca 1080
actggaatat gactacatca aagagattat tagggcagag agcttattcg acttcagta 1140
tcaaatttac ccaagaagcc gtgaataaca tgactatata tttgaggtgt tttttcaact 1200
cactaggcgg attaaatcag tgctccctct ctaattcctg caaagcttat cagaatgcgt 1260
ctaagtgtac ctctaaacag gatcacgtcc aaccagttgc ccttaagaag ttatctcaaa 1320
aggatatcaa tttcattcgt aatttagaac tatttaagat aatgaagacc cagaatgaag 1380
tcgttgatga aacaagcgca tattacatgg aaaaaccagg ttcctatatt gaatttacca 1440
tttcagaatt taacgttaat gggacattct ccgcaccttt gtcattttta gatccttctt 1500
tgttagcgga tttggatgaa atgattagaa attacaaata cgaattaaaa tcaatatata 1560
gtagtgttga catgatcttg cagaattatg gatcattgcc gataactttt catcgaaata 1620
agattcgaat acattttcca aactcaactg tgggtggaaac agaaaaacta attgcaggtc 1680
tgaatattgc tacgggtggt atttacgcag atacgtctcc cgatatcagt ctagaaggta 1740
caaatttgaa tgctctggtt aatgttgaca attcaggaag cgtatggtct tttgttaagg 1800
agccctcggt tcctcttagg agcgcttttt cacctatttt atcagatgca tcctatgata 1860
cttatgaatt ggtctag 1877

```

<210> 224

<211> 458

<212> PRT

<213> Candida albicans

<400> 224

```

Met Ile Thr Gln Pro Ala Lys Cys Pro Leu Leu Ile Arg Ile Ser Ala
  1             5             10             15

Phe Arg Ser Gly Ser Ser Phe Leu Leu Tyr Val His Cys Lys Ser Ile
      20             25             30

Asn Lys Ser Trp Gln Pro Lys Pro Gly Asn Pro Leu Arg Asn Ala Arg
      35             40             45

Leu Asn Tyr Ile Asn Ile Lys Asp Met Trp Arg Glu Ala Ser Leu Pro
      50             55             60

Ser His Phe Ala Phe His Asp Leu Lys Trp Phe Phe His Asn Arg Arg
      65             70             75             80

Ala Pro Thr Arg Asn Met Ala Val Gly Gly Asn Asn Trp Ser Met Trp
      85             90             95

Leu Arg Met Ser Arg Val His Leu Arg Gln Ile Thr Lys Ser Leu Asp
      100            105            110

```


Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr

50

55

60

Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu
65 70 75 80

Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn
85 90 95

Pro Ser Gln Arg Pro Gln Arg Arg Tyr
100 105

<210> 227

<211> 3998

<212> DNA

<213> Candida albicans

<400> 227

```

cccttcgcta aatcattaag aggtcattca tgaagttaat tcagcaccaa agttggactg 60
ttagacacga gatacacatt gcagtcacaa tgtgcagatt tttagataa ttgtcgctgc 120
acaagactgc cctccccgtc ctacagacaga cacaaaatta gattttacgt ttacataaag 180
atgtacataa cttgaaaaaa cggttaatccc tcttaaattt agaccttgta agtcttcctg 240
gccactcttt gtgatatatt gtagtgcaat atattgattc gttcttctta tttctttggt 300
cttaggcatt tccgcttttag aaaattcggt ggggtgggttc tgcgacgggt atccccctcg 360
attttgcata atgatcttca attctacaac taaaatcaag tagatacagg aaaatattcc 420
ataaattata gtgtaaatcg cctgtatac accttatcgt ttcactctcag gcaagttaaa 480
gcatttggga aacgtgctag atgacagaag aagatagaaa gctcactgta gagacagaaa 540
cagttgaggc acccggtggca aataatcttt tattgtcgaa taacagtaat gtagtagcac 600
ctaactcttc tattccctct gcctccacat ctacctctcc gctacacagg gaaatagttg 660
atgattctgt cgctactgct aacaccacca gcaacgttgt acagcataat ttgcccacca 720
tagataacaa tttaatggat tccgatgcca cgtcacataa tcaagatcat tggcattcag 780
acataaacag ggcaggaaca tcaatgtcaa cgagtgatat cccaacagat ttacatttag 840
aacatatcgg ctctgtttca tcaactaata ataatagtaa caatgcccta atcaaccaca 900
accctctgtc atctcatctt tccaatccgt catcttcatt acgaaacaag aagagctctt 960
tgttggtagc ttctaaccct gcgtttgctt cagatgttga actctcgaag aagaaacctg 1020
ccgtcatctc caataatatg cctacaagta acattgccct ttatcaaaca gcgagatcgg 1080
cgaatattca tgggccatca tcaacttccg catctaaagc gttcagaaaag gcttcggcct 1140
tctccaataa cagcggcacc agcactagta ataacatcgg ctcgaaatac cctccagctc 1200
ctcttttacc tctaccttca ctatcacaa aaaataagcc aaaaataata gagaggccca 1260
caatgcacgt cactaattca agagaaatac ttttaggtga aaacctgtta gatgatacaa 1320
aggcgaagaa tgctcccgcg aattcaacca cacacgataa tgggtccagta gcaaagtatg 1380
ggctgcgtat accgaatcac tcgaacgcag atgataatga aaataacaac aaaatgaaga 1440
agaataaaaa cattaatagt gggaaaaaatg aacgtaatga tgacaccagc aaaatatgca 1500
ctacatctac taaaacagcg ccttcaaccg cacctttggg cagtacagac aatactcagg 1560
ctctcactgc tagtgtctcc agcagtaatg ctgacaatca caataataac aagaagaaaa 1620
ccagcagcaa caacaacggc aataacagta atagtgcac caataaaaacc aatgccgata 1680
tcaagaattc taacgccgac ttgagcgctt ctacctctaa caataatgca ataaatgacg 1740
actcacatga gagtaattca gaaaaaccaa caaaggcgga ttttttcgct gcaaggctgg 1800
ctacagctgt aggtgaaaat gaaattagtg attctgagga aacatttggt tatgaatcgg 1860
cagctaattc gactaaaaac ctaatatctt ctgactcctc cagccagcag cagcagcagc 1920
aacagcaacc tccaaaacaa cagcaacagc aacaaaatca tggaataacc tcaaagataa 1980
gcgccccatt gctaaacaat aacaaaaaat tattaagccg actgaaaaat tcaagacata 2040
ttagcactgg tgccatattg aataacacaa tccgcgactat aagcacaaat ccgaacttga 2100
attctaattg gatgcagaac aataacaatc tgatgtcggg acacaatcac ctggacgagt 2160
tgagcagtat aaaacaggag ccaccgcac aattgcagca gcagcaacca ccaatggatg 2220
tacaatcggg agattcgtat acctctgaca acccagacag caatgttatt gccaaagtcg 2280

```

<400> 228																
Met	Thr	Glu	Glu	Asp	Arg	Lys	Leu	Thr	Val	Glu	Thr	Glu	Thr	Val	Glu	
1				5					10					15		
Ala	Pro	Val	Ala	Asn	Asn	Leu	Leu	Leu	Ser	Asn	Asn	Ser	Asn	Val	Val	
			20					25					30			
Ala	Pro	Asn	Pro	Ser	Ile	Pro	Ser	Ala	Ser	Thr	Ser	Thr	Ser	Pro	Leu	
		35					40					45				
His	Arg	Glu	Ile	Val	Asp	Asp	Ser	Val	Ala	Thr	Ala	Asn	Thr	Thr	Ser	
	50					55					60					
Asn	Val	Val	Gln	His	Asn	Leu	Pro	Thr	Ile	Asp	Asn	Asn	Leu	Met	Asp	
65					70					75					80	
Ser	Asp	Ala	Thr	Ser	His	Asn	Gln	Asp	His	Trp	His	Ser	Asp	Ile	Asn	
				85					90					95		
Arg	Ala	Gly	Thr	Ser	Met	Ser	Thr	Ser	Asp	Ile	Pro	Thr	Asp	Leu	His	
			100					105					110			

Glu Ser Asn Ser Glu Lys Pro Thr Lys Ala Asp Phe Phe Ala Ala Arg
 420 425 430
 Leu Ala Thr Ala Val Gly Glu Asn Glu Ile Ser Asp Ser Glu Glu Thr
 435 440 445
 Phe Val Tyr Glu Ser Ala Ala Asn Ser Thr Lys Asn Leu Ile Phe Pro
 450 455 460
 Asp Ser Ser Ser Gln Gln Gln Gln Gln Gln Gln Pro Pro Lys Gln
 465 470 475 480
 Gln Gln Gln Gln Gln Asn His Gly Ile Thr Ser Lys Ile Ser Ala Pro
 485 490 495
 Leu Leu Asn Asn Asn Lys Lys Leu Leu Ser Arg Leu Lys Asn Ser Arg
 500 505 510
 His Ile Ser Thr Gly Ala Ile Leu Asn Asn Thr Ile Ala Thr Ile Ser
 515 520 525
 Thr Asn Pro Asn Leu Asn Ser Asn Val Met Gln Asn Asn Asn Asn Leu
 530 535 540
 Met Ser Gly His Asn His Leu Asp Glu Leu Ser Ser Ile Lys Gln Glu
 545 550 555 560
 Pro Pro His Gln Leu Gln Gln Gln Gln Pro Pro Met Asp Val Gln Ser
 565 570 575
 Val Asp Ser Tyr Thr Ser Asp Asn Pro Asp Ser Asn Val Ile Ala Lys
 580 585 590
 Ser Pro Asp Lys Arg Ser Ser Leu Val Ser Leu Ser Lys Val Ser Pro
 595 600 605
 His Leu Leu Ser Ser Thr Ser Ser Asn Gly Asn Thr Ile Ser Cys Pro
 610 615 620
 Asn Val Ala Thr Asn Ser Gln Glu Leu Glu Pro Asn Asn Asp Ile Ser
 625 630 635 640
 Thr Lys Lys Ser Leu Ser Asn Ser Thr Leu Arg His Ser Ser Ala Asn
 645 650 655
 Arg Asn Ser Asn Tyr Gly Asp Asn Lys Arg Pro Leu Arg Thr Thr Val
 660 665 670
 Ser Lys Ile Phe Asp Ser Asn Pro Asn Gly Ala Pro Leu Arg Arg Tyr
 675 680 685
 Ser Gly Val Pro Asp His Val Asn Leu Glu Asp Tyr Ile Glu Gln Pro
 690 695 700
 His Asn Tyr Pro Thr Met Gln Asn Ser Val Lys Lys Asp Glu Phe Tyr
 705 710 715 720

Asn Ser Arg Asn Asn Lys Phe Pro His Gly Leu Asn Phe Tyr Gly Asp
 725 730 735
 Asn Asn Val Ile Glu Glu Glu Asn Asn Gly Asp Ser Ser Asn Val Asn
 740 745 750
 Arg Pro Gln His Thr Asn Leu Gln His Glu Phe Ile Pro Glu Asp Asn
 755 760 765
 Glu Ser Asp Glu Asn Asp Ile His Ser Met Phe Tyr Tyr Asn His Lys
 770 775 780
 Asn Asp Leu Glu Thr Lys Pro Leu Ile Ser Asp Tyr Gly Glu Asp Glu
 785 790 795 800
 Asp Val Asp Asp Tyr Asp Arg Pro Asn Ala Thr Phe Asn Ser Tyr Tyr
 805 810 815
 Gly Ser Ala Ser Asn Thr His Glu Leu Pro Leu His Gly Arg Met Pro
 820 825 830
 Ser Arg Ser Asn Asn Asp Tyr Tyr Asp Phe Met Val Gly Asn Asn Thr
 835 840 845
 Gly Asn Asn Asn Gln Leu Asn Glu Tyr Thr Pro Leu Arg Met Lys Arg
 850 855 860
 Gly Gln Arg His Leu Ser Arg Thr Asn Asn Ser Ile Met Asn Gly Ser
 865 870 875 880
 Ile His Met Asn Gly Asn Asp Asp Val Thr His Ser Asn Ile Asn Asn
 885 890 895
 Asn Asp Ile Val Gly Tyr Ser Pro His Asn Phe Tyr Ser Arg Lys Ser
 900 905 910
 Pro Phe Val Lys Val Lys Asn Phe Leu Tyr Leu Ala Phe Val Ile Ser
 915 920 925
 Ser Leu Leu Met Thr Gly Phe Ile Leu Gly Phe Leu Leu Ala Thr Asn
 930 935 940
 Lys Glu Leu Gln Asp Val Asp Val Val Val Met Asp Asn Val Ile Ser
 945 950 955 960
 Ser Ser Asp Glu Leu Ile Phe Asp Ile Thr Val Ser Ala Phe Asn Pro
 965 970 975
 Gly Phe Phe Ser Ile Ser Val Ser Gln Val Asp Leu Asp Ile Phe Ala
 980 985 990
 Lys Ser Ser Tyr Leu Lys Cys Asp Ser Asn Gly Asp Cys Thr Val Met
 995 1000 1005
 Glu Gln Glu Arg Lys Ile Leu Gln Ile Thr Thr Asn Leu Ser Leu Val
 1010 1015 1020

<211> 191
 <212> PRT
 <213> Candida albicans

<400> 230

```

Met Lys Tyr Ile Gln Thr Glu Gln Gln Ile Glu Ile Pro Glu Gly Val
 1             5             10             15

Thr Val Ser Ile Lys Ser Arg Ile Val Lys Val Val Gly Pro Arg Gly
      20             25             30

Thr Leu Thr Lys Asn Leu Lys His Ile Asp Val Thr Phe Thr Lys Val
      35             40             45

Asn Asn Gln Leu Ile Lys Val Ala Val His Asn Gly Asp Arg Lys His
      50             55             60

Val Ala Ala Leu Arg Thr Val Lys Ser Leu Val Asp Asn Met Ile Thr
      65             70             75             80

Gly Val Thr Lys Gly Tyr Lys Tyr Lys Met Arg Tyr Val Tyr Ala His
      85             90             95

Phe Pro Ile Asn Val Asn Ile Val Glu Lys Asp Gly Ala Lys Phe Ile
      100            105            110

Glu Val Arg Asn Phe Leu Gly Asp Lys Lys Ile Arg Asn Val Pro Val
      115            120            125

Arg Asp Gly Val Thr Ile Glu Phe Ser Thr Asn Val Lys Asp Glu Ile
      130            135            140

Val Leu Ser Gly Asn Ser Val Glu Asp Val Ser Gln Asn Ala Ala Asp
      145            150            155            160

Leu Gln Gln Ile Cys Arg Val Arg Asn Lys Asp Ile Arg Lys Phe Leu
      165            170            175

Asp Gly Ile Tyr Val Ser His Lys Gly Phe Ile Val Glu Asp Met
      180            185            190

```

<210> 231
 <211> 1373
 <212> DNA
 <213> Candida albicans

<400> 231

```

tcgatggata tcccatccaa gaacaggaat actggggtttt tgaagaccag aatggagatc 60
tctgaggaag aaaagatggt acgtacaata tcacggcttg acaatacgag tattgcaaac 120
agtaatggaa atggtaatga tgacacctct aatcagagaa cggaagcact ggggcgtaag 180
acgagtaatg gagggcgaat atgattacta agttaaataa atcagataca gtatttaaag 240
ttctttcaaa aaaagataat gtcatatatt ttactatcta cgcagtgaaa gagttccttc 300
taatgacaca ctattcactt cgggtaacgg atattgtgta ctgaaaaata taaaaaattt 360
tatcccgga atgcgatgag atgaaaatgc atgaagtagc gtatatattg attgcatgag 420
gttggaacttg aaagggcata tatactcggg tttatcattg attcaagtgt tcccataaat 480

```

```

aataaaacag ttaaatacgaa atgctaagaa gacaagcccc tgaaaggaga gaatatctat 540
acagaaaagc gcaagaatta caagattctc aactgcaaca aaaacgtcaa ataattaaac 600
aagcgctagc tcaggggaag ccattgccaa aggaactagc agaagatgag agttttacaaa 660
aggatttcag atatgaccaa agtttaaagg agagcgaaga agcagatgat ctacagggtg 720
atgatgaata tgctgccaca agtgggtataa tggatccaag aatcatcgtc acaacatctc 780
gtgacccaag cactcgtctc tcgcaatttg ccaaagaaat taaactgcta tttccaaatg 840
ctgtcagggt gaacagaggt aattatgtga tgccaaatct agtggatgct tgtaaaaaat 900
ccggtactac agatttggtg gtattacatg aacatagagg tgttccaact tctttgacca 960
tatcacattt tccacatgga cccactgcac agtttagttt acacaatggt gttatgagac 1020
atgatattat aaatgctggt aaccaaagcg aagtgaatcc acatctaata tttgataact 1080
ttactaccgc tttagggaaa agagttagtct gtatttttaa gcacttggtc aatgcggggc 1140
ccaaaaaaga ttccgaaaga gtaatcactt ttgcgaatag gggtgatttc attagcggtta 1200
gacagcatgt atatgtgaga acaagagagg gagtagagat tgccgaagtt ggtcctagat 1260
ttgagatgag gttgtttgaa ctgagggttg gaactttaga aaataaggac gctgatgttg 1320
agtggcagtt gagaagattc ataaggactg ccaataaaaa agactatttg tga 1373

```

<210> 232

<211> 290

<212> PRT

<213> Candida albicans

<400> 232

```

Met Leu Arg Arg Gln Ala Arg Glu Arg Arg Glu Tyr Leu Tyr Arg Lys
  1              5              10              15

```

```

Ala Gln Glu Leu Gln Asp Ser Gln Leu Gln Gln Lys Arg Gln Ile Ile
      20              25              30

```

```

Lys Gln Ala Leu Ala Gln Gly Lys Pro Leu Pro Lys Glu Leu Ala Glu
      35              40              45

```

```

Asp Glu Ser Leu Gln Lys Asp Phe Arg Tyr Asp Gln Ser Leu Lys Glu
      50              55              60

```

```

Ser Glu Glu Ala Asp Asp Leu Gln Val Asp Asp Glu Tyr Ala Ala Thr
      65              70              75              80

```

```

Ser Gly Ile Met Asp Pro Arg Ile Ile Val Thr Thr Ser Arg Asp Pro
      85              90              95

```

```

Ser Thr Arg Leu Ser Gln Phe Ala Lys Glu Ile Lys Leu Leu Phe Pro
      100              105              110

```

```

Asn Ala Val Arg Leu Asn Arg Gly Asn Tyr Val Met Pro Asn Leu Val
      115              120              125

```

```

Asp Ala Cys Lys Lys Ser Gly Thr Thr Asp Leu Val Val Leu His Glu
      130              135              140

```

```

His Arg Gly Val Pro Thr Ser Leu Thr Ile Ser His Phe Pro His Gly
      145              150              155              160

```

```

Pro Thr Ala Gln Phe Ser Leu His Asn Val Val Met Arg His Asp Ile
      165              170              175

```

```

Ile Asn Ala Gly Asn Gln Ser Glu Val Asn Pro His Leu Ile Phe Asp

```

<400>	233						
aaacacctac	ttatagacac	gaccaaactt	tccacaacct	ttcatcagag	agaaatggtg	60	
atcaagttga	atgcgtagaa	gtagcaattc	gaaacaacaa	ctacctgtca	ttctgcatag	120	
tagtagttac	gaaaggcaca	gaaaataaca	aaaaaaaaaa	aaaagtcaat	tttctacggt	180	
ctccatccgt	acctctttaa	atccgtacat	tattgttttg	cttaattttca	atatttcgga	240	
aaaagcgagc	gccctggtaa	aatgtggttc	aagcctgcga	gccttttgctt	ggtaactcac	300	
caaatgcaat	tcagtcacgt	tccacacagt	ttgggtttcc	agcctggctt	tagggaagaa	360	
tgggtctact	aggcgttcat	aatacgcgga	gggggaaata	ccaaatgcta	ttgattatgg	420	
ttaaaatatg	tgttatattga	ctttgtatat	acaaacagaa	gagaaaccaa	cacactaaag	480	
actagacaca	taactgacca	atgtcctctg	tccaatccaa	gatcttatcc	caagctccaa	540	
gtgagttgga	attacaagtc	gccaaagacct	tcatcgatct	agaaagctcc	tctccagaac	600	
taaaggctga	cttgagacca	ttgcaaataca	aatctatcag	agaagtatgt	taaaagttat	660	
ataatttgga	agcagcaaca	ttgtgatttc	ttctaiaagg	gttcttttgca	gtaatttttt	720	
caaaaaagag	tgatttttag	cagtatctgt	atgaaaattt	catgtgtctcg	agaaaaatag	780	
taattccgag	agctgtcaat	accatgaacg	ttgcgatgag	cctttgaact	ataaaggcct	840	
ccttggctcag	taccaatatc	gatgaataaa	atagaagcac	gcgaaaaaga	ccttacccca	900	
aggagaagaa	tcacaaaacc	ttttttgtta	tgaatgaacc	aattcagtta	ctaactttat	960	
ttcaacgctg	cttgattctt	attgttttaga	ttgatgtcac	cggtggttaag	aaagcactag	1020	
tcctttttgt	cccagttcca	gctttgtctg	cataccataa	ggtccaaacc	aaattgacct	1080	
gtgaattgga	aaagaaattc	cctgaccgtc	atgttatattt	cttggctgaa	agaagaatct	1140	
tgccaaaacc	atctagaaca	tctagacaag	tccaaaagag	accaagatcc	agaactttga	1200	
ctgctgttca	cgacaagggt	ttggaagaca	tggttttccc	aactgaaatt	gtcggtaaaa	1260	
tgatttagata	tttggttggt	ggtaacaaga	tccaaaagg	tttgttagac	tccaaggatg	1320	
ttcaacaat	cttagtacaag	ttggaatctt	tccaagctgt	ctacaacaag	ttgactggca	1380	
aacaaattgt	ttttgaaatt	ccaagccaga	ccaactaa			1418	

```
<210> 234
<211> 190
<212> PRT
<213> Candida albicans
```

<400> 234

Met	Ser	Ser	Val	Gln	Ser	Lys	Ile	Leu	Ser	Gln	Ala	Pro	Ser	Glu	Leu
1				5					10					15	

Glu Leu Gln Val Ala Lys Thr Phe Ile Asp Leu Glu Ser Ser Ser Pro
20 25 30

Glu Leu Lys Ala Asp Leu Arg Pro Leu Gln Ile Lys Ser Ile Arg Glu
35 40 45

Ile Asp Val Thr Gly Gly Lys Lys Ala Leu Val Leu Phe Val Pro Val
50 55 60

Pro Ala Leu Ser Ala Tyr His Lys Val Gln Thr Lys Leu Thr Arg Glu
65 70 75 80

Leu Glu Lys Lys Phe Pro Asp Arg His Val Ile Phe Leu Ala Glu Arg
85 90 95

Arg Ile Leu Pro Lys Pro Ser Arg Thr Ser Arg Gln Val Gln Lys Arg
100 105 110

Pro	Arg	Ser	Arg	Thr	Leu	Thr	Ala	Val	His	Asp	Lys	Val	Leu	Glu	Asp
		115					120					125			

Met Val Phe Pro Thr Glu Ile Val Gly Lys Arg Val Arg Tyr Leu Val
130 135 140

Gly Gly Asn Lys Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Val Gln
145 150 155 160

Gln Ile Asp Tyr Lys Leu Glu Ser Phe Gln Ala Val Tyr Asn Lys Leu
165 170 175

Thr Gly Lys Gln Ile Val Phe Glu Ile Pro Ser Gln Thr Asn
180 185 190

```
<210> 235
<211> 1333
<212> DNA
<213> Candida albicans
```

<400> 235

ttcatcacca	atatagacta	atgcgttttg	gaacgccaaa	ccgcagtgac	aaatagcaaa	60
tatgtagctg	tcatatcggc	atataataac	agttttctac	caaatgctgt	cctacattca	120
gagatcttac	atccttacat	ctaaagtaaa	acctagacat	ttacttcgag	ttatactttt	180
tttttattta	tctatttttt	ctcttgcgga	catttaaacac	ctgaattccg	cctaacgccca	240
ggactgatcc	tgccagggaa	ggagcttttg	tctagtgccca	ataggccgga	ccagtaggaa	300
ggttacagca	gctggccgcg	agagtgattg	ggtcacagga	aaatagcgca	cttctctctt	360
tgccccggaa	agggcggttca	atctaccttc	gaagggctag	tacatgagcg	cgaaggaggc	420

<400> 237
gggccacgtc agttccacac aataacattt acgtagtgtt cācgcgaagc agttacatct 60

```

caactaacat aattgctggt gagcctacaa cactgcatgc gtaaacgtca acgggattac 120
gtagtatttt ttggccgccc gtaaattctc ttgttttttt ttcttgattt cacttctttt 180
catgttcctt tggaataatc taattcctca tgattaaatg agactgtttt ttgtttccgt 240
aacatccata cctttcctgt ataataattct tgctgtaaaag tttgtttttt ttatgaaaaa 300
aacattttct tttcttgaga tgaggcgccc cgagcctttc tcccatgggc agtgggtaaat 360
tttccaaatc aatgcagctc tttgaaatac aacagcattt ttcatacatt ttaagcaatt 420
tctagtttgt agatatttgt agattagttt ttgaacattg ttttgataac tgaaaataaa 480
acagcaaaca aactacaaaa atggtcgcct taatctctaa gaaaagaaaag ctagtcgctg 540
acgggtgtctt ctacgctgaa ttgaacgaat tcttcaccag agaattagct gaagaagggt 600
actccgggtg tgaagtccgt gtcactccaa ccaagaccga agttatcatc agagctacca 660
gaactcaaga tgttttgggt gaaaacggta gaagaatcaa cgaattaact ttgttggttc 720
aaaagagatt caagtacgct ccaggtacta ttgtcttata tgctgaaaga gttcaagacc 780
gtggtttgtc cgctgtcgct caagctgaat ctatgaaatt caaattgttg aacggtttg 840
ctatcagaag agctgcttac ggtgtcgtca gatacgttat ggaatctggt gctaagggtt 900
gtgaagttgt tgtttcgggt aaactaagag ctgccagagc taaggctatg aaatttgctg 960
acggtttctt gattcactct ggtcaaccag tcaacgactt cattgacact gctactagac 1020
acgtcttgat gagacaaggt gttttgggta tcaagggttaa gattatgaga gaccagcta 1080
agagcagaac tgggtccaaag gctttgccag atgctgtcac catcattgaa ccaaaaagaag 1140
aagaaccaat tcttgctcca tctgtcaagg actacagacc agctgaagaa actgaagctc 1200
aagctgaacc agttgaagct tag 1223

```

<210> 238

<211> 240

<212> PRT

<213> Candida albicans

<400> 238

```

Met Val Ala Leu Ile Ser Lys Lys Arg Lys Leu Val Ala Asp Gly Val
  1             5             10             15

```

```

Phe Tyr Ala Glu Leu Asn Glu Phe Phe Thr Arg Glu Leu Ala Glu Glu
      20             25             30

```

```

Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Thr Lys Thr Glu Val
      35             40             45

```

```

Ile Ile Arg Ala Thr Arg Thr Gln Asp Val Leu Gly Glu Asn Gly Arg
      50             55             60

```

```

Arg Ile Asn Glu Leu Thr Leu Leu Val Gln Lys Arg Phe Lys Tyr Ala
      65             70             75             80

```

```

Pro Gly Thr Ile Val Leu Tyr Ala Glu Arg Val Gln Asp Arg Gly Leu
      85             90             95

```

```

Ser Ala Val Ala Gln Ala Glu Ser Met Lys Phe Lys Leu Leu Asn Gly
     100             105             110

```

```

Leu Ala Ile Arg Arg Ala Ala Tyr Gly Val Val Arg Tyr Val Met Glu
     115             120             125

```

```

Ser Gly Ala Lys Gly Cys Glu Val Val Val Ser Gly Lys Leu Arg Ala
     130             135             140

```

```

Ala Arg Ala Lys Ala Met Lys Phe Ala Asp Gly Phe Leu Ile His Ser
     145             150             155             160

```

Gly Gln Pro Val Asn Asp Phe Ile Asp Thr Ala Thr Arg His Val Leu
 165 170 175

Met Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Arg Asp Pro
 180 185 190

Ala Lys Ser Arg Thr Gly Pro Lys Ala Leu Pro Asp Ala Val Thr Ile
 195 200 205

Ile Glu Pro Lys Glu Glu Glu Pro Ile Leu Ala Pro Ser Val Lys Asp
 210 215 220

Tyr Arg Pro Ala Glu Glu Thr Glu Ala Gln Ala Glu Pro Val Glu Ala
 225 230 235 240

<210> 239

<211> 2168

<212> DNA

<213> Candida albicans

<400> 239

```

ctttgataaa ttaatacggg aagataccgt gtgaactatt ataataactg ccacgcttat 60
agcatgtacg ctatacatTT acgtgctgag ctccctaggaa agctcatgag cagccactgt 120
atcgtggagc ataactacaa caaagaatac acagcgtcac atagagggtt tttgagagga 180
gaagttgaaa taggacttga tcttggggga gaggggattt gaaagcacc attcaggagt 240
atgtgtctgt aattgaagtg ttagcgcgcg attcacctgt aataagagtg atgatttgat 300
agcgccattc tacatcatat ggcaaatgtt gaaaaactgt acgcgcgaaac taaaattttt 360
ttttacatcc cactaaatga aaatttttaa tccgatgccc ttccaaatat gcttattcga 420
aggacggctc tgacaagggc atatgcggtt agattgattg ttcaatattc ataaaacagg 480
atctttcaag ggacgataaa atggatgagc aagttatttt tacaacaaat acctcaggaa 540
caatagcttc tgtacactca tttgaacaga taaatttgag gcaatgctcc actcaatcaa 600
gaaatagctg tgttcaagta ggaaataaat acctttttat tgctcaagca caaaaagcat 660
taatcaatgt ctacaatctg tcaggttctt tcaaaagaga atctgttgaa cagcgcttac 720
cattacctga aatcctaaaa tgtctggaag tagttgaaaa tgatggtgtg cagtatgata 780
gaattcaagg tgtcaatcat aatttaccag acttcaatct tccgtacctt ttacttggct 840
ccaccgaatc gggtaaatgt tacatatggg agttaaattc agggatttta ttgaacgtga 900
agcctatggc tcattaccaa agtatcacca agattaagtc cattttaaac ggcaagtata 960
ttattacttc tggtaacgat tcgagagtta ttatatggca aactggtgac ttggtatcag 1020
cgtccaatga tgatccctaag cctttatgta tccttcacga tcataactcta cccgtgacag 1080
atctccaagt ttcttctagt caaggaaaaat ttttatcatg tactgatacg aaactcttca 1140
cagtatctca agatgctacc attagatgct atgatttgag tttaataggc agcaaaaaga 1200
agcagaaggc aaacgaaaaat gacgttagta ttggtaagac cccagtattg cttgcgacat 1260
ttacaactcc ttattctatc aaatccattg tactggatcc tgctgacaga gcatgctata 1320
ttggtactgc ggaaggttgt ttttcattga atttatttta taaactaaaag ggtaatgcta 1380
tcgttaactc gctacagtcc gccggagtaa acacagttca aaaaggtagg gttttttccc 1440
tagtgcaacg taactcacta actggcgggc aaaaatgaaga tttggatgca ctatatgcaa 1500
tgggccaact tgtctgtgag aatgtcctaa attcaaatgt gtcatgccta gaaatatcaa 1560
tggtatgtac attattattg atcggtgata cggaggggaa agtttctatt gcggaaattt 1620
actcaaaaca aatcattaga actatccaaa ctttaactac atcacaggat tcagttggag 1680
aagtgaccaa tctcttaacc aacccttaca gactcgaacg tggaaattta ctttttgaag 1740
gagaatccaa aggcaaacaa cctagtaata ataatggtca caattttatg aagataccaa 1800

```

<400> 240																
Met	Asp	Glu	Gln	Val	Ile	Phe	Thr	Thr	Asn	Thr	Ser	Gly	Thr	Ile	Ala	
1				5					10					15		
Ser	Val	His	Ser	Phe	Glu	Gln	Ile	Asn	Leu	Arg	Gln	Cys	Ser	Thr	Gln	
			20					25					30			
Ser	Arg	Asn	Ser	Cys	Val	Gln	Val	Gly	Asn	Lys	Tyr	Leu	Phe	Ile	Ala	
		35					40					45				
Gln	Ala	Gln	Lys	Ala	Leu	Ile	Asn	Val	Tyr	Asn	Leu	Ser	Gly	Ser	Phe	
	50					55					60					
Lys	Arg	Glu	Ser	Val	Glu	Gln	Arg	Leu	Pro	Leu	Pro	Glu	Ile	Leu	Lys	
65					70					75					80	
Cys	Leu	Glu	Val	Val	Glu	Asn	Asp	Gly	Val	Gln	Tyr	Asp	Arg	Ile	Gln	
				85					90					95		
Gly	Val	Asn	His	Asn	Leu	Pro	Asp	Phe	Asn	Leu	Pro	Tyr	Leu	Leu	Leu	
			100					105					110			
Gly	Ser	Thr	Glu	Ser	Gly	Lys	Leu	Tyr	Ile	Trp	Glu	Leu	Asn	Ser	Gly	
		115					120					125				
Ile	Leu	Leu	Asn	Val	Lys	Pro	Met	Ala	His	Tyr	Gln	Ser	Ile	Thr	Lys	
	130					135					140					
Ile	Lys	Ser	Ile	Leu	Asn	Gly	Lys	Tyr	Ile	Ile	Thr	Ser	Gly	Asn	Asp	
145					150					155					160	
Ser	Arg	Val	Ile	Ile	Trp	Gln	Thr	Val	Asp	Leu	Val	Ser	Ala	Ser	Asn	
				165					170					175		
Asp	Asp	Pro	Lys	Pro	Leu	Cys	Ile	Leu	His	Asp	His	Thr	Leu	Pro	Val	
			180					185					190			
Thr	Asp	Phe	Gln	Val	Ser	Ser	Ser	Gln	Gly	Lys	Phe	Leu	Ser	Cys	Thr	
		195					200					205				
Asp	Thr	Lys	Leu	Phe	Thr	Val	Ser	Gln	Asp	Ala	Thr	Ile	Arg	Cys	Tyr	
	210					215					220					


```

<400> 242
Met Lys Phe Ser Ser Val Thr Ala Ile Thr Leu Ala Thr Val Ala Thr
  1                      5                      10                      15

Val Ala Thr Ala Lys Lys Gly Glu His Asp Phe Thr Thr Thr Leu Thr
                20                      25                      30

Leu Ser Ser Asp Gly Ser Leu Thr Thr Thr Thr Ser Thr His Thr Thr
        35                      40                      45

His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn
  50                      55                      60

His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser
  65                      70                      75                      80

Lys Thr Pro Asn His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys

```

247

85

90

95

Thr Ser Lys Ser Lys Thr Pro Asn His Thr Gly Thr His Lys Tyr Gly
 100 105 110
 Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn His Thr Gly Thr
 115 120 125
 His Lys Tyr Gly Lys Phe Asn Lys Thr Ser Lys Ser Lys Thr Pro Asn
 130 135 140
 His Thr Gly Thr His Lys Tyr Gly Lys Phe Asn Lys Thr Lys His Asp
 145 150 155 160
 Thr Thr Thr Tyr Gly Pro Gly Glu Lys Ala Arg Lys Asn Asn Ala Ala
 165 170 175
 Pro Gly Pro Ser Asn Phe Asn Ser Ile Lys Leu Phe Gly Val Thr Ala
 180 185 190
 Gly Ser Ala Ala Val Ala Gly Ala Leu Leu Leu Leu
 195 200

<210> 243

<211> 1115

<212> DNA

<213> Candida albicans

<400> 243

gggtatacac atatatatat ttttcatttt taatgtctta gcttttgtat cttagatgaa 60
 gtttttagttc tgtatatcac gatcaagata tcatacaatc ataaattcaa ttattcttct 120
 gtttccctc ttgaggcatc aaacgagtggt ttgactgata cacaccaaca tactaaggca 180
 acttttctg ctgcccacag ctgtggcagc tatgaaactg cttttcggct gcataaaaca 240
 accatgtgga gtttttactg tattcgcatc tcgccccgct agcattcttc gttcatgcta 300
 aaaatgaggc gtgggctaatt attcagtatt aataattccg gcacccgcac agcccataacc 360
 ggaaaagggg ctggctgttg ggcttgga aaactcaat ctgagcagtc atttataaag 420
 aaagacttta atttgccttg ctaaacactt gtaagccttc caaatataga tcacttaaga 480
 caatctaaca agtgtccaaa atgtctgcaa acgaattcta ctcaagtggc caacaaggtc 540
 aatataacca gcaaaacaac caagaaagaa ctggtgctcc aaacaacggt caatatggtg 600
 ccgacaatgg taaccccaac ggtgaacgtg gtttattttc cactattgta ggtggcagtg 660
 ccggtgcgta cgctggatct aagggtgcga acaaccattc taagttgagt ggtgtgctgg 720
 gcgcatatag tggtgcattc cttgccaca agatatctga tgagcgtaaa gagcataagc 780
 aacaagagca atacggcaac tcaaacttcg gaggtgctcc tcaagggtgga cacaacaacc 840
 atcaccgtca gacaataaca acaataacgg tggatttggc ggtccaggcg gccctggcgg 900
 tcaaggtttc ggaagacaag gccacaagg atttggaggt cctggtccac aagagtttgg 960
 tgggtccagg ggccaaggat tcggtggtcc aaatcctcaa gaattcggcg gccaggtggc 1020
 caaggattcg gtggtccaaa cctcaggaa ttcgggggccc aaggtcgtca aggattcaat 1080
 ggcggttcac gttggtgaat ggctcaacag agtga 1115

<210> 244

<211> 204

<212> PRT

<213> Candida albicans


```

ccaaattggt gaaactatta gaagagctcc aggagggaaa gcaattcaac aataaaaaaca 600
tattcccgga aaaagcatta tatttgaagc tcgctcttga ttattctttc ttcagaaaga 660
atttactaga gttttgcgtc caccttgaca agataaaagg agtcattaga ccaaactatg 720
acactatata tattttgtgc ctggttgagg tggatctcct caatctggta tttaccgaca 780
atatattgga aatatgtttg cccagggttg tttcaaggga ggacttgagg gtttttaata 840
atacttttta cacatatcac gataaccgcc tacgtattct ccaagaagac ttttctcaat 900
tgttcaaaaa aatcaaaaact aaggcttctg tactatgttt tacagttgag gaaatttttc 960
tgacaaacca agaaatttta cctcaaaaact caacagtggc agaactgcaa aagagcacta 1020
ataaagtaca gacaaatggg ccgcaacggc acgatttcat agtcactcta gaaataaaaac 1080
tgaacaaaac acaaatcact ttcctcattg gagctaaagg aacgagaatt gaaagcttga 1140
gggaaaaatc aggcgccagc ataaaaataa tacctattag tgataaaatg actgcacatg 1200
aaaggaacca ccctgaatct gttcaacaaa caatactaatt ttcgggtgac ttataactcaa 1260
ttgcattagc cgtcaccagt atagagtctg cattaattac tttggattta tag 1313

```

<210> 246

<211> 270

<212> PRT

<213> Candida albicans

<400> 246

```

Met Ser Asn Gln His Ser Pro Gln Pro Phe Cys Leu Asp Thr Lys Leu
  1              5              10              15

Val Lys Leu Leu Glu Glu Leu Gln Glu Gly Lys Gln Phe Asn Asn Lys
      20              25              30

Asn Ile Phe Pro Glu Lys Ala Leu Tyr Leu Lys Leu Ala Leu Asp Tyr
      35              40              45

Ser Phe Phe Arg Lys Asn Leu Leu Glu Phe Cys Val His Leu Asp Lys
      50              55              60

Ile Lys Gly Val Ile Arg Pro Asn Tyr Asp Thr Ile Tyr Ile Leu Cys
      65              70              75              80

Leu Leu Glu Val Asp Leu Leu Asn Leu Val Phe Thr Asp Asn Ile Leu
      85              90              95

Glu Ile Cys Leu Pro Arg Phe Val Ser Arg Glu Asp Leu Arg Val Phe
      100              105              110

Asn Asn Thr Phe Tyr Thr Tyr His Asp Asn Arg Leu Arg Ile Leu Gln
      115              120              125

Glu Asp Phe Ser Gln Leu Phe Lys Lys Ile Lys Thr Lys Ala Ser Val
      130              135              140

Leu Cys Phe Thr Val Glu Glu Ile Phe Leu Thr Asn Gln Glu Ile Leu
      145              150              155              160

Pro Gln Asn Ser Thr Val Ala Glu Leu Gln Lys Ser Thr Asn Lys Val
      165              170              175

Gln Thr Asn Gly Pro Gln Arg His Asp Phe Ile Val Thr Leu Glu Ile
      180              185              190

```


251

<212> PRT

<213> Candida albicans

<400> 248

Met Val Arg Ile Leu Pro Ile Ile Leu Ser Ala Leu Ser Ser Lys Leu
 1 5 10 15

Val Ala Ser Thr Ile Leu His Ser Ser Ile His Ser Val Pro Ser Gly
 20 25 30

Gly Glu Ile Ile Ser Ala Glu Asp Leu Lys Glu Leu Glu Ile Ser Gly
 35 40 45

Asn Ser Ile Cys Val Asp Asn Arg Cys Tyr Pro Lys Ile Phe Glu Pro
 50 55 60

Arg His Asp Trp Gln Pro Ile Leu Pro Gly Gln Glu Leu Pro Gly Gly
 65 70 75 80

Leu Asp Ile Arg Ile Asn Met Asp Thr Gly Leu Lys Glu Ala Lys Leu
 85 90 95

Asn Asp Glu Lys Asn Val Gly Asp Asn Gly Ser His Glu Leu Ile Val
 100 105 110

Ser Ser Glu Asp Met Lys Ala Ser Pro Gly Asp Tyr Glu Phe Ser Ser
 115 120 125

Asp Phe Lys Glu Met Arg Asn Ile Ile Asp Ser Asn Pro Thr Leu Ser
 130 135 140

Ser Gln Asp Ile Ala Arg Leu Glu Asp Ser Phe Asp Arg Ile Met Glu
 145 150 155 160

Phe Ala His Asp Tyr Lys His Gly Tyr Lys Ile Ile Thr His Glu Phe
 165 170 175

Ala Leu Leu Ala Asn Leu Ser Leu Asn Glu Asn Leu Pro Leu Thr Leu
 180 185 190

Arg Glu Leu Ser Thr Arg Val Ile Thr Ser Cys Leu Arg Asn Asn Pro
 195 200 205

Pro Val Val Glu Phe Ile Asn Glu Ser Phe Pro Asn Phe Lys Ser Lys
 210 215 220

Ile Met Ala Ala Leu Ser Asn Leu Asn Asp Ser Asn His Arg Ser Ser
 225 230 235 240

Asn Ile Leu Ile Lys Arg Tyr Leu Ser Ile Leu Asn Glu Leu Pro Val
 245 250 255

Thr Ser Glu Asp Leu Pro Ile Tyr Ser Thr Val Val Leu Gln Asn Val
 260 265 270

Tyr Glu Arg Asn Asn Lys Asp Lys Gln Leu Gln Ile Lys Val Leu Glu
 275 280 285

253

<400> 250

Met Phe Phe Lys Val Ser Asn Phe Thr Ser Leu Thr Leu Leu Ser Leu
 1 5 10 15

Ile Pro Ile Val Gly Pro Ile Leu Ala Asn Gln Leu Met Ala Pro Lys
 20 25 30

Arg Thr Phe Thr Tyr Leu Gln Arg Tyr Phe Leu Leu Lys Gly Phe Ser
 35 40 45

Lys Lys Gln Ala Lys Asp Phe Gln Tyr Glu His Tyr Ala Ser Phe Ile
 50 55 60

Cys Phe Gly Met Ser Ala Gly Leu Leu Glu Leu Ile Pro Phe Phe Thr
 65 70 75 80

Ile Val Thr Ile Ser Ser Asn Thr Val Gly Ala Ala Lys Trp Cys Thr
 85 90 95

Ser Leu Leu Lys Gly Glu Arg Lys Lys Glu
 100 105

<210> 251

<211> 1256

<212> DNA

<213> Candida albicans

<400> 251

acatttccca aaaaagacat ttctgtccaa aagtagaagg caagaaaacc ctggaggaat 60
 cataggcaaa gaaagaaaag aagaagttca tctttaaaac tacctttcaa gcctttattc 120
 gttcctcgta aaggacacac gaaaaaata aacagtacct tgcagaagga gtgcagagtt 180
 aggtcgagg gaatccttga aagccaagag ttttttttcc gtaatgatct cccaaagcaa 240
 ccatcaacat tgtggtgcaa agtttagtgt aagatgttct actgaactat cttaatagct 300
 gagcatcatg tgagtaaacy agtaagcaag aaaacaacaa agtaatgttc aactttcgta 360
 actacggaaa ataatatata agtagttaac gaaattcgaa caatgagagc tctcacatat 420
 catcttcttt tccagtttag ccattatcag cacaataata caaaacacac tcgtacactc 480
 gcttcaacta taacaaaaaa atggcttaca tcaagatcgc tttattagct gctatcgctg 540
 ctttggttcc tgcccaaact caggaagaaa ttgacgaatt gaacgttatt ttgaatgacg 600
 ttaagtccaa cttgcaagaa tatattagtt tggctgaaga ttcttcatct ggattttcct 660
 taagcagtct gccatctggt gtttttagaca tcggttttagc tttggcttcc gccactgatg 720
 actcctacac tactttgtac tctgaggttg actttgctgc tgttagcaag atggtgacca 780
 tggttccatg gtattcttcc aggtcttctac cagaattgga atccttggtta ggaacttcta 840
 ccaccgctgc ctcttctact gaagcttctt ctgctgctac ttcttccgct gttgcttcc 900
 ccagtgaac tacttcttct gccgtcgctt cctccagtga agctacttct tctgcccgtc 960
 cttcttccag tgaagcttct tcttctgctg ctacttcttc tgctgtcgct tcttccagt 1020
 aggtacctc ttccaccgtc gcttcttcta ccaaggetgc ctcttccact aaggcttctt 1080
 cctctgctgt ttcttcagct gttgcttctt ccaccaaagc ctccgccatt tctcaaata 1140
 gtgatggtca agttcaagcc actagcactg tttccgaaca aactgaaaac ggtgctgcca 1200
 aggtgtcat cggatatggg gctgggtgtca tggccgctgc cgccatgtta ttataa 1256

<210> 252

<211> 251

<212> PRT

<213> Candida albicans

<400> 252

Met Ala Tyr Ile Lys Ile Ala Leu Leu Ala Ala Ile Ala Ala Leu Ala
 1 5 10 15
 Ser Ala Gln Thr Gln Glu Glu Ile Asp Glu Leu Asn Val Ile Leu Asn
 20 25 30
 Asp Val Lys Ser Asn Leu Gln Glu Tyr Ile Ser Leu Ala Glu Asp Ser
 35 40 45
 Ser Ser Gly Phe Ser Leu Ser Ser Leu Pro Ser Gly Val Leu Asp Ile
 50 55 60
 Gly Leu Ala Leu Ala Ser Ala Thr Asp Asp Ser Tyr Thr Thr Leu Tyr
 65 70 75 80
 Ser Glu Val Asp Phe Ala Ala Val Ser Lys Met Leu Thr Met Val Pro
 85 90 95
 Trp Tyr Ser Ser Arg Leu Leu Pro Glu Leu Glu Ser Leu Leu Gly Thr
 100 105 110
 Ser Thr Thr Ala Ala Ser Ser Thr Glu Ala Ser Ser Ala Ala Thr Ser
 115 120 125
 Ser Ala Val Ala Ser Ser Ser Glu Thr Thr Ser Ser Ala Val Ala Ser
 130 135 140
 Ser Ser Glu Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Ser
 145 150 155 160
 Ser Ser Ala Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Thr
 165 170 175
 Ser Ser Thr Val Ala Ser Ser Thr Lys Ala Ala Ser Ser Thr Lys Ala
 180 185 190
 Ser Ser Ser Ala Val Ser Ser Ala Val Ala Ser Ser Thr Lys Ala Ser
 195 200 205
 Ala Ile Ser Gln Ile Ser Asp Gly Gln Val Gln Ala Thr Ser Thr Val
 210 215 220
 Ser Glu Gln Thr Glu Asn Gly Ala Ala Lys Ala Val Ile Gly Met Gly
 225 230 235 240
 Ala Gly Val Met Ala Ala Ala Ala Met Leu Leu
 245 250

<210> 253

<211> 2693

<212> DNA

<213> Candida albicans

<400> 253

```

cattgatctc gagcacagct gctcttttct ctcaatgaat tacgttatat gttaatcaca 60
caagcatcag tttttcatcg caaaagaaaa tatttagagt tcttgcaatt cagatgtacc 120
tcaattaata actcaatcac ctctatgtt cttgctggta gtactgcttt tgtcttaatt 180
actgctgaat cagccttcta gaagaccgtt ctgtttcagc cgctcgcccc ttttcaaagc 240
ttgcgcggct gagttttatg aggggcggct tttttgtgaa tggcaatcta ccattattag 300
tagcaatatg atttgcagat agatacatat atatccttct gggttcatgt ctcgttacca 360
tccacactaa tgcataggac cagaaagaaa ggacatcgaa tccaacacgt attaaaaataa 420
ggactcctca ttaaaaaggc ttttaatat caacttgcta tagatcacgc acccttttgg 480
caagtcaacc ttaaattatt atgatttctg tttgcccaca aaatgacttg caaaaatgct 540
acagaagcct cacattcgat gtccaggac aacaattcga agagagaaat gaacaaaacc 600
ttaaaaaacg ggccaaaaag aaaggcagtt tccaaccatc tgttgccctt gacacagtgc 660
cttccaccgc tggttattct tctatagacg acagcaggga aggattcaaa ggtgtacctg 720
ttcccaacta ttacacgatg gaagagtgtc atgacgatga aacagactct ttttcgccaa 780
atttgcaata ttatttgaga gatacattcc aatcatcacc ttttctgaat actagaaaag 840
agaacaaatc tgaatccagt agttttccaa tgagatcctc aaagttgttg gaaaaagaatt 900
ctgacatcaa aaaatatttc ttggtatcca agaattggaa aatagtggag agagactatc 960
caagcaccgc agtaattgtc aacgaaacgt tgatgataaa caggtttgaa aagaactgga 1020
taaagttatg gcgccaaaag aaactacaaa taaatgaaag gctgaatgac aaaaaaaat 1080
ggtttactta cccagaactt atcttctctg aagagcgtat taaaccgtta tatagaggag 1140
atgatatgtc accatgtaca aaagaacaaa aaagaaagca taaaatactt caacaaaagg 1200
tcggatatcc caataaccct aagacaatag tttgtcacat taacggaaaa aaacatacgt 1260
gggttgccct agactggaca gtctacaagt ttgcacgaaa tcttgatcac attgttgtca 1320
taactacact gccaaaaatg atttctaaca ggaaaaaaac tgcaaaagat gatacagaat 1380
gggcaccggg atatcaaaaa gaagtaatag atcaaaaatt aaacgacatt tttgattata 1440
ttttacagct agtaaaaagt gtcaaaatat ccgtcaaaat tactttagaa ataattgtag 1500
gcaaaattaa aaaaagtctg gtagatgtca ttaatgtcca tactccagat ttcttagttc 1560
ttgctacttt aaagcacgag cgaaatgaga atctttattac atataaatcc aaaaagctga 1620
cagatgtctt tctgttagt tatccgattc ccacatttgt tgttccctcg aaacgaatgt 1680
attcgttcga actgaatcta caaagagaag taaatgaaca ttatgtctca aaaaatcata 1740
tgaagcacga acacactgac gttgagagca tgagcagttc aatgttcaaa aaaaatacaa 1800
tatcagatat ttcttcacat atttccgtag attcgtacgc cgaagatttc aaaaggcaag 1860
gtctacatcaa aaagcagttc aacacctcta atgattccat tccaagaaaa ttgaccggtc 1920
tcgcccagca ttcaagaagg aagatcacgg gtgatataga aaaattacaa gacgatgaga 1980
aagatagaga atgtactaag gaaaaacttt tgttgaagaa aattgatatc ataattagag 2040
agtcattgaa gtcttcttta gcgatagaga cgttgcctgg taaaaatgta tcgcagtcca 2100
gtcacggtga ccaaatttcc agctttaaga atgctttgat aggcaatggg tcgaaaaaca 2160
caaagtttag aaaatcttta ataccatatt ctctctcaga ggaacaaaat accacaacaa 2220
ctattaaact cagtagctcg cctacgtccc aaatcaagtt tgcaacctct gtaaaacaca 2280
aagatggaag agccgccctt ggcaaagcca gaaatctgcc tgatataagg cacagtattt 2340
ccttcgacaa agaaaattcc tttgatccat ctgataaaaag cagtagtgtt gataatagca 2400
ttcctttgag gaaagttaaa agtgccggtg cgtaagaaa agtcaaaact aatgactcct 2460
caagtagtgc aggggtcaaag aaaagctcgt ctagtttttag tactgtgaac accttactg 2520
ggggtggagt tgggattttt aagggtgtta aaagtggaag ttctcttggg aataaatcat 2580
ccagtagaag gaatagtagc agtggcgatg tttttgaaag tgatgatcgt aacgacaaga 2640
aaaagaagaa gaaaaaaaag aagaaatcat tgttcttatt cggcaaaata tga 2693

```

<210> 254

<211> 730

<212> PRT

<213> *Candida albicans*

<400> 254

Met Ile Ser Val Cys Pro Gln Asn Asp Leu Gln Lys Cys Tyr Arg Ser
1 5 10 15

Leu Thr Phe Asp Val Pro Gly Gln Gln Phe Glu Glu Arg Asn Glu Gln
 20 25 30
 Asn Leu Lys Lys Arg Ala Lys Lys Lys Gly Ser Phe Gln Pro Ser Val
 35 40 45
 Ala Phe Asp Thr Val Pro Ser Thr Ala Gly Tyr Ser Ser Ile Asp Asp
 50 55 60
 Ser Arg Glu Gly Phe Lys Gly Val Pro Val Pro Asn Tyr Tyr Thr Met
 65 70 75 80
 Glu Glu Cys Tyr Asp Asp Glu Thr Asp Ser Phe Ser Pro Asn Leu Gln
 85 90 95
 Tyr Tyr Leu Arg Asp Thr Phe Gln Ser Ser Pro Phe Leu Asn Thr Arg
 100 105 110
 Lys Glu Asn Lys Ser Glu Ser Ser Ser Phe Pro Met Arg Ser Ser Lys
 115 120 125
 Leu Leu Glu Lys Asn Ser Asp Ile Lys Lys Tyr Phe Leu Val Ser Lys
 130 135 140
 Asn Gly Lys Ile Val Arg Arg Asp Tyr Pro Ser Thr Pro Val Ile Val
 145 150 155 160
 Asn Glu Thr Leu Met Ile Asn Arg Phe Glu Lys Asn Trp Ile Lys Leu
 165 170 175
 Trp Arg Gln Arg Lys Leu Gln Ile Asn Glu Arg Leu Asn Asp Lys Lys
 180 185 190
 Lys Trp Phe Thr Tyr Pro Glu Leu Ile Phe Ser Glu Glu Arg Ile Lys
 195 200 205
 Pro Leu Tyr Arg Gly Asp Asp Ser Ala Pro Cys Thr Lys Glu Gln Lys
 210 215 220
 Arg Lys His Lys Ile Leu Gln Gln Lys Val Gly Tyr Pro Asn Asn Pro
 225 230 235 240
 Lys Thr Ile Val Cys His Ile Asn Gly Lys Lys His Thr Trp Val Ala
 245 250 255
 Leu Asp Trp Thr Val Tyr Lys Phe Ala Arg Asn Leu Asp His Ile Val
 260 265 270
 Val Ile Thr Thr Leu Pro Lys Met Ile Ser Asn Arg Lys Lys Thr Ala
 275 280 285
 Lys Asp Asp Thr Glu Trp Ala Pro Gly Tyr Gln Lys Glu Val Ile Asp
 290 295 300
 Gln Lys Leu Asn Asp Ile Phe Asp Tyr Ile Leu Gln Leu Val Lys Val
 305 310 315 320

Val Lys Ile Ser Val Lys Ile Thr Leu Glu Ile Ile Val Gly Lys Ile
 325 330 335
 Lys Lys Ser Leu Val Asp Val Ile Asn Val His Thr Pro Asp Phe Leu
 340 345 350
 Val Leu Ala Thr Leu Lys His Glu Arg Asn Glu Asn Leu Ile Thr Tyr
 355 360 365
 Lys Ser Lys Lys Leu Thr Asp Val Phe Pro Val Ser Tyr Pro Ile Pro
 370 375 380
 Thr Phe Val Val Pro Ser Lys Arg Met Tyr Ser Phe Glu Leu Asn Leu
 385 390 395 400
 Gln Arg Glu Val Asn Glu His Tyr Val Ser Lys Asn His Met Lys His
 405 410 415
 Glu His Thr Asp Val Glu Ser Met Ser Ser Ser Met Phe Lys Lys Asn
 420 425 430
 Thr Ile Ser Asp Ile Ser Ser His Ile Ser Val Asp Ser Tyr Ala Glu
 435 440 445
 Asp Phe Lys Arg Gln Gly Tyr Ile Lys Lys Gln Phe Asn Thr Ser Asn
 450 455 460
 Asp Ser Ile Pro Arg Lys Leu Thr Gly Leu Ala Gln His Ser Arg Arg
 465 470 475 480
 Lys Ile Thr Gly Asp Ile Glu Lys Leu Gln Asp Asp Glu Lys Asp Arg
 485 490 495
 Glu Cys Thr Lys Glu Lys Leu Leu Leu Lys Lys Ile Asp Ile Ile Ile
 500 505 510
 Arg Glu Ser Leu Lys Ser Ser Leu Ala Ile Glu Thr Leu Pro Gly Lys
 515 520 525
 Asn Val Ser Gln Ser Ser His Gly Asp Gln Ile Ser Ser Phe Lys Asn
 530 535 540
 Ala Leu Ile Gly Asn Gly Ser Lys Asn Thr Lys Phe Arg Lys Ser Leu
 545 550 555 560
 Ile Pro Tyr Ser Ser Ser Glu Glu Gln Asn Thr Thr Thr Thr Ile Lys
 565 570 575
 Leu Ser Ser Ser Pro Thr Ser Gln Ile Lys Phe Ala Thr Ser Val Lys
 580 585 590
 His Lys Asp Gly Arg Ala Ala Leu Gly Lys Ala Arg Asn Leu Pro Asp
 595 600 605
 Ile Arg His Ser Ile Ser Phe Asp Lys Glu Asn Ser Phe Asp Pro Ser
 610 615 620

Asp Lys Ser Ser Ser Val Asp Asn Ser Ile Pro Leu Arg Lys Val Lys
 625 630 635 640
 Ser Ala Gly Ala Leu Arg Lys Val Lys Thr Asn Asp Ser Ser Ser Ser
 645 650 655
 Ala Gly Ser Lys Lys Ser Ser Ser Ser Phe Ser Thr Val Asn Thr Phe
 660 665 670
 Thr Gly Gly Gly Val Gly Ile Phe Lys Val Phe Lys Ser Gly Ser Ser
 675 680 685
 Ser Gly Asn Lys Ser Ser Ser Arg Arg Asn Ser Ser Ser Gly Asp Val
 690 695 700
 Phe Glu Ser Asp Asp Arg Asn Asp Lys Lys Lys Lys Lys Lys Lys Lys
 705 710 715 720
 Lys Lys Ser Leu Phe Leu Phe Gly Lys Ile
 725 730

<210> 255

<211> 2270

<212> DNA

<213> Candida albicans

<400> 255

aattttcccc ccgtcataag ttctataaca cggttggtct tgatggcata atttcatgct 60
 ggaacctaca aaccgcgaag aaaataaaaa atttcgcca atttaacgaa gacagcgtgg 120
 ttaaaattgc ttgttcggac aatattctat gtctggcaac ttctgatgat actttcaaga 180
 caaacgccgc aattgaccaa actattgaac taaacgcgaag ttcaatatac ataattttg 240
 actatgagaa ctgatattct cgtgaagatt cgtgtagtat gatagaacat tccagaaaaa 300
 aaattcagat tcatcgtctt ctcttcgctt ctctcctttt aaggaataaa gaaaaaatca 360
 catacataga ttaagtaaat aggatctgct agaaaaatta tatatagatc aatcatctta 420
 ttaagggtatc ttgtttaagc ccaaaagtct gtccecaaat tcctcactgt agctactaaa 480
 acaacctata cgcaagaaag atgtcattga cagccgatga atacaaacaa caaggtaacg 540
 ctgcatttac cgctaaggat tacgataaag cgatagagct cttcactaaa gctattgaag 600
 tttctgaaac tccaaccat gttttatatt ctaacagggtc cgctgttat acttcttta 660
 agaaatttag tgacgcattg aatgatgcta atgaatgtgt caaatcaat ccattctgg 720
 ctaagggtta taatagactc ggtgccgccc acttaggtct tggcgatctc gacgaagctg 780
 aaagcaacta caaaaagcc ttggagttgg atgccagtaa caaggccgcc aaagaaggat 840
 tggatcaggt tcatcgtacc caacaggcaa gacaggcaca gcctgattta ggggtgacac 900
 agttgtttgc tgacccaaat ttaattgaaa atttaaagaa gaaccacaaa actagcgaaa 960
 tgatgaagga ccctcaatta gtggctaaac tgattgggta caaacaaaat ccgcaagcta 1020
 ttggccaaga tctgtttact gatccaagat taatgaccat catggctaca ttgatggggg 1080
 ttgatttaaa catggatgat ataaaccaat caaactccat gccaaaggaa ccggaaacca 1140
 gtaaaagcac tgaacaaaag aaagatgctg aaccacaaag cgattccact acgagcaagg 1200
 aaaattcctc taaagcacca cagaaagaag aaagtaagga atccgagcca atggaagttg 1260
 atgaagatga ctctaaaatt gaggcgcaca aggaaaaggc cgaaggtaac aagttttaca 1320
 aggcacgtca attcgatgaa gctatagagc actacaacaa ggcgtgggaa ctgcataaag 1380
 atattaccta ttaaacacac cgtgctgctg ctgaatacga aaaaggcgaa tacgagacag 1440
 ctatttctac cttgaatgat gctgttgagc aaggtagaga aatgagagcg gattacaagg 1500
 tcatttccaa atcatttgcg cgtattggta atgcctatca caaattgggt gacttgaaga 1560
 aaactataga atactaccaa aaatcattga ccgaacatcg tactgctgac attttgacca 1620
 agttaaggaa tgctgaaaaa gaattgaaga aagctgaggc ggaggcgtat gttaaccttg 1680

aaaaggcgga ggaagcccgt cttgaaggta aggaatatatt taccaagagt gattggccga 1740
 atgctgttaa ggcttacact gaaatgatca aaagggcacc tgaagatgct agaggatatt 1800
 ctaatagagc tgctgcacta gcgaagttaa tgtctttccc tgaagctatc gcagattgta 1860
 acaaagccat tgaaaaagat ccaaatttcg tgagagctta tatcagaaaag gccaccgcac 1920
 aaattgctgt taaagaatat gcttcgctt tggaaacact agatgcggcc agaaccaaag 1980
 atgctgaagt gaataatggt tctagtgcga gggaaattga tcaactgtac tacaaggcaa 2040
 gccaacaaaag attccaacct ggtaccagta acgaaacccc agaagaaacc tatcaaaggg 2100
 ccatgaaaga tcctgaagtg gctgcatca tgcaagatcc tgttatgcaa agtattttgc 2160
 agcaggccca acagaatccc gctgctttac aagaacacat gaaaaatcca gaagtattca 2220
 aaaagattca gacgttgatc gctgctggta tcatccggac tggccgctaa 2270

<210> 256

<211> 589

<212> PRT

<213> Candida albicans

<400> 256

Met Ser Leu Thr Ala Asp Glu Tyr Lys Gln Gln Gly Asn Ala Ala Phe
 1 5 10 15
 Thr Ala Lys Asp Tyr Asp Lys Ala Ile Glu Leu Phe Thr Lys Ala Ile
 20 25 30
 Glu Val Ser Glu Thr Pro Asn His Val Leu Tyr Ser Asn Arg Ser Ala
 35 40 45
 Cys Tyr Thr Ser Leu Lys Lys Phe Ser Asp Ala Leu Asn Asp Ala Asn
 50 55 60
 Glu Cys Val Lys Ile Asn Pro Ser Trp Ser Lys Gly Tyr Asn Arg Leu
 65 70 75 80
 Gly Ala Ala His Leu Gly Leu Gly Asp Leu Asp Glu Ala Glu Ser Asn
 85 90 95
 Tyr Lys Lys Ala Leu Glu Leu Asp Ala Ser Asn Lys Ala Ala Lys Glu
 100 105 110
 Gly Leu Asp Gln Val His Arg Thr Gln Gln Ala Arg Gln Ala Gln Pro
 115 120 125
 Asp Leu Gly Leu Thr Gln Leu Phe Ala Asp Pro Asn Leu Ile Glu Asn
 130 135 140
 Leu Lys Lys Asn Pro Lys Thr Ser Glu Met Met Lys Asp Pro Gln Leu
 145 150 155 160
 Val Ala Lys Leu Ile Gly Tyr Lys Gln Asn Pro Gln Ala Ile Gly Gln
 165 170 175
 Asp Leu Phe Thr Asp Pro Arg Leu Met Thr Ile Met Ala Thr Leu Met
 180 185 190
 Gly Val Asp Leu Asn Met Asp Asp Ile Asn Gln Ser Asn Ser Met Pro
 195 200 205

<210> 259
 <211> 1474
 <212> DNA
 <213> *Candida albicans*

<400> 259
 aaacccatac acaatgaacc ttatcacacc caaacatatg atatggtatt aaaaaatgaa 60
 aaaaattcat tattcttttag cgtaattatt gaagaaaaaa cagtgcgcgc ggtaattttt 120
 tgtcactcag taactagaga gaagccgaat gtactcccc ggctagctgg agaccatggc 180
 tctgcctagg atttctctta tgctttcctt tcaccaatca ctttgttccg gcgaggcccc 240
 cgaagctcgc tttctttcag cctagcaatc atgttcttgc cagcgtcgta gactactgta 300
 tggcagttgc tgcacttgcc atgaatatcc tagtgaagcc tctatgcaat aatccagtta 360
 ctgcgcttaga atcctggtaa aatgtctaata cttattacat tacagcaacg tattagattt 420
 tgattgaaaa ttagtccttg cgacttggtg tatatcttat ttttaagaaag ctgaaaggaa 480
 gaaagatcat cacgaacaac atgtctgctc cacaagccaa gattttgtct caagctccaa 540
 ctgaattgga attacaagtt gctcaagctt tcggtgaatt ggaaaattct tctccagaat 600
 tgaaagctga gttgagacct ttgcaattca agtccatcag agaagtatgt tattaatttg 660
 aatctaaact taagaataat ggagagtaac aaaggaaaaa agtgtgaacg ggacgatacc 720
 agaatgtttc aatctagaaa agtataaaaag ataaggacta ggactcaaat gtatttggct 780
 gactatcgcc tgaaccttga tgctaagcaa ataccatata ttcaagaaaa agcctactcc 840
 agtgtttaag aagaagggaa cgatttacta gatcatgcta tacgcagtaa ggttctgata 900
 gttaattaca atcgggtccaa gttctaagcg gtgtcgtcca tgcataatc atttacaagt 960
 tactggcgct aactcttcaa atattcaaaa tatcacctaa tcaaacttac taacattttc 1020
 cttttttggt ttccttcttt tatagatcga cgttgctggg ggtaagaagg ctttggccat 1080
 ttttggtcca gtcccatctt tggtctggtt ccacaagggt caaactaagt tgacccgtga 1140
 attgaaaaag aaattccaag accgtcatgt catcttcttg gctgaaagaa gaatcttgcc 1200
 aaagccatct agaacatcta gacaagtcca aaagagacca agatccagaa ccttgactgc 1260
 tgttcatgac aagatcttgg aagacttagt cttcccaact gaaatcgttg gtaagagagt 1320
 tagatatttg gttggtggta acaagatcca aaaggttttg ttagactcaa aggatgtcca 1380
 acaaatcgac tacaaattgg aatctttcca agctgtttac aacaaattga ctggtaaagca 1440
 aattgttttc gaaattccaa gtgaaactca ttag 1474

<210> 260
 <211> 190
 <212> PRT
 <213> *Candida albicans*

<400> 260
 Met Ser Ala Pro Gln Ala Lys Ile Leu Ser Gln Ala Pro Thr Glu Leu
 1 5 10 15
 Glu Leu Gln Val Ala Gln Ala Phe Val Glu Leu Glu Asn Ser Ser Pro
 20 25 30
 Glu Leu Lys Ala Glu Leu Arg Pro Leu Gln Phe Lys Ser Ile Arg Glu
 35 40 45
 Ile Asp Val Ala Gly Gly Lys Lys Ala Leu Ala Ile Phe Val Pro Val
 50 55 60
 Pro Ser Leu Ala Gly Phe His Lys Val Gln Thr Lys Leu Thr Arg Glu
 65 70 75 80

Leu Glu Lys Lys Phe Gln Asp Arg His Val Ile Phe Leu Ala Glu Arg
 85 90 95
 Arg Ile Leu Pro Lys Pro Ser Arg Thr Ser Arg Gln Val Gln Lys Arg
 100 105 110
 Pro Arg Ser Arg Thr Leu Thr Ala Val His Asp Lys Ile Leu Glu Asp
 115 120 125
 Leu Val Phe Pro Thr Glu Ile Val Gly Lys Arg Val Arg Tyr Leu Val
 130 135 140
 Gly Gly Asn Lys Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Val Gln
 145 150 155 160
 Gln Ile Asp Tyr Lys Leu Glu Ser Phe Gln Ala Val Tyr Asn Lys Leu
 165 170 175
 Thr Gly Lys Gln Ile Val Phe Glu Ile Pro Ser Glu Thr His
 180 185 190

<210> 261
 <211> 803
 <212> DNA
 <213> Candida albicans

<400> 261
 acccatttta caaatttttt ttgctatttg agccatagta cccattaata ggtctcgtcc 60
 attcccttgt ttttttttta ttgtttcaat tacactacat aattaaaaat cacatcactt 120
 tcaactctcac cttagtcggt ctttatcaac caaaaataaa aaaatgcttc aatccgttgt 180
 ctttttcgct cttttaacct tcgcaagttc tgtgtcagcg atttattcaa acaatactgt 240
 ttctacaact accacttttag cgcccagcta ctcttggtg cccaagaga ctaccatata 300
 gtacgccgac gacaccacta ccttttttgt cacctcaacg gtctactcca cgagctgggt 360
 cacctcaact tcagccacca ttaccaatgc ggctctctcc tccttgcca cctcttcggc 420
 ctctggatct gtaacccag aatccacca tgaaattacc tccacctga ctatcacgtc 480
 cactttgctg ctaacccttc atgactccac tactttgtct ccatcatcta ctgcagcaag 540
 tgtcagtgc gaagattcaa acaacaaaga tgcaaagggtc aagtcctttg aacaggcttc 600
 aacttccaat gggtgcgtcc caatcacaaa gtttgctact gtcaccaatg agcccggtac 660
 ccagtacgtt acagtcaccc caaatacgac tacacaatac gttactgtca ccggtgcacc 720
 ttctgttacc actaccttc caggtaacgt acaatgggtac aacaccactt cgattactaa 780
 ttcgaccagt tgggtgaatta tga 803

<210> 262
 <211> 100
 <212> PRT
 <213> Candida albicans

<400> 262
 Met Thr Pro Leu Leu Cys Leu His His Leu Leu Gln Gln Val Ser Val
 1 5 10 15
 Thr Lys Ile Gln Thr Thr Lys Met Gln Arg Ser Ser Pro Leu Asn Arg
 20 25 30

265

Glu Glu Ile Asp Thr Lys Asn Leu Tyr Val Ile Lys Ala Leu Gln Ser
 35 40 45
 Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr
 50 55 60
 Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu
 65 70 75 80
 Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn
 85 90 95
 Pro Thr Gln Arg Pro Gln Arg Arg Tyr
 100 105

<210> 265
 <211> 1432
 <212> DNA
 <213> Candida albicans

<400> 265
 tatttacaag ctagataaaa aaaaaatcaa atagcaagct attctgtcat atcttaagggt 60
 gctgattggt tgtaggcacg aagtaaacia gctcttcccc aaaacaataa atacgggtttt 120
 cgggactggt caccgcgtaca ttttacgttt ccgacggcgc gatgctatct ttgaattttt 180
 atctctttca ggtaacccca tgaccagtag ggcggcttac taccgaagag aaaaatgtcc 240
 gcggcctaga cagttacttc ccaggccagg gccaggccac acggacagag gcagattcca 300
 agttgttccg catagtctgt ctagctcttt ctcaattttc cgccagattc tgtctaattt 360
 ctttcgctc gagttggcaa cagtacgaag aagtaactct aatagataga tataaccggt 420
 tttagaggca ttatttttgc agaagataat agaagagaac cgtaacaaag gaatcaagca 480
 aagaaaaagt atgtaataga atgtattgta tgcttggtga atgaatgtca atgtagctat 540
 tttatatggt gagctcaa atgaatgaaca tatcgtggaa atttaaaata ctgaagaata 600
 cccaataagt caatgcaacc tgtgaatggt tttcctgaaa tacgccgaat actgaatacg 660
 attattacca taaattgctt ctagaaggaa ggcgggtgtac catttaatac tgatgatatg 720
 gttaatatca tttgagaagt cttcacatga ggactataga actaccatcc aggaattata 780
 gaggaatata actgaatcag agatctatgt tgaaacattc atttacatgt aattgtctgc 840
 aataaagcaa tatgttgtaa atattgcaaa gaataaattc ttttttctgt 900
 tttatcttta acagtggctc atttcaaaga ataccaagtc attggtcgtc gtttaccac 960
 tgaatccggt ccagaaccaa agttgttcag aatgagaatt tttgcttcaa atgaagtc 1020
 cgccaagtct cgttactggt atttcttgca aaaattgcac aagggttaaga aggtctctgg 1080
 tgaaattggt tccatcaacc aaatcaacga agctcaccca accaagggtca agaacttcgg 1140
 tgtttgggtt agatacagatt ccagatctgg tactcacaac atgtacaagg aaatcagaga 1200
 cgtatccaga gttgctgccg tcgaaacctt ataccaagac atggctgcta gacacagagc 1260
 tagattttag tctattcaca tcttgaaagg tgctgaaatt gaaaagactg ctgatgtcaa 1320
 gagacaatac gtcaagcaat tcttgaccaa ggatttataa tccccattac ctcacagagt 1380
 ccaaaaatct accaagactt tctcttataa gagaccatca accttctact aa 1432

<210> 266
 <211> 174
 <212> PRT
 <213> Candida albicans

<400> 266
 Met Tyr Leu Ala His Phe Lys Glu Tyr Gln Val Ile Gly Arg Arg Leu

1	5	10	15
Pro Thr Glu Ser Val Pro Glu Pro Lys Leu Phe Arg Met Arg Ile Phe	20	25	30
Ala Ser Asn Glu Val Ile Ala Lys Ser Arg Tyr Trp Tyr Phe Leu Gln	35	40	45
Lys Leu His Lys Val Lys Lys Ala Ser Gly Glu Ile Val Ser Ile Asn	50	55	60
Gln Ile Asn Glu Ala His Pro Thr Lys Val Lys Asn Phe Gly Val Trp	65	70	75
Val Arg Tyr Asp Ser Arg Ser Gly Thr His Asn Met Tyr Lys Glu Ile	85	90	95
Arg Asp Val Ser Arg Val Ala Ala Val Glu Thr Leu Tyr Gln Asp Met	100	105	110
Ala Ala Arg His Arg Ala Arg Phe Arg Ser Ile His Ile Leu Lys Val	115	120	125
Ala Glu Ile Glu Lys Thr Ala Asp Val Lys Arg Gln Tyr Val Lys Gln	130	135	140
Phe Leu Thr Lys Asp Leu Lys Phe Pro Leu Pro His Arg Val Gln Lys	145	150	155
Ser Thr Lys Thr Phe Ser Tyr Lys Arg Pro Ser Thr Phe Tyr	165	170	

<210> 267

<211> 932

<212> DNA

<213> Candida albicans

<400> 267

```

cttcttacaa gttaatgaat agtatatata tgtaaaaaaa aattctgctt catgtatata 60
cgcacctcgt tattgaggta ttgcgaatgt agcagttgaa taagcaaaga cgaggtttgt 120
acatcttggc atattaaatg gttatttcgg ggtttgtttc ggctcaacgg tgatataaaa 180
agaaatccag tactgtttac cattgtgcat ccgtacattt gatttgttta caacatcttc 240
acatttccat tgtggaatca ttttattttt ttcagaatac cttaccgcga agcaaacttt 300
caagcaaact tacaatttgc aaaatttcac cgaattctcc gcaggacata ttataaaaagt 360
tatgtcatct cttatcacaa caggtctata agtgttcctt gttcaattgt ttttcccaat 420
tcaaaactct tcacggagca gtttaattat cttactgtcg aagaagtcaa aaactagact 480
atatattatt gagaagaaaa atgtctgacg ttgaagaagt cggtgaagtt caagaagaaa 540
ctggtgttga acaaactgcc gaagttacta tcgaagatgc tttgaagggt gttttgagaa 600
ccgctttggt tcacgatggt ctagctagag gtttgagaga atctaccaag gctttaacca 660
gaggtgaagc tttattgggt gttttgggtc gctctgttac tgaagctaac attatcaagt 720
tggttgaagg tttggctaac gaccagaaa acaaggttcc attgatcaag gttgctgatg 780
ctaagcaatt aggtgaatgg gctggtttgg gtaagatcga ccgtgaagggt aacgccagaa 840
aggttgtcgg tgccctcggt gttgttgcga agaactgggg tgctgaaact gatgaattgt 900
ccatgatcat ggaacacttc tccaacaat aa 932

```


ggtctaactg acactactgt tccaaagaga ttgggtccaa agagagctaa caacatcaga 1320
 aagttcttcg gtttgtccaa ggaagatgac gtctgtgatt tcgtcatcag aagagaagtc 1380
 accaagggtg aaaagactta caccaaggct ccaaagatcc aaagattggt tactcctcaa 1440
 agattgcaaa gaaagagaca ccaaagagct ttgaagggtca gaaacgctca agctcaaaga 1500
 gaagctgctg ccgaatacgc tcaattgttg gctaagagat tgtctgaaag aaaggctgag 1560
 aaggctgaaa tcagaaagag aagagcttct tctttgaagg cttaa 1605

<210> 272

<211> 236

<212> PRT

<213> Candida albicans

<400> 272

Met	Lys	Leu	Asn	Ile	Ser	Tyr	Pro	Val	Asn	Gly	Ser	Gln	Lys	Thr	Phe
1				5					10					15	
Glu	Ile	Asp	Asp	Glu	His	Arg	Ile	Arg	Val	Phe	Phe	Asp	Lys	Arg	Ile
		20					25						30		
Gly	Gln	Glu	Val	Asp	Gly	Glu	Ala	Val	Gly	Asp	Glu	Phe	Lys	Gly	Tyr
		35					40						45		
Val	Phe	Lys	Ile	Ser	Gly	Gly	Asn	Asp	Lys	Gln	Gly	Phe	Pro	Met	Lys
	50					55					60				
Gln	Gly	Val	Leu	Leu	Pro	Thr	Arg	Ile	Lys	Leu	Leu	Leu	Thr	Lys	Asn
	65				70					75					80
Val	Ser	Cys	Tyr	Arg	Pro	Arg	Arg	Asp	Gly	Glu	Arg	Lys	Arg	Lys	Ser
			85						90					95	
Val	Arg	Gly	Ala	Ile	Val	Gly	Pro	Asp	Leu	Ala	Val	Leu	Ala	Leu	Val
			100					105					110		
Ile	Val	Lys	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Gly	Leu	Thr	Asp	Thr	Thr
		115					120						125		
Val	Pro	Lys	Arg	Leu	Gly	Pro	Lys	Arg	Ala	Asn	Asn	Ile	Arg	Lys	Phe
		130				135					140				
Phe	Gly	Leu	Ser	Lys	Glu	Asp	Asp	Val	Arg	Asp	Phe	Val	Ile	Arg	Arg
	145				150					155					160
Glu	Val	Thr	Lys	Gly	Glu	Lys	Thr	Tyr	Thr	Lys	Ala	Pro	Lys	Ile	Gln
				165					170					175	
Arg	Leu	Val	Thr	Pro	Gln	Arg	Leu	Gln	Arg	Lys	Arg	His	Gln	Arg	Ala
			180					185					190		
Leu	Lys	Val	Arg	Asn	Ala	Gln	Ala	Gln	Arg	Glu	Ala	Ala	Ala	Glu	Tyr
		195					200					205			
Ala	Gln	Leu	Leu	Ala	Lys	Arg	Leu	Ser	Glu	Arg	Lys	Ala	Glu	Lys	Ala
	210					215					220				
Glu	Ile	Arg	Lys	Arg	Arg	Ala	Ser	Ser	Leu	Lys	Ala				

Asn	Gly	Ser	Ser	Thr	Gln	Phe	Val	Arg	Lys	Lys	Arg	Ser	Thr	Ser	Ile
	130					135					140				
Ser	Asn	Ala	Val	Val	Ser	Ser	Lys	Pro	Arg	Leu	Ala	Ser	Ser	Ala	Ile
145					150					155					160
Asn	Ala	Thr	Ala	Ser	Ser	Ser	Val	Gly	Lys	Gly	Lys	His	Pro	Pro	Ile
				165					170					175	
Ser	Ser	Pro	Ser	Asn	Ala	Thr	Leu	Lys	Arg	Ser	Asn	Ser	Thr	Ser	Gly
			180					185					190		
Glu	Lys	Thr	Lys	Arg	Ser	Ile	Phe	Gly	Ser	Leu	Phe	Ser	Lys	Arg	Ser
	195						200					205			
Thr	Ser	Ser	Ser	Ala	Ser	Thr	Ala	Lys	Lys	Pro	Leu	Pro	Val	Val	Asn
210						215					220				
Thr	Ser	Thr	Thr	Glu	Asn	Glu	Ser	Gly	Gly	Ile	Lys	Ala	Val	Ala	Thr
225					230					235					240
Pro	Asp	Pro	Arg	Val	Lys	Glu	Ile	Ser	Ser	Pro	Met	Arg	Gly	Val	Ala
				245					250					255	
Pro	Thr	Ala	Ser	Lys	Pro	Gln	Thr	Pro	Ile	Leu	Pro	Ser	Pro	Ala	Leu
			260					265					270		
Ala	Val	Lys	Asp	Leu	Ser	Thr	Val	Ser	Leu	Lys	Arg	Val	Ser	Phe	Ala
		275					280					285			
Val	Asp	Lys	Phe	Glu	Ser	Asp	Pro	Pro	Gln	Gln	Leu	Pro	Ser	Arg	Thr
	290					295					300				
Pro	Lys	Lys	Gly	Asn	Ile	Leu	Ile	Pro	Asp	Asp	Met	Ile	Ser	Glu	Val
305				310						315					320
Pro	Ser	Ile	Ser	Val	Gly	Ile	Ser	Ser	Ser	Asn	Gln	Ser	Ala	Lys	Ser
				325					330					335	
Thr	Asn	Ser	Asn	Ile	Lys	Gly	Pro	Leu	Tyr	Thr	Lys	Lys	Ser	Lys	Glu
			340					345					350		
Tyr	Ile	Leu	Ala	Leu	Glu	Asn	Gln	Lys	Leu	Ala	Leu	Arg	Glu	Ala	Ala
		355					360					365			
Lys	His	Gln	Gln	Glu	Ala	His	Phe	Ala	Ala	Asn	Arg	Ile	Ala	Phe	Glu
	370					375					380				
Val	Ala	Asn	Phe	Lys	Thr	Ala	Ser	Asp	Ala	Gly	Gly	Lys	Leu	Thr	Glu
385					390					395					400
Lys	Ser	Ser	Glu	Gly	Thr	Ile	Thr	Lys	Gln	Arg	Glu	Glu	Val	Ser	Pro
				405					410					415	
Pro	Asn	Val	Glu	Ala	Asp	Arg	Glu	Leu	Glu	Asn	Asn	Lys	Leu	Ala	Glu
			420					425					430		

Asn Leu Ser Lys Ala Gly Ile Asp Lys Pro Ile His Met His Glu His
435 440 445

Tyr Phe Lys Glu Pro Asp Gln Asp Lys Tyr Gln Asp Gly His Ser Ile
450 455 460

Glu Asn Asn Glu Val Thr Leu Asp Val Ile Tyr Thr Arg Cys Cys His
465 470 475 480

Leu Arg Glu Ile Leu Pro Ile Pro Ser Thr Leu Arg Gln Val Lys Asp
485 490 495

Lys Thr Ala Pro Leu Gln Ile Leu Lys Phe Leu Asn Pro Lys Pro Thr
500 505 510

Leu Ile Asp Ile Leu Ser Phe Cys Asp Phe Ile Thr Ile Ala Pro Ile
515 520 525

His Thr Ile Val Phe Asp Asn Val Ala Leu Asn Gln Asp Met Phe Arg
530 535 540

Ile Ile Ile Ser Ala Leu Val Asn Ser Thr Val Leu Asp Lys Leu Ser
545 550 555 560

Leu Arg Asn Val Arg Ile Asp Gln Asp Gly Trp Lys Leu Leu Cys Lys
565 570 575

Phe Leu Leu Leu Asn Lys Ser Leu Asn Lys Leu Asp Ile Ser Gln Thr
580 585 590

Lys Ile Lys Ser Asp Leu Ala Glu Ser Leu Tyr Arg His Asn Met Asp
595 600 605

Trp Asn Leu Phe Thr Asp Val Leu Ser Gln Arg Ser His Lys Pro Ile
610 615 620

Glu Glu Leu Leu Phe Asn Gly Ile Gln Phe Ser Lys Ile Pro Tyr Ser
625 630 635 640

Cys Phe Ala Arg Leu Leu Thr Ser Phe Ala Thr Gln Lys Asn Phe Pro
645 650 655

Glu Ser Gly Ile Arg Leu Gly Leu Ala Gly Ala Thr Thr Ser Asn Ile
660 665 670

Ser Gln Asp Cys Leu Lys Phe Ile Phe Asn Trp Met Ser Gln Tyr Asn
675 680 685

Val Gln Gly Val Asp Leu Ala Phe Asn Asp Leu Ser Thr Met Ile Lys
690 695 700

Pro Met Val Gly Lys Leu Ser Ala Leu Ser Tyr Asp Asn Leu Arg Tyr
705 710 715 720

Phe Ile Leu Asn Ser Thr Asn Ile Ser Thr Ser Tyr Asp Leu Ala Leu
725 730 735

Leu Leu Lys Tyr Leu Ser Lys Leu Pro Asn Leu Ile Phe Leu Asp Leu
 740 745 750
 Ser Asn Leu Ser Gln Cys Phe Pro Asp Ile Leu Pro Tyr Met Tyr Lys
 755 760 765
 Tyr Leu Pro Arg Phe Pro Asn Leu Lys Arg Ile His Leu Asp Ser Asn
 770 775 780
 Asn Leu Thr Leu Lys Glu Leu Ala Val Val Cys Asn Ile Leu Ile Lys
 785 790 795 800
 Cys Lys Ser Leu Ser His Val Ser Met Thr Asn Gln Asn Val Glu Asn
 805 810 815
 Phe Tyr Leu Met Asn Gly Thr Asp Ser Pro Val Gln Gln Thr Asn Thr
 820 825 830
 Asp Gly Asp Leu Asp Ser Ser Ser Thr Leu Asp Val Lys Gly Gln Phe
 835 840 845
 Ala Lys Asn Ser Phe Ser Ser Thr Leu Tyr Ala Phe Ala Arg Asp Ser
 850 855 860
 Pro Asn Leu Ile Gly Leu Asp Phe Asp Tyr Asp Leu Ile Ser Glu Glu
 865 870 875 880
 Ile Gln Ser Arg Ile Ala Leu Cys Leu Met Arg Asn Met Lys Arg Thr
 885 890 895
 Met Asp Ser Thr Phe Gln Leu Asp Glu Leu Asp Ser Gln Asp Asp Leu
 900 905 910
 Leu Phe Asp Gly Ser Leu Val Thr Met Thr Ala Glu Ser Val Leu Glu
 915 920 925
 Lys Leu Asn Leu Leu Ser Asp Lys Ser Thr Lys Val Lys Lys Asp Thr
 930 935 940
 Thr Lys Arg Tyr Leu Leu Lys Lys Tyr Ile Glu Lys Phe His Ile Leu
 945 950 955 960
 His His Asn Val Gln His Thr Ile Asp Thr Met Phe Glu Lys Arg Lys
 965 970 975
 Ser Gly Glu Leu Pro Leu Gln Glu Lys Glu Asn Leu Val Arg Leu Leu
 980 985 990
 Leu Leu Glu Gln Asn Leu Cys Asn Ile Leu Glu Leu Phe Ser His Asn
 995 1000 1005
 Pro Asn Leu Asn Asp Val Leu Gly Ser Ser Arg Asp Asp Ser Lys Glu
 1010 1015 1020
 Ser Val Asp Ser Ser Glu Asp Ser Lys Leu Pro Ala Leu Lys His Val
 1025 1030 1035 1040


```

tcaacgtatc aaccataaga accataatca taataattgt ttaccttaat ggcgatatcg 240
ccttttatca ccatcgacga taacaaacgc ctattctgtc taccgtttct ttttttcgct 300
cgcaatatca gaatcgttta tcccaaaggg tagttatagc aactatttaa ataacttaga 360
tgtttcttta acttattccg tcatacgtac acaaacaccc gctagatata gcactccttg 420
ctgtcgaaca ttataaagggt gcttttataaa ctactaatcg tatattcagc aggtcagaac 480
gcaaagtcgg acgataaaact atgttgaagc tagctcgtcc atttattccg cctttatcaa 540
ggaacaatgc catttcttca ggaatagttc tcacttctag aagatttcag tcttccttta 600
cgttcttaag taaccagtct ttactatcta aaaatcaaat gaaatccaaa agaaaaaagg 660
gcagtaaaaaa ggcagcgtac catcgtcaac ccccggaaca cgaacatact gcaccactta 720
taaagcaaaa caagacaatc acaaagaaag aacatagcga tgtgagaggt tctcatttaa 780
aaaagaaaag aagcgatttt tcgtggctac caagagtacc atccacctca catttaaagc 840
agagtgcacat gaccacaaat gtactctatt ctggatatag acccttattc atcaatccca 900
atgacccgaa gctaaaggaa gacaccgga gtacgttata cgaatttgcg atgaagcttg 960
aagattttaa tgaacctcta tcaccatgga tttcctctgc cactggactt gaattctttt 1020
cagagtggga gaatatacct agtgaactac tgaaaaattt gaagcctttt catccacctt 1080
aggaaaaatc aatgaacaca aatgagctta ttcatgtaag tgctaagaga aatacattag 1140
ttgacaataa aacaagttag acgcttcagc ggaaaatgga tgaattttca aagagaagag 1200
gaaaggggag aaaaaagtca gtagtgacgt tgctccaaat gaagaaaaaa cttgagggat 1260
ga

```

<210> 276

<211> 253

<212> PRT

<213> Candida albicans

<400> 276

```

Met Leu Lys Leu Ala Arg Pro Phe Ile Pro Pro Leu Ser Arg Asn Asn
  1             5             10             15

```

```

Ala Ile Ser Ser Gly Ile Val Leu Thr Ser Arg Arg Phe Gln Ser Ser
      20             25             30

```

```

Phe Thr Phe Leu Ser Asn Gln Ser Leu Leu Ser Lys Asn Gln Met Lys
    35             40             45

```

```

Ser Lys Arg Lys Lys Gly Ser Lys Lys Ala Ala Tyr His Arg Gln Pro
    50             55             60

```

```

Pro Glu His Glu His Thr Ala Pro Leu Ile Lys Gln Asn Lys Thr Ile
    65             70             75             80

```

```

Thr Lys Lys Glu His Ser Asp Val Arg Gly Ser His Leu Lys Lys Lys
      85             90             95

```

```

Arg Ser Asp Phe Ser Trp Leu Pro Arg Val Pro Ser Thr Ser His Leu
    100            105            110

```

```

Lys Gln Ser Asp Met Thr Thr Asn Val Leu Tyr Ser Gly Tyr Arg Pro
    115            120            125

```

```

Leu Phe Ile Asn Pro Asn Asp Pro Lys Leu Lys Glu Asp Thr Gly Ser
    130            135            140

```

```

Thr Leu Tyr Glu Phe Ala Met Lys Leu Glu Asp Leu Asn Glu Pro Leu
    145            150            155            160

```


Ser Pro Trp Ile Ser Ser Ala Thr Gly Leu Glu Phe Phe Ser Glu Trp
165 170 175

Glu Asn Ile Pro Ser Glu Leu Leu Lys Asn Leu Lys Pro Phe His Pro
180 185 190

Pro Lys Glu Lys Ser Met Asn Thr Asn Glu Leu Ile His Val Ser Ala
195 200 205

Lys Arg Asn Thr Leu Val Asp Asn Lys Thr Ser Glu Thr Leu Gln Arg
210 215 220

Lys Met Asp Glu Phe Ser Lys Arg Arg Gly Lys Gly Arg Lys Lys Ser
225 230 235 240

Val Val Thr Leu Leu Gln Met Lys Lys Lys Leu Glu Gly
245 250

<210> 277

<211> 1940

<212> DNA

<213> Candida albicans

<400> 277

acgttatTTTT caaaacacat acgaaatcgc tggacttttct cactaaaggc ttccggagacc 60
tgcggttctt ccatcccat ctcttccaca tataccgggg gttctgatgg cattcctata 120
gcttgctcaa agtcctgcga gtttagctca tcttgtagt tatttgctgg ttcttcaaca 180
ttcgggaagag tagtgtagcc cctagtattc accatatacct ttgtatactc atatgcgaac 240
ttgtctaata caatgtatac caaaaataac agcttgaaaa aaatctcagg gtcttttcat 300
tgaataatct cattctgcta ttttaagttt ttcgtttgca acccgagact gtcgagctag 360
aaaatttcat tgatacgatt taaaaataat cgatgccagt aatagcctca aaaaacttat 420
gcaaaaatac gagatactat aaactacagc ttagctaaact ctaacattat tatataaaac 480
aatgggcttc aatatagcgt atgtctagct cacagcatgt gttccaaata cattaaagaa 540
gatctctttt gttgttgata ctaaccagta aagttgagag ttataacaat gaaaatagga 600
tgctgtgcga ctttttttat ccacagttag gtggagtcga attccatata tatcatttat 660
cgcagaaact aatcgatttg ggccattctg tcgtcattat aactcacgct tacaagatc 720
gagtcggcgt acgacatctt accaacggtc taaaggctca tcacgtacca ttttttgtga 780
ttttcagaga aaccactttt cccactgttt tttcaacatt tccaataata aggaatatc 840
ttctcagaga gcagatccaa attgttcatt ctcatggtag cgcttccacg ttcgctcacg 900
aggggaattct tcatgctaata actatgggat tgagaactgt gttcacggac cattcactct 960
acgggttttaa taacttaacg tcgatttggg tgaataagtt gctaacattt accttgacaa 1020
acatagatcg gggtatatgt gtttctaata catgcaaaga aaatatgatt gttagaacag 1080
aattaagtcc tgatataatc tcagtaattc ccaacgcagt ggtgagcgaa gatttcaaac 1140
caagggatcc tactgggtggc accaagagaa acaaagtag ggataagata gtgacgtgg 1200
tcacggaag gctctttcca acaaaaggtt ccgatttact tactcgcata attccgaaag 1260
tttgttcctc acatgaagat gtcgaattta tagtagcggg cgatgggtcca aagttcatag 1320
attttcaaca aatgattgaa agtcatagac tacaaaaacg tgtgcaactc ttaggctctg 1380
ttccacatga gaaagtcagg gatgtattat gtcaagggtga catatattta cacgctagtt 1440
taacagaagc atttggtaca attctagttg aggccgcac ttgtaatttg ctaattgtaa 1500
cgacacaagt cggaggaatt cccgaagtgt taccaaata gatgactgtt tatgcagaac 1560
agacatccgt ttctgacctt gttcaagcaa caaataaagc tatcaatata ataagaagta 1620
aagcttttga cacttctctt tttcatgata gcgtgtctaa aatgtacgac tggatggacg 1680
tagccaaaag gacagtagag atatatacta atatatcttc tacttcttcc gctgatgata 1740
aagattggat gaaaatggta gcaaatcttt acaaaagaga tggaaatctgg gctaaacatc 1800
tttatctggt atgtggaatt gtagagtaca tgcttttttt cctcttagag tggctatacc 1860

Phe Gln Gln Met Ile Glu Ser His Arg Leu Gln Lys Arg Val Gln Leu
 260 265 270
 Leu Gly Ser Val Pro His Glu Lys Val Arg Asp Val Leu Cys Gln Gly
 275 280 285
 Asp Ile Tyr Leu His Ala Ser Leu Thr Glu Ala Phe Gly Thr Ile Leu
 290 295 300
 Val Glu Ala Ala Ser Cys Asn Leu Leu Ile Val Thr Thr Gln Val Gly
 305 310 315 320
 Gly Ile Pro Glu Val Leu Pro Asn Glu Met Thr Val Tyr Ala Glu Gln
 325 330 335
 Thr Ser Val Ser Asp Leu Val Gln Ala Thr Asn Lys Ala Ile Asn Ile
 340 345 350
 Ile Arg Ser Lys Ala Leu Asp Thr Ser Ser Phe His Asp Ser Val Ser
 355 360 365
 Lys Met Tyr Asp Trp Met Asp Val Ala Lys Arg Thr Val Glu Ile Tyr
 370 375 380
 Thr Asn Ile Ser Ser Thr Ser Ser Ala Asp Asp Lys Asp Trp Met Lys
 385 390 395 400
 Met Val Ala Asn Leu Tyr Lys Arg Asp Gly Ile Trp Ala Lys His Leu
 405 410 415
 Tyr Leu Leu Cys Gly Ile Val Glu Tyr Met Leu Phe Phe Leu Leu Glu
 420 425 430
 Trp Leu Tyr Pro Arg Asp Glu Ile Asp Leu Ala Pro Lys Trp Pro Lys
 435 440 445
 Lys Thr Val Ser Asn Glu Thr Lys Glu Ala Arg Glu Thr
 450 455 460

<210> 279

<211> 2900

<212> DNA

<213> Candida albicans

<400> 279

ctcaatggga attgagtga gatcagctctg atcgagagga atttgtacga ttcgtggaaa 60
 accagcattt cgtagaaaaa gttgatacga tttacaacgg ttataatgaa agtctatcaa 120
 tgatggacga cctgactaga gagttactac tatgggagaa aaaatattca aataacacta 180
 atgccattca ataaacgcaa aacactgcaa tattattctc aaccaaagta taactgtaat 240
 gaggcgaaca aacacatcta tacatatata tacatctata tggatataaa aacgactaat 300
 tcaacgttgt ttttatcaac cgagcttact cttgtacggg taaccgcaag gatagctagt 360
 tgcggatggg atagcgattt ggctggcacg atgattaagg aatccaaaca tctaattggac 420
 tagcacattc tatcgattta cgggtcaggt aaacatagat attgggatat atcatatatc 480
 cttactgagt aactataatt atgggttcac gaggaaggac tttgaagtca gacactgatg 540

Arg Val Leu Thr His Asp Gly Thr Leu Asp Asn Asp Tyr Phe Asn Lys
50 55 60

His Asn Val Ser Gln Lys Cys Lys Ser Ser Asp Ala Leu Phe Arg Lys
65 70 75 80

Arg Thr Ile Ser Gly Leu Asn Met Thr Ala Leu Thr Arg Val Lys Ser
85 90 95

Asn Gln Gly Lys Arg Ser Ala Ser Phe His Ser Pro Val His Asn Thr
100 105 110

Leu Leu Ser Pro Lys Asn Ser Ser His Ser Asn Thr Gly Thr Ala Gly
115 120 125

Phe Gly Leu Lys Pro Arg Arg Ser Lys Ser Thr Gln Ser Val Leu Ser
130 135 140

Leu Arg Asp Ala Gln Glu Ser Lys Lys Ser Glu Ser Thr Thr Asp Glu
145 150 155 160

Glu Val Glu Cys Phe Ser Glu Asp Asn Ile Glu Asp Gly Lys Val Asn
165 170 175

Asn Asp Lys Val Ile Ala Glu His Val Met Pro Glu Glu Lys Lys Asn
180 185 190

Val Gln Gln Leu Asn Gln Asn Glu Leu Gln Ser Pro Asp Ser Ile Asp
195 200 205

Glu Gln Glu Glu Asp Lys Ser Gly Thr Asp Gly Lys Glu Asn His Arg
210 215 220

Ala Val Ser Leu Pro Leu Pro His Leu Ser Ser Asn Asn Tyr Phe Gly
225 230 235 240

Glu Ser Ser His Ser Ile Glu His Gln Lys Asp Gly Glu Thr Ser Pro
245 250 255

Ser Ser Ile Glu Thr Lys Leu Asn Ala Thr Ser Val Ile Asn Glu Glu
260 265 270

Gly Gln Ser Lys Val Thr Lys Glu Ala Asp Ile Asp Asp Leu Ser Ser
275 280 285

His Ser Gln Asn Leu Arg Ala Ser Leu Val Lys Ala Gly Asp Asn Ile
290 295 300

Ser Glu Ala Pro Tyr Asp Lys Glu Lys Lys Ile Leu Asp Val Gly Asn
305 310 315 320

Thr Leu Ala Ala His Lys Ser Asn Gln Lys Pro Ser His Ser Asp Glu
325 330 335

Gln Phe Asp Gln Glu Asp His Ile Asp Ala Pro Arg Ser Asn Ser Ser
340 345 350


```

gcgaaagttt cattgtttga tacatcttga tagtaaccgc aggtttcttt cttagttcat 420
attttattgt atttcaacta atattatttt tttttcagtg gaagggaagg tgaaccaaga 480
acatacaaac atagccaaag atgtctgcca aagctcaaaa ccctatgctg gatttgaaga 540
tcgaaaagtt ggtcttaaac atttctgttg gtgaatctgg tgacagattg accagagcct 600
ccaaggtttt agagcaatta tctgggtcaaa ctccagttca atccaaggcc agatacactg 660
tcagaacttt cggatatcaga agaaacgaaa aaattgctgt tcacgttacc gtcagagggtc 720
caaaggctga agaaattttg gaaagagggt tgaagggtcaa ggaataccaa ttgagagaca 780
gaaacttctc tgctaccggt aacttcggtt tcggtattga cgaacacatt gacttgggta 840
tcaagtatga cccatccatc ggtattttcg gtatggattt ctatgtcgtc atgaacagac 900
cagggtgctag agtcactaga agaaagagat gtaagggtac cgttggtaac tcccacaaga 960
caactaagga agacaccgtc tcttggttca agcaaaagta cgatgctgat gttttggaca 1020
aataa                                     1025

```

<210> 284

<211> 174

<212> PRT

<213> Candida albicans

<400> 284

```

Met Ser Ala Lys Ala Gln Asn Pro Met Arg Asp Leu Lys Ile Glu Lys
  1              5              10              15

Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg
      20              25              30

Ala Ser Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser
      35              40              45

Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys
      50              55              60

Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu
      65              70              75              80

Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Asp Arg Asn Phe
      85              90              95

Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu
      100             105             110

Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Phe Gly Met Asp Phe Tyr
      115             120             125

Val Val Met Asn Arg Pro Gly Ala Arg Val Thr Arg Arg Lys Arg Cys
      130             135             140

Lys Gly Thr Val Gly Asn Ser His Lys Thr Thr Lys Glu Asp Thr Val
      145             150             155             160

Ser Trp Phe Lys Gln Lys Tyr Asp Ala Asp Val Leu Asp Lys
      165             170

```

<210> 285

<211> 1229

<212> DNA

<213> *Candida albicans*

<400> 285

```

agagaacgta ttgaagagga gaaaagggag aaaagaggtc aattggaaga acaacatcgt 60
tctgcatcaa atgcttctat ggcttcttta ttgtcagctg cttcaactac agcagcaact 120
aaaaatttga gtgtggctgg cacaaatcct tctcatacca ctgaaagaat gtttttaaat 180
ttacctttta acaattccct gttcaatgcc ccaccagtag aaattaattt taatgatctt 240
gaagttttgg aattgtacac tcaattagta ttataccgag atgatattac caaatctact 300
tttgaattag ctatatcacc agcaaatttg aatatttctc aacggaaaat catatcaatt 360
ttatgtaatt atttgaattt attagaattg tttgataatg gggtgataat aattagaaga 420
aaaccaggat acattgctca gtgtataact caacaatcta ttattcctaa ttctcaacag 480
gtgtctgggc caactcacc gcaacaacat caacagaatc aacttcaaca acagcaacag 540
caacaacatc aacatcaaca tccttcacat tcatcatcga tgatgaacct tcatcaattg 600
ggtggtacat tagctgttcc agcgcacctt gaattattaa gatcccaatc gcaatcagca 660
ttaccgttgc caagattgag acagcaaacc tctacaccaa ttcaacaaaa tcaacaagtt 720
cagcaccaaa atcaaccacc acaacaacaa cagcaacagc atgttcaacc acaatataat 780
tattacaatt agcaatctat tcaaagccaa ccacattctg cgagacctta ttctcaatca 840
tataatattt atcaacaaca acagcaacag cagcaacaac aagctcaaca acaagctcaa 900
caacaacaac aacaacaatt acaatatcaa cagggacacc agtcacaagt ttcaaacact 960
acattgaatt cttctagtgc tgctgcatta cttagatcaa gtagcagtag atcatttgtt 1020
gatgtgagat ccacacctcc cacaagtagt tttgctcaac agcaacaaca acaacaacaa 1080
caacagcaac agccgccact aacttcatca atccatgatt ctccaacacc acatcatcat 1140
ttaccacttc aacagcagcc accacaacca aatcattacc tatccaatta ccatcagggg 1200
gttggtatctc aaccaaaaac tccattggc 1229

```

<210> 286

<211> 409

<212> PRT

<213> *Candida albicans*

<400> 286

```

Arg Glu Arg Ile Glu Glu Glu Lys Arg Glu Lys Arg Gly Gln Leu Glu
 1             5             10             15

Glu Gln His Arg Ser Ala Ser Asn Ala Ser Met Ala Ser Leu Leu Ser
          20             25             30

Ala Ala Ser Thr Thr Ala Ala Thr Lys Asn Leu Ser Val Ala Gly Thr
 35             40             45

Asn Pro Ser His Thr Thr Glu Arg Met Phe Leu Asn Leu Pro Phe Asn
 50             55             60

Asn Ser Ser Phe Asn Ala Pro Pro Val Glu Ile Asn Phe Asn Asp Leu
 65             70             75             80

Glu Val Leu Glu Leu Tyr Thr Gln Leu Val Leu Tyr Arg Asp Asp Ile
          85             90             95

Thr Lys Ser Thr Phe Glu Leu Ala Ile Ser Pro Ala Asn Leu Asn Ile
 100             105             110

Ser Gln Arg Lys Ile Ile Ser Ile Leu Cys Asn Tyr Leu Asn Leu Leu
 115             120             125

```


<211> 2153
 <212> DNA
 <213> *Candida albicans*

<400> 287

```

ataaacaaaa aagaagcacg aactgtgggc aacaacaaca acaacaacaa caaaaaaaaaa 60
aaattttctgg aaaatcaaaa ttgaactcca accagcagcg gcggcggcga cagaaaaata 120
tattaacaga atactttttt gtattcaact ctctaactct ttctattttt tttttttttc 180
tatatacact gttaaatcaa tcaacaatag caggatatcc attcatatac aaatagataa 240
actgtttaat taattaatta actgatttga ttggggaaaa aacaaatfff atatttggag 300
aattgaatff caatcatttt aacaaattca aagctttaat tcccacctat caaatffcat 360
tattatffff ttttcattat tttttttttc cttttctttc tttctttctt tcttttttgg 420
aacaaagtaa tagccgataa aataaataat tcacatagcc caattcatat tacattgact 480
tttgacaaga ggtatatata atggatttta gaaatttatc aactacaccg aatcaaatgg 540
gcactgtaat gcaacgtcgt ccctctctat catcattatc gtcagcctcg ggctattctt 600
cttccaatta tgggtgaaat cctacaccca atcccaacaa ttccaatacc aataacaata 660
gtatgggcaa tagtaataac aacactcatg gcaataaacac tcccaaatfa tcaactcaaa 720
gattgacaaa taataggaat ttacaatcct tgtggataaa ccaaccatct attgctcctt 780
ctaattgtgt tccttgggtg gaacagcaac aacaacaaac ccttgatctg ttggaaaata 840
atactaaaac agactccagt aatgatgctt ctgctactaa taataataat gttaatgtta 900
atgttaatgc caatgccaat gttaatgcca atgccaatat ccatgccccaa acccatgtca 960
acacaaatgt taatgcaaac acaacagcaa ctagtattaa tgcttccacg attttaaata 1020
ctacaccaag tattaatgac actaatgata atgccccaaa aattaatgtt tccatgatta 1080
gtaataacaa taacaataac agtaacaata ataacaacaa cactaacaat agtagtacag 1140
gaagttctaa cattgcaaac atgcttctct ctgtttctaa tgcaacgaca atgaataaca 1200
gtaatagtat caatagcacc acaacaata ctacaattaa cgaagctgat gatgacgagt 1260
taattcctac tgcgattgtg attaaaaata ttccatttgc cattaaaaag gaacaattgt 1320
tagatgtgat gacaaaatta aacttgccat taccatatgc ctttaattat cattttgata 1380
atgggtgtgt tcgtggatta gcatttgcca atttcacatc tacagatgag acatcagcag 1440
tagtaaacca attgaatgga agagaaatag gtggaagaaa attacgtgtt gaatacaaaa 1500
aaatgcttcc ggcacaagaa agagaacgta ttgaaagaga gaaaagggag aaaagaggtc 1560
aattggaaga acaacatcgt tctgcatcaa atgcttcttt ggcttcttta ttgtcagctg 1620
cttcaactac agcagcaact aaaaatttga gtgtggctgg cacaaatcct tctcatacca 1680
ctgaaagaat gtttttaaat ttacctttta acaattccct gttcaatgcc ccaccagtag 1740
aaattaatff taatgatctt gaagttttgg aattgtacac tcaattagta ttataccgag 1800
atgatattac caaatctact tttgaattag ctatatcacc cagcatatff gaatatttct 1860
caacggaaaa tcatatcaat ttatgtaatt atttgaattt attagaattg ttgataatg 1920
ggttgctact aattagaaaa aaaccaggat ccattgctca gtgtataact caaaaatcta 1980
ttattcctaa ttctcaacag gtgtctgggc caactcacc gcaccaccat caaaagaatc 2040
aacttcacca acagcaacag caacacacat caacatcaac atccttaaca ttcatcctcg 2100
atgatgaacc ttcatcaatt ggggtgtaca ttagctgttc cagcgcacca tga 2153

```

<210> 288
 <211> 550
 <212> PRT
 <213> *Candida albicans*

<400> 288

```

Met Asp Phe Arg Asn Leu Ser Thr Thr Pro Asn Gln Met Gly Thr Val
  1              5              10              15

Met Gln Arg Arg Pro Ser Leu Ser Ser Leu Ser Ser Ala Ser Gly Tyr
      20              25              30

Ser Ser Ser Asn Tyr Gly Gly Asn Pro Thr Pro Asn Pro Asn Asn Ser
      35              40              45

```



```

catccccctac accaaccaaac ccacaaacccc cattgccatt acttccagct caaactaaac 600
ctgtaaactc aaaaagaaaa tcagcagcca gtacacctgg aaatgaatca aagaaatcaa 660
gaaaatcaaaa ttctacagct tcaacaccca acagtgtctac accaacatca gtcggaacac 720
ctccacagaa aacttccaaa ccaacagggtc ataggccagt gacttcatgt actttttgtc 780
gtcaacataa aatcaaatgt aatgcttcag ataattatcc aaacccatgt gaaagatgta 840
aaaaaatggg tttgaaatgt gaaattgacc ccgaatttag acctcgcaaa gggtcacaaa 900
tccaatcatt gaaactggat gttgatgaat tgaaggccaa gattgaaatg ttgactaaaa 960
atgaatcttt gctcacacaa gctttgaatc aacacaattt gaaccacgct tcgcaacagc 1020
aacaactgtc tggatcgcaa tctcaacaac aacatcctcc aaatccacaa cgtgcattgt 1080
catatacgct tgcaaaactca tcaccacaag ttgcatttag caatgcatcg ccaattcctt 1140
ctgtgacaag tattcaacaa aatgcaccgt tgactcacga aaattccgac aattctccat 1200
acgctttaaa tacaccagaa aacattgaag aattacaacc aatctcagaa tttatttttg 1260
gtgacgttac tttgccatta aacagggcca atgagttaca cgacaagttt atgaccacac 1320
atttaccatt tttgccataa ataatatctc gatctgccac cgaattgtat cataaatctc 1380
aattgctttt ctgggcccgtg attcttaccg caagcttatac agaaccagaa cccaaacttt 1440
atatgtcgtt ggcattcctta attaaacaa tagcaattga aacatggttg attaaaaaac 1500
caagatcaac tcatgttatc caagccttga tcatactttc aatatggccg ttacctaatg 1560
aaaaagtttt ggatgattgc tcttatagat ttggttgatt ggcaaagaac ttgtcattac 1620
aattaggtct acatcgtggg ggagaattca ttcaagaatt tagtcggaat caagtaagtc 1680
taggacctga tgcagaaagg tggaggactc gttcatgggt agcagttttc ttttgtgaac 1740
agttttgggt atcattgttg gggttgccac cttcaataaa cactactgat tatttattag 1800
agaatgctcg tgttgataaa tcggtgccta aaaatttccg ttgtttgatt tcgctatcta 1860
ttttccaatg caaattagtt aatattatgg gtattagcgt tactagacca gacggtttat 1920
tggagcctct gaatcgtgct ggttcactta gtttattgga tagagaattg gaaagattaa 1980
gatttaaaact tcaatttgaa gaaggggggc caattgaagt atattatttg tatattaaat 2040
tgatgatctg ctgctttgcc tttttaccag gtacacctat cgaggatcaa gtcaagtatg 2100
tcagttttgc atattttatc gcaacaagaa tcgtgacaat cgtttctaaa atggtgaatg 2160
acatttcatt gattgaattg ccaatatata tcagacaagc agtgacatat agtgttttca 2220
tgttgttcaa attacatttg tcaagatatt tgattgacaa gtatgtggat agtgctagac 2280
agctgattgt tactgtgcat cgtttattta gaaacacggt gagttcctgg aaagatttgc 2340
aaaacgatat ttctcgaaca gccaaagttc tagaaaattt gaacatggtg ttgtataatt 2400
atcctgaaat atttttaaat gatctggaaa atgaggattc aagtattatc accagaatga 2460
ggtcacattt gacagcatct ttattctatg atttggttg gtgtgtacat gaggcaagaa 2520
gacgatcagt acttgataag gggaaaagac aggtctcagc taacaagaaa atcttgccct 2580
tgccatttta caaccaaatc actaaggatg atttcaagac aattaccacg acatcaccta 2640
atggaactac tattactaca ttagttccaa ctgatcaagc tatgaatcaa gcaaaactga 2700
aatcttttga ttccagcaaa ccacttgaaa taaatggat tcccttacct atgcttgaag 2760
ctactggttc aacaagagaa gtttttagatt ctttaccctc gcaatcttta ccatcacaag 2820
caccaactct tcagcagtat ccaatgcagc aagatcaaca acagcaagaa ccatcacaac 2880
aacaacaaca aaagcacctg cagcaactgc agcaatacca acaacagcag caatcgaatc 2940
aacagcaacc acatcttcaa catcaaagac agtttcaaca atcaccacca ccgcaatttt 3000
caatgatttc ttcaacgcgc ccccttcagc aaccaccttt tattttggca aactcacctg 3060
taccacaaac ttatttgcca aagattgatg aaatgaatat gtcaccagaa gtaaaacaag 3120
aaaactctgt tgctccattt gcattctcaa tcaccaactt ttttgatcaa caaacaagtg 3180
gatggtttta taatgataac caagatgacg actttttggg ttggtttgat gttaatatga 3240
tgcaagagaa ataa 3254

```

<210> 290

<211> 917

<212> PRT

<213> Candida albicans

<400> 290

Met Lys Phe Glu Lys Gly Lys Val Arg Ile Leu Pro Lys Pro Ser Pro

1

5

10

15

Thr	Pro	Thr	Asn 20	Pro	Gln	Thr	Pro	Leu 25	Pro	Leu	Leu	Pro	Ala 30	Gln	Thr
Lys	Pro	Val 35	Asn	Ser	Lys	Arg	Lys 40	Ser	Ala	Ala	Ser	Thr 45	Pro	Gly	Asn
Glu	Ser 50	Lys	Lys	Ser	Arg	Lys 55	Ser	Asn	Ser	Thr	Ala 60	Ser	Thr	Pro	Asn
Ser 65	Ala	Thr	Pro	Thr	Ser 70	Val	Gly	Thr	Pro	Pro 75	Gln	Lys	Thr	Ser	Lys 80
Pro	Thr	Gly	His	Arg 85	Pro	Val	Thr	Ser	Cys 90	Thr	Phe	Cys	Arg	Gln 95	His
Lys	Ile	Lys	Cys 100	Asn	Ala	Ser	Asp	Asn 105	Tyr	Pro	Asn	Pro	Cys 110	Glu	Arg
Cys	Lys	Lys 115	Met	Gly	Leu	Lys	Cys 120	Glu	Ile	Asp	Pro	Glu 125	Phe	Arg	Pro
Arg	Lys 130	Gly	Ser	Gln	Ile	Gln 135	Ser	Leu	Lys	Ser	Asp 140	Val	Asp	Glu	Leu
Lys 145	Ala	Lys	Ile	Glu 150	Met	Leu	Thr	Lys	Asn	Glu 155	Ser	Leu	Leu	Thr	Gln 160
Ala	Leu	Asn	Gln	His 165	Asn	Leu	Asn	His	Ala 170	Ser	Gln	Gln	Gln	Gln	Ser 175
Ser	Gly	Ser	Gln 180	Ser	Gln	Gln	Gln	His 185	Pro	Pro	Asn	Pro	Gln 190	Arg	Ala
Leu	Ser	Tyr 195	Thr	Ser	Ala	Asn	Ser 200	Ser	Pro	Gln	Val	Ala 205	Phe	Ser	Asn
Ala	Ser 210	Pro	Ile	Pro	Ser	Val 215	Thr	Ser	Ile	Gln	Gln 220	Asn	Ala	Pro	Leu
Thr 225	His	Glu	Asn	Ser	Asp 230	Asn	Ser	Pro	Tyr	Ala 235	Leu	Asn	Thr	Pro	Glu 240
Asn	Ile	Glu	Glu 245	Leu	Gln	Pro	Ile	Ser	Glu 250	Phe	Ile	Leu	Gly	Asp 255	Val
Thr	Leu	Pro	Leu 260	Asn	Arg	Ala	Asn	Glu 265	Leu	His	Asp	Lys	Phe 270	Met	Thr
Thr	His	Leu 275	Pro	Phe	Leu	Pro	Ile 280	Ile	Ile	Ser	Arg	Ser 285	Ala	Thr	Glu
Leu	Tyr 290	His	Lys	Ser	Gln	Leu 295	Leu	Phe	Trp	Ala	Val 300	Ile	Leu	Thr	Ala
Ser 305	Leu	Ser	Glu	Pro	Glu 310	Pro	Lys	Leu	Tyr	Met 315	Ser	Leu	Ala	Ser	Leu 320

Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile Lys Thr Pro Arg Ser
 325 330 335
 Thr His Val Ile Gln Ala Leu Ile Ile Leu Ser Ile Trp Pro Leu Pro
 340 345 350
 Asn Glu Lys Val Leu Asp Asp Cys Ser Tyr Arg Phe Val Gly Leu Ala
 355 360 365
 Lys Asn Leu Ser Leu Gln Leu Gly Leu His Arg Gly Gly Glu Phe Ile
 370 375 380
 Gln Glu Phe Ser Arg Asn Gln Val Ser Leu Gly Pro Asp Ala Glu Arg
 385 390 395 400
 Trp Arg Thr Arg Ser Trp Leu Ala Val Phe Phe Cys Glu Gln Phe Trp
 405 410 415
 Ser Ser Leu Leu Gly Leu Pro Pro Ser Ile Asn Thr Thr Asp Tyr Leu
 420 425 430
 Leu Glu Asn Ala Arg Val Asp Lys Ser Leu Pro Lys Asn Phe Arg Cys
 435 440 445
 Leu Ile Ser Leu Ser Ile Phe Gln Cys Lys Leu Val Asn Ile Met Gly
 450 455 460
 Ile Ser Val Thr Arg Pro Asp Gly Leu Leu Glu Pro Ser Asn Arg Ala
 465 470 475 480
 Gly Ser Leu Ser Leu Leu Asp Arg Glu Leu Glu Arg Leu Arg Phe Lys
 485 490 495
 Leu Gln Phe Glu Glu Gly Gly Pro Ile Glu Val Tyr Tyr Leu Tyr Ile
 500 505 510
 Lys Leu Met Ile Cys Cys Phe Ala Phe Leu Pro Gly Thr Pro Ile Glu
 515 520 525
 Asp Gln Val Lys Tyr Val Ser Phe Ala Tyr Leu Ser Ala Thr Arg Ile
 530 535 540
 Val Thr Ile Val Ser Lys Met Val Asn Asp Ile Ser Leu Ile Glu Leu
 545 550 555 560
 Pro Ile Tyr Ile Arg Gln Ala Val Thr Tyr Ser Val Phe Met Leu Phe
 565 570 575
 Lys Leu His Leu Ser Arg Tyr Leu Ile Asp Lys Tyr Val Asp Ser Ala
 580 585 590
 Arg Gln Ser Ile Val Thr Val His Arg Leu Phe Arg Asn Thr Leu Ser
 595 600 605
 Ser Trp Lys Asp Leu Gln Asn Asp Ile Ser Arg Thr Ala Lys Val Leu
 610 615 620

[illegible]

<210> 291
 <211> 908
 <212> DNA
 <213> Candida albicans

<400> 291
 ttattattac tatgacacac acttactctc ttctatgtct ccgcttacat cacacatcat 60
 acgtttgaaa acacccaccc cctttttctt atctacaaaa aaaaaataac aaactcacta 120
 taactactaa accttttttt ttattttatt attttgtatt ttgttatatt aatcaaacta 180
 ttatcattca tctatatata catccccatc gattcatctg acataatagt atgtatgatc 240
 atacagaggg aaaatcaccc tttttattat taccaagggtc tcaatgatta gtgtggctag 300
 cgtctgttac tacttacctc gtgtttgtag ataattgcc aacaatcttt aattgaccat 360
 cgaccacaaa aataatatgg aaataatact aacagaactt agaaacatca ctcataatga 420
 gatcaccaatt caaagacgag catccttttg gtatgtatta catgattttt agtcctctga 480
 atcttcttcc gatcatcata tactaacatt ttcgtgggtg ttattcttta atagaaaaga 540
 gacaagccga ggcagccaga attgctcaga ggttcaagga tagagtacca gtcactctgtg 600
 aaaagggttg gaattccgat atccccgaaa ttgataaacg taaatattta gtgccagtgg 660
 atttgactgt tgggtcaattt gtttacgtta ttagaaaaag aatcaagtta ccaagcgaaa 720
 aagccatttt catctttgtc aatgacatat taccaccaac cgctgcatta atcagtacaa 780
 tctacgaaga acacaaggac gaagatggtt tcttatacgt tttatactct ggagagaata 840
 cttttggcga gaaactagca attgacattt catcattaga tttcagtgat atccctgatt 900
 atgttttaa 908

<210> 292
 <211> 135
 <212> PRT
 <213> Candida albicans

<400> 292
 Met Arg Ser Gln Phe Lys Asp Glu His Pro Phe Glu Lys Arg Gln Ala
 1 5 10 15
 Glu Ala Ala Arg Ile Ala Gln Arg Phe Lys Asp Arg Val Pro Val Ile
 20 25 30
 Cys Glu Lys Val Glu Asn Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys
 35 40 45
 Tyr Leu Val Pro Val Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile
 50 55 60
 Arg Lys Arg Ile Lys Leu Pro Ser Glu Lys Ala Ile Phe Ile Phe Val
 65 70 75 80
 Asn Asp Ile Leu Pro Pro Thr Ala Ala Leu Ile Ser Thr Ile Tyr Glu
 85 90 95
 Glu His Lys Asp Glu Asp Gly Phe Leu Tyr Val Leu Tyr Ser Gly Glu
 100 105 110
 Asn Thr Phe Gly Glu Lys Leu Ala Ile Asp Ile Ser Ser Leu Asp Phe
 115 120 125
 Ser Asp Ile Pro Asp Tyr Val

130

135

<210> 293
 <211> 2891
 <212> DNA
 <213> Candida albicans

<400> 293
 gtggcacatc ccaggaagta gagcatggac agttcgtatg gtattgctgt gcatacgata 60
 caaaaaaaaaac agaaacgaga aaaaaaatcg atcgtcaacc tttatcaact catctacagc 120
 agcagcaaag ttcgcccta aatatgagtc aagtcaca gaaacccaaa tcgtttggta 180
 gattgtatac catgtactac tttcattttc catttggtat gcttacgaca actgaaacca 240
 tgctacttca tacgtttgta ttgatgtttg ccttattggg tgccatggg atctacgctt 300
 atttgccttc aagtatcatg tttgcaatct ccagagcata ctattatggt tttggcatgg 360
 atattagtag catcaacggt tatgcaaagt agcgtgtct acttagtttt atagtttaaa 420
 aatttggttaa tataaaccca aagtttctaa caggctctgt ttgctcgact aaaaaagaat 480
 tttgtcaaac gcgtatcaga atgtttaccc tttttttttt taccacagat caaatgaatg 540
 ttcgacctaa tgctccgttt cggcctccta gaccaataaa ggggggtgtt gcggtggtgc 600
 agaaagtagt aaaacgaaaa ttgccacta ccaccaatcc taaacctgca aagattttga 660
 ctaccgatcc cggtcaaca aaatcgtga tccaatggag aaagaaaact tcaaagaaga 720
 acaaaacatg ggacggtgat gggtagccg tgattaaaca gcttgagaat ggggcatgcg 780
 agatatctat caagaactct gatggcaaac ctatggggaa aagagtgttt actgcgacac 840
 ctaaccttga cgacgtgatt agtgtgggac cctatgaatt agaattagac gaaaaagtag 900
 ggtctaactc aactccccag acagtgcacac gtgttaccca ccagttcaaa aagggtgctc 960
 ctcccacagc tagtagtcgg aaaccgcttt atgacgactg tgccgatgcc atcgcgttgc 1020
 ctccctctcc aaaagccaaa gattatgtca aagtaaatat cgatccacat ttggcaaaag 1080
 tgcttcgtcc gcatacaggt gaaggtgtga agtttatgta tgagtgttta atgggggtacc 1140
 gtgggttttg cgggcacggg tgtttgttag cagatgaaat ggggttggg aaaacggtga 1200
 tgacaatcac tacaacttg acgttgctca aacaaaaccc gtttatggaa aaagggtgcag 1260
 tggtaataaa ggtattgggt gtgtgtcctg tcacgcttat ttccaattgg agacaggagt 1320
 ttaggaaatg gttaggtgct aataagctaa acgtgttgac gctcaacaac ccaatgtcaa 1380
 acgagaaaca ggatatactc aattttggaa agttgaatgt gtaccaagt ttagtggtga 1440
 attatgaaaa acttggtgga cttttgatg aactctcagc ggtcaagttt gatttggttag 1500
 tgtgtgacga gggccatcgt ttgaagaata gtgcaaataa agtattgaat aatcttatca 1560
 agctcaatat tccgaagaaa attgttttga cgggtacgcc gattcaaaac gaggttgtag 1620
 agtttcacac gttgatctcg ttctcaacc cgggtgtgct tcccagacta aaattgtttc 1680
 agcgaaactt tataacacct atatctaggg ccgagatat caactgtttt gacctgaag 1740
 tgaagaaacg cgggtgaagag atatcgcagc agttgattga attgactcag agttttattc 1800
 ttagacgtac acaagcgatt ttggctaatt acttgacaca gaaaactgac attttggtgt 1860
 ttgttccacc tacatcgttg cagctcaagt tgttcgacta tataaccaac ttgaagaaat 1920
 ttaatcagtt tgaggcattt accatgatca atttgtttaa aaagatttgc aattcccctt 1980
 cgttgttggc cgacgacgag ttatttaaaa agattgttga agaaaagttt aatttgggga 2040
 tggcatccgg taaaataaac attcttgtgc cgttgctatt ggaaattgct tcgcttgggg 2100
 aaaagattgt cttaatttcc aactacacca agactttgga cttgttggaa caggttttgc 2160
 gcaagggtcag cctaacattt tcgagattag atgggtcgac cccaacaat gtgcgtagca 2220
 agttggttaa tcagttaa acgaaccccg acataaacgt atttttattg tcgtcgaaat 2280
 ctggcgggat ggggatcaac ttgttcgggg cttcgaggtt gattttgttt gacaatgact 2340
 ggaacccagc gaccgatttg caatcgatgt cgcaattca cagagacgga caattgaaac 2400
 cgtgtttcat ttataggcta ttcaccacgg ggtgtattga cgagaaaatc tttcagcgac 2460
 agctcgtgaa gaacaaattg agttccaagt ttttggacaa tgacgccacg tccaaatctg 2520
 atgtgtttga caatgatgat ttgaagaata tttttgagat agatacatcg acaatatcca 2580
 atactcatga tttattagag tgtgtgtgtg agggcgacgg gtcgatgttg agtcagccaa 2640
 ccatagagga aagcgaacca ccccaaaaac aagcatgggt tactgcatta gagcttaaga 2700
 agaagattga cgatggtgag gcgctaaaga ggacggctgt taaatttgcc ttgaacgatt 2760
 atcgacacta caatccagag gtgaaccgta atttggtatt tgattctgcg ctacaccgaa 2820

297

ttgctaacaa ttcaagctat gaaaataagc aattgccaat tacatttata atgctgagag 2880
taactaatta a 2891

<210> 294

<211> 796

<212> PRT

<213> Candida albicans

<400> 294

Met	Phe	Thr	Leu	Phe	Phe	Phe	Thr	Thr	Asp	Gln	Met	Asn	Val	Arg	Pro	
1				5					10					15		
Asn	Ala	Pro	Phe	Arg	Pro	Pro	Arg	Pro	Ile	Lys	Gly	Gly	Val	Ala	Val	
			20					25					30			
Val	Gln	Lys	Val	Val	Lys	Arg	Lys	Leu	Pro	Thr	Thr	Thr	Asn	Pro	Lys	
		35					40					45				
Pro	Ala	Lys	Ile	Leu	Thr	Thr	Asp	Pro	Gly	Ser	Thr	Lys	Tyr	Val	Ile	
	50					55					60					
Gln	Trp	Arg	Lys	Lys	Thr	Ser	Lys	Lys	Asn	Lys	Thr	Trp	Asp	Gly	Asp	
65					70					75					80	
Gly	Tyr	Ala	Val	Ile	Lys	Gln	Leu	Glu	Asn	Gly	Ala	Cys	Glu	Ile	Ser	
				85					90					95		
Ile	Lys	Asn	Ser	Asp	Gly	Lys	Pro	Met	Gly	Lys	Arg	Val	Phe	Thr	Ala	
		100						105					110			
Thr	Pro	Asn	Leu	Asp	Asp	Val	Ile	Ser	Val	Gly	Pro	Tyr	Glu	Leu	Glu	
		115					120						125			
Leu	Asp	Glu	Lys	Val	Gly	Ser	Asn	Ser	Thr	Pro	Gln	Thr	Val	Thr	Arg	
	130					135					140					
Val	Thr	His	Gln	Phe	Lys	Lys	Val	Ala	Pro	Pro	Thr	Ala	Ser	Ser	Arg	
145					150					155					160	
Lys	Pro	Leu	Tyr	Asp	Asp	Cys	Ala	Asp	Ala	Ile	Ala	Leu	Pro	Pro	Pro	
				165					170					175		
Pro	Lys	Ala	Lys	Asp	Tyr	Val	Lys	Val	Asn	Ile	Asp	Pro	His	Leu	Ala	
			180					185					190			
Lys	Val	Leu	Arg	Pro	His	Gln	Val	Glu	Gly	Val	Lys	Phe	Met	Tyr	Glu	
		195					200					205				
Cys	Leu	Met	Gly	Tyr	Arg	Gly	Phe	Gly	Gly	His	Gly	Cys	Leu	Leu	Ala	
	210					215					220					
Asp	Glu	Met	Gly	Leu	Gly	Lys	Thr	Leu	Met	Thr	Ile	Thr	Thr	Ile	Trp	
225					230					235					240	
Thr	Leu	Leu	Lys	Gln	Asn	Pro	Phe	Met	Glu	Lys	Gly	Ala	Val	Val	Asn	
				245					250					255		

Ser Arg Leu Asp Gly Ser Thr Pro Asn Asn Val Arg Ser Lys Leu Val
 565 570 575
 Asn Gln Phe Asn Thr Asn Pro Asp Ile Asn Val Phe Leu Leu Ser Ser
 580 585 590
 Lys Ser Gly Gly Met Gly Ile Asn Leu Val Gly Ala Ser Arg Leu Ile
 595 600 605
 Leu Phe Asp Asn Asp Trp Asn Pro Ala Thr Asp Leu Gln Ser Met Ser
 610 615 620
 Arg Ile His Arg Asp Gly Gln Leu Lys Pro Cys Phe Ile Tyr Arg Leu
 625 630 635 640
 Phe Thr Thr Gly Cys Ile Asp Glu Lys Ile Phe Gln Arg Gln Leu Val
 645 650 655
 Lys Asn Lys Leu Ser Ser Lys Phe Leu Asp Asn Asp Ala Thr Ser Lys
 660 665 670
 Ser Asp Val Phe Asp Asn Asp Asp Leu Lys Asn Ile Phe Glu Ile Asp
 675 680 685
 Thr Ser Thr Ile Ser Asn Thr His Asp Leu Leu Glu Cys Val Cys Glu
 690 695 700
 Gly Asp Gly Ser Met Leu Ser Gln Pro Thr Ile Glu Glu Ser Glu Pro
 705 710 715 720
 Pro Pro Lys Gln Ala Trp Val Thr Ala Leu Glu Leu Lys Lys Lys Ile
 725 730 735
 Asp Asp Gly Glu Ala Leu Lys Arg Thr Ala Val Lys Phe Ala Leu Asn
 740 745 750
 Asp Tyr Arg His Tyr Asn Pro Glu Val Asn Arg Asn Leu Asp Phe Asp
 755 760 765
 Ser Ala Leu His Arg Ile Ala Asn Asn Ser Ser Tyr Glu Asn Lys Gln
 770 775 780
 Leu Pro Ile Thr Phe Ile Met Ser Arg Val Thr Asn
 785 790 795

<210> 295

<211> 2643

<212> DNA

<213> Candida albicans

<400> 295

aaagaatttc aaatttagtt ttaggtgata attatcggtc gtcctttcct aacctaccaa 60
 ttttgacttt gtgtactcat acgatggttg ttattagtta aagttgcttt gctttgcttt 120
 tcaatttcaa tttcacaatt gaatttcaga atagaattag tttcaccttt tcttacaatc 180

300

```

ggctaagatt ttttttcatt cttctaattt agtttacaga atagaaagaa tagtttgctt 240
gtttgctcat atttacaatc aattgggttat tgggtgtttat tatttttttt tggttcctct 300
ttttaccccc ctttccgtct aattgagtta ttgtttggaa taatttatta cttattcaat 360
atattttttt tcttcttcc cttcttcaac ttcttcttta tacatttcaa tcaaccttcc 420
aacaatccta taattactta cttaccttct tcaattggat taattggatt tgaattgtta 480
caattgaata cttcaacgag atgactttac caattcagga tttagaacct gattattata 540
tttccgtcaa ttatcctacc accgataatg gatcaccaac cccacaagct gaaaaatcat 600
tgaaaacatt aattgattta ttatacgata aagggtttgc cgcccaaatt agacctgggtg 660
atthagacca tttgttagtc tttgttaaatt tgtcttcata caagttttct gaagaagctg 720
aaaaagattt aattaaaaat tatgaatttg gtgtcacggg taaagatgac gtgttagctt 780
ctaaacttag aattatttat caatacttaa cttatccaca atcagttggg ggatgtggta 840
ttactcctaa ttctggggat tggaaatttg tcaccagtat tgttccaatt actaatgcct 900
ttaatgaaac cacttttagt gaagatttaa aaattaatgt tactcaacca aatttatcaa 960
ttgccactat caaaaagaca tatggagttg aagttgctct ttattttgaa tatataaaac 1020
ataacgattt cctgttaaact ttgccttta tcaatttgc ttgggggggtt ttattccttg 1140
catcatggca tagaagagaa caacatttgg ttaatgtatg ggggtgttcaa aatagtcatt 1200
taattgaaac acataatttc gaattggcta aagtcaatga aagatatgaa gaaaaatcaa 1260
cttatttcca tgcaaataat accaatggat tcagattttt aaaacaattg gcatttatcc 1320
ccattgcctt ggtgtttgtt ggtgttttga ttagttatca attgagttgt ttctgtattg 1380
aaatcttttt aaccgatatt tatgatggcc cgggaaatc tttattgact ttattacca 1440
cggttttaat cagtgtattt gtgccaattt tgaccattgt ttataatgct gtcacggata 1500
ttattattaa atgggaaaat catgataacc aatatagcaa aaataattct attcttgta 1560
aaacctttgt gttgaatttc ttgactgggt atgttccatt aatcatcact tcattcatat 1620
atttaccatt tgtcatttg gtgcaacctc atttaggtga tattaacc accattgcca 1680
catatgctgg tgaaaataga ttctacacca aatacttgtt gaaattaaag agtcaagaag 1740
aatttaaaat caatcaagg agattagatg ctcaattctt ttatttcatt gtcacaaatc 1800
aagttataca attgggtattg aaatatattc tccattggg ttaagattt gtatttaatt 1860
ttattgaaac gaaaattcag aagaaacctc aattacaaac taaagatgat aacctgatg 1920
aatctatttg gttacataat gtcagattat cgttgaaact tctgaatat aatgttgatg 1980
atgattttag aggattagtt ttacaatttg gatatttgat aatgtttggg ccagtttggc 2040
cattggcacc attggtttgt attattttca atttaatttt tttcaagttg gataatttta 2100
aattattgaa tggtaaatat ttcaaaccac cagttccaag aagagttgat tctattcatc 2160
catggaattt agcccttttc ttgttagcat ggattggatc aattatttcc ccgtgggtca 2220
cggcatttta ccgtcatggt actgctccac caaatctat ggggtcaattt gcccttgata 2280
aagctagtgt tcatgtttca tcctcagttt tcttggtttt attaatgttt gtttcagaac 2340
atggattttt gattttgagt tatcttttat ttgaattctc ttctttgttc aagagtcaag 2400
ttgaatggga aaatgatttt gttgataatg atattaaatt gagacatgat tattattctg 2460
ggaaagtaaa accaacttat aaagtcact cggatgagtt gtgggagaag tttaccccac 2520
aatcaacttt gaatttcact ggtcctaacc caaccgcaga aactgatgat aaagttgaaa 2580
aaattgcttc taccgaagat gcttatctga cttctgcaga aaaatctact actactgcta 2640
ctt 2643

```

<210> 296

<211> 714

<212> PRT

<213> Candida albicans

<400> 296

```

Met Thr Leu Pro Ile Gln Asp Leu Glu Pro Asp Tyr Tyr Ile Ser Val
  1             5             10             15

```

```

Asn Tyr Pro Thr Thr Asp Asn Gly Ser Pro Thr Pro Gln Ala Glu Lys
      20             25             30

```

```

Ser Leu Lys Thr Leu Ile Asp Leu Leu Tyr Asp Lys Gly Phe Ala Ala

```


35					40					45						
Gln	Ile	Arg	Pro	Gly	Asp	Leu	Asp	His	Leu	Leu	Val	Phe	Val	Lys	Leu	
50					55					60						
Ser	Ser	Tyr	Lys	Phe	Ser	Glu	Glu	Ala	Glu	Lys	Asp	Leu	Ile	Lys	Asn	
65					70					75					80	
Tyr	Glu	Phe	Gly	Val	Thr	Gly	Lys	Asp	Asp	Val	Leu	Ala	Ser	Lys	Leu	
85					90					95						
Arg	Ile	Ile	Tyr	Gln	Tyr	Leu	Thr	Tyr	Pro	Gln	Ser	Val	Gly	Gly	Cys	
100					105					110						
Gly	Ile	Thr	Pro	Asn	Ser	Gly	Asp	Trp	Lys	Phe	Val	Thr	Ser	Ile	Val	
115					120					125						
Pro	Ile	Thr	Asn	Ala	Phe	Asn	Glu	Thr	Thr	Leu	Val	Glu	Asp	Leu	Lys	
130					135					140						
Ile	Asn	Val	Thr	Gln	Pro	Asn	Leu	Ser	Ile	Ala	Thr	Ile	Lys	Lys	Thr	
145					150					155					160	
Tyr	Gly	Val	Glu	Val	Ala	Leu	Tyr	Phe	Glu	Tyr	Ile	Lys	His	Tyr	Thr	
165					170					175						
Phe	Trp	Leu	Leu	Leu	Leu	Ser	Ile	Ile	Gly	Leu	Val	Ser	His	Phe	Arg	
180					185					190						
Lys	Asp	Lys	Arg	Phe	Ser	Leu	Thr	Phe	Ala	Phe	Ile	Asn	Leu	Leu	Trp	
195					200					205						
Gly	Val	Leu	Phe	Leu	Ala	Ser	Trp	His	Arg	Arg	Glu	Gln	His	Leu	Val	
210					215					220						
Asn	Val	Trp	Gly	Val	Gln	Asn	Ser	His	Leu	Ile	Glu	Glu	His	Asn	Ser	
225					230					235					240	
Glu	Leu	Ala	Lys	Val	Asn	Glu	Arg	Tyr	Glu	Glu	Lys	Ser	Thr	Tyr	Phe	
245					250					255						
His	Ala	Asn	Asn	Thr	Asn	Gly	Phe	Arg	Phe	Leu	Lys	Gln	Leu	Ala	Phe	
260					265					270						
Ile	Pro	Ile	Ala	Leu	Val	Phe	Val	Gly	Val	Leu	Ile	Ser	Tyr	Gln	Leu	
275					280					285						
Ser	Cys	Phe	Cys	Ile	Glu	Ile	Phe	Leu	Thr	Asp	Ile	Tyr	Asp	Gly	Pro	
290					295					300						
Gly	Lys	Ser	Leu	Leu	Thr	Leu	Leu	Pro	Thr	Val	Leu	Ile	Ser	Val	Phe	
305					310					315					320	
Val	Pro	Ile	Leu	Thr	Ile	Val	Tyr	Asn	Ala	Val	Thr	Asp	Ile	Ile	Ile	
325					330					335						
Lys	Trp	Glu	Asn	His	Asp	Asn	Gln	Tyr	Ser	Lys	Asn	Asn	Ser	Ile	Leu	

340	345	350
Val Lys Thr Phe Val Leu Asn Phe Leu Thr Gly Tyr Val Pro Leu Ile 355 360 365		
Ile Thr Ser Phe Ile Tyr Leu Pro Phe Ala His Leu Val Gln Pro His 370 375 380		
Leu Gly Asp Ile Lys Thr Thr Ile Ala Thr Tyr Ala Gly Glu Asn Arg 385 390 395 400		
Phe Tyr Thr Lys Tyr Leu Leu Lys Leu Lys Ser Gln Glu Glu Phe Lys 405 410 415		
Ile Asn Gln Gly Arg Leu Asp Ala Gln Phe Phe Tyr Phe Ile Val Thr 420 425 430		
Asn Gln Val Ile Gln Leu Val Leu Lys Tyr Ile Leu Pro Leu Gly Leu 435 440 445		
Arg Phe Val Phe Asn Phe Ile Glu Thr Lys Ile Gln Lys Lys Pro Gln 450 455 460		
Leu Gln Thr Lys Asp Asp Asn Pro Asp Glu Ser Ile Trp Leu His Asn 465 470 475 480		
Val Arg Leu Ser Leu Lys Leu Pro Glu Tyr Asn Val Asp Asp Asp Phe 485 490 495		
Arg Gly Leu Val Leu Gln Phe Gly Tyr Leu Ile Met Phe Gly Pro Val 500 505 510		
Trp Pro Leu Ala Pro Leu Val Cys Ile Ile Phe Asn Leu Ile Phe Phe 515 520 525		
Lys Leu Asp Asn Phe Lys Leu Leu Asn Gly Lys Tyr Phe Lys Pro Pro 530 535 540		
Val Pro Arg Arg Val Asp Ser Ile His Pro Trp Asn Leu Ala Leu Phe 545 550 555 560		
Leu Leu Ala Trp Ile Gly Ser Ile Ile Ser Pro Val Val Thr Ala Phe 565 570 575		
Tyr Arg His Gly Thr Ala Pro Pro Lys Ser Met Gly Gln Phe Ala Leu 580 585 590		
Asp Lys Ala Ser Val His Val Ser Ser Ser Val Phe Leu Val Leu Leu 595 600 605		
Met Phe Val Ser Glu His Gly Phe Leu Ile Leu Ser Tyr Leu Leu Phe 610 615 620		
Glu Phe Ser Ser Leu Phe Lys Ser Gln Val Glu Trp Glu Asn Asp Phe 625 630 635 640		
Val Asp Asn Asp Ile Lys Leu Arg His Asp Tyr Tyr Ser Gly Lys Val		

	645		650		655
Lys Pro Thr	Tyr Lys Val His Ser Asp Glu Leu Trp Glu Lys Phe Thr				
	660		665		670
Pro Gln Ser Thr Leu Asn Phe Thr Gly Pro Lys Pro Thr Ala Glu Thr					
	675		680		685
Asp Asp Lys Val Glu Lys Ile Ala Ser Thr Glu Asp Ala Tyr Ser Thr					
	690		695		700
Ser Ala Glu Lys Ser Thr Thr Thr Ala Thr					
705			710		

<210> 297

<211> 1784

<212> DNA

<213> Candida albicans

<400> 297

```

cggtaattat gtcacaaaaa caaacaaatca acatattaaa tcgttatccc aactttgtca 60
gttttactaa caccttttat tttgtgttat acaaattgca caatcaatta ctataacttt 120
tttttgaaac gtgggctctg tttagttaa cttctttag tagttattatt ccgattgggt 180
tagctcaata actgcatttc gtacaataat gtttaattcaa ttctaaattc cgatgaaccg 240
aacacacaaa aaacatccag ttctggagag atttttcaaa acttctatta taaatagaac 300
cctataagtc cataataatt caattgaagg attattttct tttccctttt ctgattactt 360
tcaccaatth tcttctctcc aaaaaaaaca ccttcttcat ggtttctgtt tctaaattaa 420
tcaataacgg gttgttatta actagtcaaa gtgttttcca agatgttgct actccgcaac 480
aagcttctgt gcaacaatac aatatactca attttcttgg cggtagtgcc ccttatattc 540
aaagaaacgg atattgggatt tctactgata tccctgctgg ttgtgaaatt gctcaaattc 600
aattgtattc aagacatggg gaaagatacc caagtaaaag taatggtaaa agtttagaag 660
caatttatgc taaatttgaa aactacaaag gtacttttaa aggtgatttg tcattcttaa 720
atgattacac ttattttgtc aaagaccaga gtaactatgc taaggaaact agcccaaaaa 780
attctgaagg aacctatgcc ggtacaacca atgccttgcg tcatgggtgct gcgttttagag 840
ccaaatatgg atccttatac aaggaaaaact caactttacc aatcttcaca tccaattcta 900
acagagtaca tgaaacttca aagtatttctg ctagagggtt tttaggtgat gattatgaag 960
aaggtaaaac tgtcaagttt aacatcatct ctgaagatgc tgatcttggg gccaatagtt 1020
tgactcctag aagtgcattg tccaagaaca aagaactgag cagtagtact gccaaaaaat 1080
ataacacaaac atattttaa gctattgctg aaagattagt taaaccaaac ccaggtttga 1140
atttgactac aagtgatgtc aacaatttat tcagttgggtg tgcttatgaa atcaacgtca 1200
gaggaagttc accattctgt gatttattca ccaatgaaga attcattaag aactcttatg 1260
gtaacgatct ttccaaatat tattctaata gtgctggtaa taattacacc agaattcattg 1320
gttcagtgat tttgaattca tccttgggaa ttttgaagga cactaagaac tctaatacaag 1380
tatgggtatc atttgctcat gatactgatt tggaaatttt ccattctgct ttaggattat 1440
tggaaccagc tgaagattta ccaacatctt acatcccatc ccctaaccga tacgtccatt 1500
cttctattgt tccacaagggt gccagaatat acacagaaaa acttcaatgt ggaaacgatg 1560
cttatgttag atacattatc aacgatgctg tcgtgccaat tccaaaatgt gctactgggtc 1620
cagggttctc ttgtaaactt gatgattttg aaaatttcgt taaagaaaaga attggagatg 1680
ttgactttgt taacaatgt ggtgtcaata gtacctaccc atctgagctt actttctact 1740
gggattataa aaatgtcact tacagtgtc ctttagaatt gtaa 1784

```

<210> 298

<211> 461

<212> PRT

<213> Candida albicans

<400> 298

Met Val Ser Val Ser Lys Leu Ile Asn Asn Gly Leu Leu Leu Thr Ser
1 5 10 15

Gln Ser Val Phe Gln Asp Val Ala Thr Pro Gln Gln Ala Ser Val Gln
20 25 30

Gln Tyr Asn Ile Leu Asn Phe Leu Gly Gly Ser Ala Pro Tyr Ile Gln
35 40 45

Arg Asn Gly Tyr Gly Ile Ser Thr Asp Ile Pro Ala Gly Cys Glu Ile
50 55 60

Ala Gln Ile Gln Leu Tyr Ser Arg His Gly Glu Arg Tyr Pro Ser Lys
65 70 75 80

Ser Asn Gly Lys Ser Leu Glu Ala Ile Tyr Ala Lys Phe Glu Asn Tyr
85 90 95

Lys Gly Thr Phe Lys Gly Asp Leu Ser Phe Leu Asn Asp Tyr Thr Tyr
100 105 110

Phe Val Lys Asp Gln Ser Asn Tyr Ala Lys Glu Thr Ser Pro Lys Asn
115 120 125

Ser Glu Gly Thr Tyr Ala Gly Thr Thr Asn Ala Leu Arg His Gly Ala
130 135 140

Ala Phe Arg Ala Lys Tyr Gly Ser Leu Tyr Lys Glu Asn Ser Thr Leu
145 150 155 160

Pro Ile Phe Thr Ser Asn Ser Asn Arg Val His Glu Thr Ser Lys Tyr
165 170 175

Phe Ala Arg Gly Phe Leu Gly Asp Asp Tyr Glu Glu Gly Lys Thr Val
180 185 190

Lys Phe Asn Ile Ile Ser Glu Asp Ala Asp Leu Gly Ala Asn Ser Leu
195 200 205

Thr Pro Arg Ser Ala Cys Ser Lys Asn Lys Glu Ser Ser Ser Ser Thr
210 215 220

Ala Lys Lys Tyr Asn Thr Thr Tyr Leu Asn Ala Ile Ala Glu Arg Leu
225 230 235 240

Val	Lys	Pro	Asn	Pro	Gly	Leu	Asn	Leu	Thr	Thr	Ser	Asp	Val	Asn	Asn
				245					250					255	

Leu Phe Ser Trp Cys Ala Tyr Glu Ile Asn Val Arg Gly Ser Ser Pro
260 265 270

Phe Cys Asp Leu Phe Thr Asn Glu Glu Phe Ile Lys Asn Ser Tyr Gly
275 280 285

305

Asn Asp Leu Ser Lys Tyr Tyr Ser Asn Gly Ala Gly Asn Asn Tyr Thr
 290 295 300
 Arg Ile Ile Gly Ser Val Ile Leu Asn Ser Ser Leu Glu Leu Leu Lys
 305 310 315 320
 Asp Thr Lys Asn Ser Asn Gln Val Trp Leu Ser Phe Ala His Asp Thr
 325 330 335
 Asp Leu Glu Ile Phe His Ser Ala Leu Gly Leu Leu Glu Pro Ala Glu
 340 345 350
 Asp Leu Pro Thr Ser Tyr Ile Pro Phe Pro Asn Pro Tyr Val His Ser
 355 360 365
 Ser Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Leu Gln Cys
 370 375 380
 Gly Asn Asp Ala Tyr Val Arg Tyr Ile Ile Asn Asp Ala Val Val Pro
 385 390 395 400
 Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp
 405 410 415
 Phe Glu Asn Phe Val Lys Glu Arg Ile Gly Asp Val Asp Phe Val Lys
 420 425 430
 Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp
 435 440 445
 Asp Tyr Lys Asn Val Thr Tyr Ser Ala Pro Leu Glu Leu
 450 455 460

<210> 299

<211> 1871

<212> DNA

<213> Candida albicans

<400> 299

gagtttttatg ggattggggtt tttcaattaa agactcttcg tgataatgca ataccaaaac 60
 caaaatztat ttaacgatgc aataattatt tcaatgtgag ctatccatga atcagtgaga 120
 atctttatta tggaagaaat tgggtcaaaat ttgacaatgt ttagtaactt tatatcttgg 180
 tgttgggatg gtgccacaaa tggagattgt tgagtgtaca tgaaaaatac gtagttaaat 240
 tttgtttctt gtttttatta tttagccact tttttatccg attcttcata ttacctttgg 300
 taaagtgata agattaatat catattagta aaacaccccc aatgatgaat gtttgtattt 360
 atagccagac tataaaaatt acgggggattt aattcgcgac tcacccacgt tctcacacag 420
 tatgtgcttt tttcataagt atgatttgaa ccctaaaata tcaactttca taataaacat 480
 aattctttcc agacaactaa atgggtgggt tatcacgagt acttaatgct gggttttattc 540
 taagtggaca atctgttttc caggatgttg ctgccccaca tcaagcatca attgaacaat 600
 ataatatgt caagtacctt ggtggcagcg gtccatatat tcaaaattca gggtagtgga 660
 tttctactga tataccagaa aaatgcacta ttgaacaagt tcaaatgatt agtagacatg 720
 gtgagcgatt tcttagtaaa ggagatggga aatactttaa ttcagtgatg gaagttttca 780
 agagatatgg tgaatttcat ggagatttat cttttttaaa tgactatgag tatttcgtta 840
 ctaatccaga ttattatgaa aaggagacta ctcctaaaaa ctcaaaagggt ccatattttg 900
 gaactacaaa tttattacga catggagctt atttttagaaa aagatatcaa tcactatttg 960

Val Phe Thr Ser Asn Ser Gly Arg Cys Tyr Gln Ser Gly Val Tyr Phe
165 170 175

<210> 301

Ser Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Leu Gln Cys
370 375 380

Gly Asn Asp Ala Tyr Val Arg Tyr Ile Ile Asn Asp Ala Val Val Pro
385 390 395 400

Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp
405 410 415

Phe Glu Asn Phe Val Lys Glu Arg Ile Gly Asp Val Asp Phe Val Lys
420 425 430

Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp
435 440 445

Asp Tyr Lys Asn Val Thr Tyr Asn Ala Pro Leu Gly Asp Phe
450 455 460

<210> 303

<211> 1886

<212> DNA

<213> *Candida albicans*

<400> 303

```
actacttaaa ttggcatatc caaacaaaact tgaagtagga gtttccttat ttttattttg 60
tatttatata tttgattgcg attaatgtca taaatttttag ttcggttaatt atgtcacaaa 120
aacaacaat caacatatta aatcgttatc ccaactttgt cagttttact aacacctttt 180
atthttgtgt atacaaaattg cacaatcaat tactataact tttttttgaa acgtgggctc 240
tggttagttt aactttctgt agttttatta ttccgattgg gttagctcaa taactgcatt 300
tcgtacaata atgttaattc aattctaaat tccgatgaac cgaacacaca aaaaacatcc 360
agttctggag agatttttca aaacttctat tataaataga accctataag tccataataa 420
ttcaattgaa ggattattht cttttccctt ttctgattac tttcaccaat tttcttctct 480
ccaaaaaaa caccttcttc atggtttctg tttctaaatt aatcaataac ggggttggtat 540
taactagtca aagtgttttc caagatgttg ctactccgca acaagcttct gtgcaacaat 600
acaatatact caatthttctt ggcggttagtg ccccttatat tcaaagaaac ggatatggga 660
tttctactga tatccctgct ggttgtgaaa ttgctcaaat tcaattgtac tcaagacatg 720
gtgaaagatt ccaacagca agtagtgga aagattatga gaaaatttat gctaaattta 780
aaaactacaa tggtagattc aaaggtgatt tgtcattctt aaatgattac acttattttg 840
tcaaagacca gagtaactat gctaaggaaa ctagcccaaa aaattctgaa ggaacctatg 900
ccggtacaac caatgccttg cgtcatgggt ctgctgttag agccaaatat ggatccttat 960
acaaggaaaa ctcaacttta ccaatcttca catccaattc taacagagta catgaaactt 1020
caaagtatth cgctagaggg ttttttaggtg atgattatga agaaggtaaa actgtcaagt 1080
ttaacatcat ctctgaagat gctgatcttg gtgccaatag tttgactcct agaagtgcatt 1140
gttccaagaa caaagaactg agcagtagta ctgccccaaa atataacaca acatatttaa 1200
atgctattgc tgaagagatta gttaaaccaa acccagggtt gaatttgact acaagtgatg 1260
tcaacaatth attcagttgg tgtgcttatg aaatcaacgt cagaggaagt tcaccattct 1320
gtgatttatt caccaatgaa gaattcatta agaactctta tggtaatgat ctttccaaat 1380
attattctaa tgggtgctgg aataattaca ccagaatcat tgggttcagt attttgaatt 1440
catccttgga actttttaaaa gacaccgaga actctaata agtatgggtta tcatttgctc 1500
atgatactga tttagaaatt ttccattctg ctttaggatt attggaacca gctgaagatt 1560
taccaacatc ttacatccca ttccctaacc catacgtcca ttcttctatt gttccacaag 1620
gtgccagaat atacacagaa aaacttcaat gtggaaacga tgcttatggt agatacatta 1680
tcaacgatgc tgtcgtgcca attccaaaat gtgctactgg tccagggttc tcttgtaaac 1740
ttgatgattt tgaataattc gttaaagaaa gaattggaga tgttgacttt attaaacaat 1800
tggtgtgcaa tagtacctac ccatctgagc ttactttcta ctgggattat aaaaatgtca 1860
```

cttacaatgc tccttttagaa ttgtaa

1886

<210> 304

<211> 461

<212> PRT

<213> Candida albicans

<400> 304

Met	Val	Ser	Val	Ser	Lys	Leu	Ile	Asn	Asn	Gly	Leu	Leu	Leu	Thr	Ser
1				5					10					15	

Gln	Ser	Val	Phe	Gln	Asp	Val	Ala	Thr	Pro	Gln	Gln	Ala	Ser	Val	Gln
			20					25					30		

Gln	Tyr	Asn	Ile	Leu	Asn	Phe	Leu	Gly	Gly	Ser	Ala	Pro	Tyr	Ile	Gln
		35					40					45			

Arg	Asn	Gly	Tyr	Gly	Ile	Ser	Thr	Asp	Ile	Pro	Ala	Gly	Cys	Glu	Ile
	50					55					60				

Ala	Gln	Ile	Gln	Leu	Tyr	Ser	Arg	His	Gly	Glu	Arg	Phe	Pro	Thr	Ala
65					70					75					80

Ser	Ser	Gly	Lys	Asp	Tyr	Glu	Lys	Ile	Tyr	Ala	Lys	Phe	Lys	Asn	Tyr
			85						90					95	

Asn	Gly	Thr	Phe	Lys	Gly	Asp	Leu	Ser	Phe	Leu	Asn	Asp	Tyr	Thr	Tyr
			100					105					110		

Phe	Val	Lys	Asp	Gln	Ser	Asn	Tyr	Ala	Lys	Glu	Thr	Ser	Pro	Lys	Asn
		115					120					125			

Ser	Glu	Gly	Thr	Tyr	Ala	Gly	Thr	Thr	Asn	Ala	Leu	Arg	His	Gly	Ala
	130					135					140				

Ala	Phe	Arg	Ala	Lys	Tyr	Gly	Ser	Leu	Tyr	Lys	Glu	Asn	Ser	Thr	Leu
145				150						155					160

Pro	Ile	Phe	Thr	Ser	Asn	Ser	Asn	Arg	Val	His	Glu	Thr	Ser	Lys	Tyr
				165					170					175	

Phe	Ala	Arg	Gly	Phe	Leu	Gly	Asp	Asp	Tyr	Glu	Glu	Gly	Lys	Thr	Val
			180					185					190		

Lys	Phe	Asn	Ile	Ile	Ser	Glu	Asp	Ala	Asp	Leu	Gly	Ala	Asn	Ser	Leu
		195					200					205			

Thr	Pro	Arg	Ser	Ala	Cys	Ser	Lys	Asn	Lys	Glu	Ser	Ser	Ser	Ser	Thr
	210						215				220				

Ala	Lys	Lys	Tyr	Asn	Thr	Thr	Tyr	Leu	Asn	Ala	Ile	Ala	Glu	Arg	Leu
225				230						235					240

Val	Lys	Pro	Asn	Pro	Gly	Leu	Asn	Leu	Thr	Thr	Ser	Asp	Val	Asn	Asn
				245					250					255	


```

ggagtttttaa acaggataat tggattcaat aagaggaaaa atttttttatc gtcgtgatta 660
taacaaatac aaagaaatta agcaatgaag tgatataagc aaatgaagga ctagttttatt 720
aggggtgaca ttttttagact acgtaaaagt acttttcgatt caaggaaaaac caaatTTtag 780
tatctatcaa caaactacaa atcaatttag ttaacttcaa taatgacaat aatttttaatc 840
actgaaaaca ataaacatgc aaacaagcaa aactagtcaa gctttacgaa teagtcaata 900
ctaacaatac ttttttttgt ttcatttttag ttaaaccatct catatccagc caacggtact 960
caaaaatcta tggatatcga tgatgacaca aaattacgtg tttctacgga aaaaagaatg 1020
ggtcaagaag ttgaagggtga ctcagttgga gatgaattca aagggttacat cttcaaaatc 1080
actggtggtga acgataaaca aggtgtccca atgaaacaag gtggttatgca cccaaccaga 1140
gttagattat tattatctaa aggtcactct tgttacagac caagaagaac tggtgaaaga 1200
aaaagaaaaat ccgtagagg ttgtattgtt gctcaagatt tgtcagtttt ggctttgtct 1260
attgttaaac aagggtgacaa tgaaattgaa ggattaactg acaccactgt tccaaaaaga 1320
ttaggtccaa agagagctaa ccacattaga aaattctttg gtttaactaa agaagatgat 1380
gttagagatt tcgttggttag aagagaagtt actaaagggtg acaaaactta caccaaagct 1440
ccaaagattc aaagattagt tactccacaa actttacaaa gaaagagagc tttgaaagct 1500
aaaaaagtca agaatgctca acaacaaaga gatgctgctg ctgaatacgc tcaattgttg 1560
gctaagagat tgcataaaaag aaaagaagaa agagctgaaa ttaaaaagaa gagagctgaa 1620
tctttaaaga actaa 1635

```

<210> 306

<211> 236

<212> PRT

<213> Candida albicans

<400> 306

Met Lys Leu Asn Ile Ser Tyr Pro Ala Asn Gly Thr Gln Lys Ser Met
1 5 10 15

Asp Ile Asp Asp Asp Thr Lys Leu Arg Val Ser Thr Glu Lys Arg Met
20 25 30

Gly Gln Glu Val Glu Gly Asp Ser Val Gly Asp Glu Phe Lys Gly Tyr
35 40 45

Ile Phe Lys Ile Thr Gly Gly Asn Asp Lys Gln Gly Val Pro Met Lys
50 55 60

Gln Gly Val Met His Pro Thr Arg Val Arg Leu Leu Leu Ser Lys Gly
65 70 75 80

His Ser Cys Tyr Arg Pro Arg Arg Thr Gly Glu Arg Lys Arg Lys Ser
85 90 95

Val Arg Gly Cys Ile Val Ala Gln Asp Leu Ser Val Leu Ala Leu Ser
100 105 110

Ile Val Lys Gln Gly Asp Asn Glu Ile Glu Gly Leu Thr Asp Thr Thr
115 120 125

Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn His Ile Arg Lys Phe
130 135 140

Phe Gly Leu Thr Lys Glu Asp Asp Val Arg Asp Phe Val Val Arg Arg
145 150 155 160

Glu Val Thr Lys Gly Asp Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln

	165		170		175
Arg Leu Val Thr Pro Gln Thr Leu Gln Arg Lys Arg Ala Leu Lys Ala					
	180		185		190
Lys Lys Val Lys Asn Ala Gln Gln Gln Arg Asp Ala Ala Ala Glu Tyr					
	195		200		205
Ala Gln Leu Leu Ala Lys Arg Leu His Glu Arg Lys Glu Glu Arg Ala					
	210		215		220
Glu Ile Lys Lys Lys Arg Ala Glu Ser Leu Lys Asn					
	225		230		235

<210> 307
 <211> 1520
 <212> DNA
 <213> Candida albicans

<400> 307

gtgacgagaa	cttctgtcat	ctcgagtctg	ccaactgcct	ctaacagcaa	caacaataag	60
aacaatgata	acggaggagg	attatcccat	acaaacagaa	tagttgttgg	tgtagtgtgt	120
ggggttggtg	gttctatatt	aattggtttg	ttggccgttt	tattttactt	gagaaagaga	180
aacaaccgtg	attatgaagg	tggatggact	ttctggagaa	agaatgagaa	attgggaagt	240
gatgagttct	tcaatggtga	attgggtgtc	agagacagaa	atattaatca	aggatcaa	300
ttttaaacaa	ggcttatttt	ggatgagggt	ggtttttttt	ataagtattt	tgtagtgtga	360
tttaaaat	tgtaccttaa	agtcttttaa	tttaatttta	ataaaaagt	gtgatttggc	420
aaacttcaag	agtatatatt	gtgaaaaaaa	aaaaaaaaat	tggaaactgaa	cgcgtctaac	480
atcttatacc	tctaagcaaa	atgtcagagt	actctgtgta	tcaacagttg	aatgaagata	540
caaacgcaac	taaatatact	tataaattac	tacagctacc	atcaaagata	ctaaatcaac	600
ttgaatccaa	gtcaactaac	ttgtatataa	aatctgat	caattcccta	gcattatgca	660
ctgattcaga	aactttcaag	ttacgacaaa	tgaaccattc	caatacagtc	ttgctattga	720
acaaagaacc	tgacaacaag	ttaattgggt	ttcagaaaac	cagttatgaa	tatgagttga	780
cagaaatcaa	aggttcgatc	gatacgtccg	atatccctat	tttcaacgga	caaacagcac	840
agcaacctat	tgattttgata	gcatttgaag	ataattcgat	ttgttcacat	caagagtttt	900
tatcgaattg	gtatgagttg	ggagggttgt	aaattgataa	tggagcatat	ataatgagtg	960
cagatattat	tactgaacta	ttatatctat	taatacacc	attgatgagt	ttacaagtgc	1020
acgagttttc	tccggaagat	gtttcatcca	tcatcacgcc	cccttataat	gactcaatgg	1080
taacatcaat	catacacaaa	ttttgcacta	tagaaagtga	gaaatatcaa	ttgaatgatt	1140
taaaaattac	acagtgggtt	ggcattgttg	agatgtcaaa	aatcaatcat	aaaatgaccg	1200
atatttcaga	gttcttattg	aattggaaaa	ctagtttgcc	gtcattctat	aaccctccat	1260
tggacatcag	tcaattggca	ggctattact	gctccccaat	cgaaaacaaa	atattgtatg	1320
tcgaccaga	atctttatca	gaaaatttga	gtcaacgatt	caaagaattg	tttgaattgg	1380
ataaaagt	gaactatgat	gagtttattc	cattcattaa	aaagtttgtt	cctgccggtg	1440
aaaaggtcga	ctcaattatt	ttaaagtatg	gcaagaagaa	gaaagttggt	agagatagat	1500
ttatagtctg	tcctagataa					1520

<210> 308
 <211> 339
 <212> PRT
 <213> Candida albicans

<400> 308

Met Ser Glu Tyr Ser Val Tyr Gln Gln Leu Asn Glu Asp Thr Asn Ala

1	5	10	15
Thr Lys Tyr Thr Tyr Lys Leu Leu Gln Leu Pro Ser Lys Ile Leu Asn	20	25	30
Gln Leu Glu Ser Lys Ser Thr Asn Leu Tyr Ile Lys Ser Asp Ile Asn	35	40	45
Ser Leu Ala Leu Cys Thr Asp Ser Glu Thr Phe Lys Leu Arg Gln Met	50	55	60
Asn His Ser Asn Thr Val Leu Leu Leu Asn Lys Glu Pro Asp Asn Lys	65	70	75
Leu Ile Gly Phe Gln Lys Thr Ser Tyr Glu Tyr Glu Leu Thr Glu Ile	85	90	95
Lys Gly Ser Ile Asp Thr Ser Asp Ile Pro Ile Phe Asn Gly Gln Thr	100	105	110
Ala Gln Gln Pro Ile Asp Leu Ile Ala Leu Glu Asp Asn Ser Ile Cys	115	120	125
Ser His Gln Glu Phe Leu Ser Asn Trp Tyr Glu Leu Gly Gly Cys Glu	130	135	140
Ile Asp Asn Gly Ala Tyr Phe Met Ser Ala Asp Ile Ile Thr Glu Leu	145	150	155
Leu Tyr Leu Leu Ile Thr Lys Leu Met Ser Leu Gln Val His Glu Phe	165	170	175
Ser Pro Glu Asp Val Ser Ser Ile Ile Thr Pro Pro Tyr Asn Asp Ser	180	185	190
Met Val Thr Ser Ile Ile His Lys Phe Cys Thr Ile Glu Ser Glu Lys	195	200	205
Tyr Gln Leu Asn Asp Leu Lys Ile Thr Gln Trp Phe Gly Ile Val Glu	210	215	220
Met Ser Lys Ile Asn His Lys Met Thr Asp Ile Ser Glu Phe Leu Leu	225	230	235
Asn Trp Lys Thr Ser Leu Pro Ser Phe Tyr Asn Pro Pro Leu Asp Ile	245	250	255
Ser Gln Leu Ala Gly Tyr Tyr Cys Ser Pro Ile Glu Asn Lys Ile Leu	260	265	270
Tyr Val Asp Pro Glu Ser Leu Ser Glu Asn Leu Ser Gln Arg Phe Lys	275	280	285
Glu Leu Phe Glu Leu Asp Lys Ser Trp Asn Tyr Asp Glu Phe Ile Pro	290	295	300
Phe Ile Lys Lys Phe Val Pro Ala Gly Lys Lys Val Asp Ser Ile Ile			


```

<400> 312
Met Ala Gly Val Arg Gln Leu Arg Ile Ile Ala Leu Thr Ala Phe Val
  1                               10                      15

Leu Gly Leu Ile Phe Thr Leu His Lys Val Gly Ser Asn Ala Ala Ser
      20                      25                      30

Leu Val His Ala Gln Ala Ser Asp Gln Gln Pro Asn Lys His Asn Thr
      35                      40                      45

Lys Ser Thr Thr Tyr Thr Ala Thr Asn Asp Glu Ser Val Ala Asn Leu
  50                      55                      60

Ile Asp Ser Lys Asn Asp Pro Gln Thr Asp Asp Lys Ile Asn Gln Lys
  65                      70                      75                      80

```

<400> 313						
agtggttggt	caataatggt	aagttcttgg	aaatagccat	tgttgctttc	tggtggttag	60
acttgttagga	agtagaactg	ttttccaatg	aaaagtagtt	ttaattagaa	aaattttcaa	120
agtgcgtgaa	gcccagttctg	aatgtgcgag	gaagcccagt	cagttagtag	tgtccttccc	180
tccactgtct	gtaatacaaaa	atttcacctta	gtgaaaatgc	gaaatatatc	tgtactggga	240
accccccgga	aaaaaaaaaaa	cctatgctca	aaactatatg	tactgtacac	aatctagggc	300
tatagcccta	atattgtaca	ggaagaactt	taactatggt	gcgaagagcg	tttccaattt	360
tttttttttc	aggtgtatgc	tgttctatgg	caactactgt	gttagtagag	agtgtctcgc	420
actaacagaa	catttttttc	agaacaggaa	aatttttgaa	atctaacatc	ttttactgaa	480
agccaagcat	caacacaata	atgtcaaccc	aatctgttca	agtatgtaaa	cgaattgaaa	540
taaagagata	gagagatggt	ttattatcaa	aatacgaaag	gaaaggcaat	taaaaaagga	600
aatcaaaaag	tcccaacctt	gcagtagaag	aattgaggta	tatgaatttg	atagatagcc	660
agaacggtgt	tacataaatg	ggatatagaa	caaaactata	cgaggagttt	gtttcaacga	720
tcattcaata	accagaaaac	gataatattt	tagcgaccat	taaatgacac	ttgaaggctc	780
actgggccaa	tagaatatct	ccatatacac	ttttgaacta	tttactaaca	atttactttt	840
gtttctagac	ttttggtaaa	aagaagactg	ccactgccgt	tgtctatggt	aaagccggtg	900
aagggttaat	taaaattaac	ggttccccaa	tcaccttggt	ccaaccagaa	atcttaagat	960
tcaaagttta	cgaaccattg	actttggttg	gttttagataa	attccaaggt	atcgacatca	1020
cgattaaagt	cactcgttgg	ggtcacgttt	ctcaagtcta	cgccatcaga	caagctattg	1080
gtaaaqgttt	ggttgcttac	cacaaaaaat	acgttgacga	agcttctaag	aacgaattaa	1140

319

agaaaatttt cgcttcttac gataagacct tgtagttgc cgactcaaga agaattggaac 1200
 caaagaaatt cgggtggtcgt ggtgccagag caagattcca aaaatcttac cgtaa 1256

<210> 314
 <211> 142
 <212> PRT
 <213> Candida albicans

<400> 314
 Met Ser Thr Gln Ser Val Gln Thr Phe Gly Lys Lys Lys Thr Ala Thr
 1 5 10 15
 Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Ile Asn Gly
 20 25 30
 Ser Pro Ile Thr Leu Val Gln Pro Glu Ile Leu Arg Phe Lys Val Tyr
 35 40 45
 Glu Pro Leu Thr Leu Val Gly Leu Asp Lys Phe Gln Gly Ile Asp Ile
 50 55 60
 Arg Val Lys Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala Ile
 65 70 75 80
 Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr Val
 85 90 95
 Asp Glu Ala Ser Lys Asn Glu Leu Lys Lys Ile Phe Ala Ser Tyr Asp
 100 105 110
 Lys Thr Leu Leu Val Ala Asp Ser Arg Arg Met Glu Pro Lys Lys Phe
 115 120 125
 Gly Gly Arg Gly Ala Arg Ala Arg Phe Gln Lys Ser Tyr Arg
 130 135 140

<210> 315
 <211> 959
 <212> DNA
 <213> Candida albicans

<400> 315
 gtggttaagat atagaaagct taccactttg acaagtttga aataggatgg gtgaaaattt 60
 ggacatcttg aataacttaaa attctgaact tgatcaccag atccttttct tttacataat 120
 tagatatgat ggatagggtta gaatcgtctt taaagagaag gtataatatc taactgattt 180
 ggcgagggtg tggaaaagtc actccactgt atatattctc ggagttttaac gtactacagt 240
 tcagtggggg gaatacctaa ataggggggt agaatacgaa ctcctacaaa ttttaaggag 300
 actatgaccc gaaaagagaa gaaaaattta ttactctaag aactttatat acctccacaa 360
 ctacttttt ctttagtttc attctgctt ttttttctta cacatcttaa ggtcaaacaa 420
 ttttaacttat tagcttggtga aaatctcact tcaattcaag ttctctttca attgacatta 480
 tagtattttcc caattcaatt atggcttctc atgcttctct tatattctgt aaaattatca 540
 aagggtgaaat tccttctttc aagttaattg aaactgcaaa gacttattcc ttcttgga 600
 ttcaaccaat tgctgaagcc cacgttttaa ttatccctaa acaccatggg gcaaagttgc 660
 acaacattcc agacgactac cttagtgaac ttttaccagt tgtcaaaaaa ttgacaaaag 720

tcttgaaatt ggacgaaaat aatactccag aaggtgaagg ttataacgtt ttacagaaca 780
 acggaagaat tgctcatcaa gttgttgatc acgttcactt ccatttgatt cctaaaaagg 840
 atgaggctac aggttttaggt gttggttggc ctgctgaagc cactgatttt gataaattag 900
 gaaaattgca tgagaaatta aaggaagaat tggctaaggt agataatgaa aaattataa 959

<210> 316
 <211> 152
 <212> PRT
 <213> Candida albicans

<400> 316
 Met Ala Ser His Ala Ser Cys Ile Phe Cys Lys Ile Ile Lys Gly Glu
 1 5 10 15
 Ile Pro Ser Phe Lys Leu Ile Glu Thr Ala Lys Thr Tyr Ser Phe Leu
 20 25 30
 Asp Ile Gln Pro Ile Ala Glu Ala His Val Leu Ile Ile Pro Lys His
 35 40 45
 His Gly Ala Lys Leu His Asn Ile Pro Asp Asp Tyr Leu Ser Asp Ile
 50 55 60
 Leu Pro Val Val Lys Lys Leu Thr Lys Val Leu Lys Leu Asp Glu Asn
 65 70 75 80
 Asn Thr Pro Glu Gly Glu Gly Tyr Asn Val Leu Gln Asn Asn Gly Arg
 85 90 95
 Ile Ala His Gln Val Val Asp His Val His Phe His Leu Ile Pro Lys
 100 105 110
 Lys Asp Glu Ala Thr Gly Leu Gly Val Gly Trp Pro Ala Glu Ala Thr
 115 120 125
 Asp Phe Asp Lys Leu Gly Lys Leu His Glu Lys Leu Lys Glu Glu Leu
 130 135 140
 Ala Lys Val Asp Asn Glu Lys Leu
 145 150

<210> 317
 <211> 297
 <212> DNA
 <213> Candida albicans

<400> 317
 cataattatt acatataaac tcgcactata attttttttt tttctattct gtgtgtgtgt 60
 gtgtgtgaga gccagagaaa ccaaactgac tgagtgatcg tctctcaaca atttatttct 120
 cctcgtctta ttttttttct ttcttttctt ttctcttctt tcttcttctt cttctttttc 180
 ttcttctttt cttcttttacc aaaacactag tattttcaaca tgagagataa gtggagaaaa 240
 aagagagtta gaagattaaa gagaaagaga cggaagggtta gagctagatc caagtaa 297

321

<210> 318
 <211> 25
 <212> PRT
 <213> Candida albicans

<400> 318
 Met Arg Asp Lys Trp Arg Lys Lys Arg Val Arg Arg Leu Lys Arg Lys
 1 5 10 15

Arg Arg Lys Val Arg Ala Arg Ser Lys
 20 25

<210> 319
 <211> 1303
 <212> DNA
 <213> Candida albicans

<400> 319
 tattgtctga tgctatacgg aatgggcggt acaaatatac aaacttatat ttgaaagtaa 60
 attctattat tttcttctat cgtatgcata ccgattatta tcacaaggac aattgcctat 120
 tggtgtgtgg aataaattta aaatccttct tattggtgtc tagactttgc tttttgtggt 180
 gattagggct ttagccctat cacgtgaaat actgtatata aaaaattcct tatagcgcg 240
 taaaacatat tttttttccg tattaacaaa tatgtgtgaa gttttgtcct ggtgttttct 300
 cactgttttt cttttttttt ctggtagtat caattaacgc ttagatccaa tacagttttg 360
 gtaacttgta cacgaacaaa atctcaaatt tgttactgtg tgaaccaaca aggaagagaa 420
 aaaaaaaccc atacaaaaat ttttcagtat caaggaatta gaagagacgt ttaaatcaac 480
 aaagttcaaa tctatcaaca atggtatggt taatatcgat attatccata gatgtacatg 540
 tatecctaag ggtttcatta tttggaaagt tatgtttatg ggagttctat ttattaagat 600
 atgggataag aattaaagta ttggatgagt agtacaagac caacaaagag aaatagcccc 660
 ctttccctcc actattcaat atactcaaca acattatcaa gttaaaagtt cagaagatac 720
 acgtaaatga aaagtttaata ccaagaagaa tacaaattac cagtcatac cgtgtttggg 780
 tttagattac tatattttac aagaaacata ttatatgaaa tgatacccaa tccacagcga 840
 cttttcagat agccaaataa ctaagcaact caagataaca taggatcatg catcaatcac 900
 aaatgaaaca ttaataactaa ctaacttttt ttttatttat taggccggtg ttaaaaacttt 960
 cgaattaaga actaaatcta aggaacaatt agaattctcaa ttggttgaat tgaaacaaga 1020
 attggccact ttaaaagttc aaaaattaca aagaccaagt ttaccaagaa ttcacactgt 1080
 tcgtaaaaaac attgctagag tattgactgt tattaacttg aatcaaagag aaaatgttcg 1140
 tgcctttttac gctggtaaaa aatacattcc aaaagattta agagctaaaa agactagagc 1200
 ttttaagaaga aaattgacta aatttgaagc ttctcaagaa actgaaaaag ctagaaaaca 1260
 aagaattgct tttccacaaa gaaaatttgc tattaaagct taa 1303

<210> 320
 <211> 120
 <212> PRT
 <213> Candida albicans

<400> 320
 Met Ala Gly Val Lys Thr Phe Glu Leu Arg Thr Lys Ser Lys Glu Gln
 1 5 10 15

Leu Glu Ser Gln Leu Val Glu Leu Lys Gln Glu Leu Ala Thr Leu Lys
 20 25 30

Val Gln Lys Leu Gln Arg Pro Ser Leu Pro Arg Ile His Thr Val Arg

35	40	45
Lys Asn Ile Ala Arg Val Leu Thr Val Ile Asn Leu Asn Gln Arg Glu		
50	55	60
Asn Val Arg Ala Phe Tyr Ala Gly Lys Lys Tyr Ile Pro Lys Asp Leu		
65	70	75
Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Lys Leu Thr Lys Phe Glu		
	85	90
Ala Ser Gln Glu Thr Glu Lys Ala Arg Lys Gln Arg Ile Ala Phe Pro		
100	105	110
Gln Arg Lys Phe Ala Ile Lys Ala		
115	120	

<210> 321
 <211> 2690
 <212> DNA
 <213> Candida albicans

<400> 321

ctctgtgtaa	attgatgaaa	tccacacaat	aaaaattttc	tttcttcttt	taagaaccta	60
aaaacagaat	caacattatt	tgccccatac	atatccaaga	attaaatact	tattagttct	120
aagtggata	gaagagaatc	aaacttaaca	ttactgttac	gcaacgtcaa	gagggcattt	180
tttttagttt	taatttgttt	catttcaatt	gaatctttta	gaatcaccga	gtatacatat	240
tttcttttgt	attttatcag	ggaagccaca	tccaaccacc	agttacatcc	cacaaaatcc	300
cttaatcttg	ttcttagttg	tattattaat	ctattgaatt	taagtttgat	atgcgagaga	360
atattgtgga	ttgtataagt	tttgaactgg	acttgaatac	tttgaggggc	ttaatcatat	420
attgcatttt	ataccctact	cgcggtgttg	cttaccacac	tgactagtat	gatcctttctg	480
agatttctag	ccaataaatt	atgagtgata	tttatattat	tattcatatt	tctactacct	540
gtgatgactc	gccgacattt	gtcactaagg	attcttccga	gttaattgaa	tttgcttgagg	600
aaacagtcga	tagtgtcact	ttggaaactt	tatacaaagg	atcaaacttg	gttcgtccaa	660
ccaacacacc	tatcacacct	tactgctcga	agattcatag	aataacatgg	gacaatgtca	720
aaaatgctgg	gtcgttcaaa	gacgccatca	caaactttga	tcaatacgta	caagaacaca	780
taatttccaa	gaaaaaggag	ttttcaattg	tgatgtttga	catttccaaa	ttgagagttc	840
agttggttcg	tgaagctaga	gacaaatccg	tggtttttacc	ctcgtatcta	caacatccaa	900
ggatttttga	tttaccaaga	gaatatttaa	attggcaatc	tagccaccct	gaaacattat	960
cataccccc	aacttcttta	actaatatta	ttactgcatt	agaagttgag	gttgagaata	1020
tatctgaata	tgtcgacttg	ccaaactttt	cttccacacc	atcaccatca	aaagcttcag	1080
caacaacgac	gacgacaact	gcaaattgtc	cagccattga	cgtcctttcc	agtgaacacg	1140
aaccaaatgg	taaagtcatt	gcaaatttgc	acgccaaaat	tgccaaacaa	ttgatcaaaa	1200
aatccatccc	tgttgagaat	caccctaatt	tattttacaag	accttttgat	tcgggtcaag	1260
atatcactgc	ttttacatca	gaaagatcaa	aagtactcta	tctttccaac	ttgccaaacg	1320
acaccacaca	atcagagttg	gaatcatggt	tactcagta	tggtggaaga	ccagggtggg	1380
tttggaactt	taagtctgca	gatgataaca	ataataataa	caacaacaat	agcaatggcg	1440
ggaaaggata	tcagaatgcg	agaaaatatg	gtatttcagg	gtttgtggcc	tttaatactc	1500
atgaggaagc	agttgattgt	ttagctttga	atgggagagt	gttgaatgat	cgtcctattg	1560
aagttcaagc	gtcttctagt	aaagtgtttg	atatggccat	ggataaattg	ttgttgactc	1620
tgttcccact	ctcaaagaac	agaoctagac	ccgggggattg	gacttggtta	tcttgtgggt	1680
tttccaattt	ccagagaaga	acacactggt	tcagggtgctc	ttttgcgcca	gtggcggttc	1740
aggatgtttt	taacagtaat	acaggcaatt	ccaacggtaa	tggcaatggt	agcggcaacc	1800
acaaccacaa	ccacaatagt	ggagctcgcc	gtggcatgaa	tttacagcct	gctcaagcta	1860
atgagaaaaat	tggaacaggc	aatattagta	ttcctttctta	caacgatcca	atcaagggtc	1920

aatagcattg	aacaagaaga	agaggacaac	gatagaccaa	ggttggtttt	agccaatcct	60
gattatgata	gtgatgacag	ttcatagaca	atttacagcc	ttaaattggat	atatatgtat	120
atttaataat	aaaggacttg	tttttttttag	taactagtgt	gatctctttt	ctgggtgtac	180
atttcggata	gccaaccaag	ttatatttta	gcagtttata	gacagtgtta	tcgatgggta	240

Met 1	Ser	Asp	Ser	Gly 5	Tyr	Thr	Leu	Ile	Tyr 10	Glu	Pro	Asn	Thr	Ala 15	Thr
Lys	Val	Ser	Val 20	Asn	Glu	Phe	Lys	Asn 25	Leu	Leu	Glu	Lys	Gly 30	Lys	Asp
Asp	Val	Lys 35	Val	Asp	Thr	Met	Lys 40	Lys	Ile	Leu	Ile	Thr 45	Ile	Leu	Asn
Gly	Asp 50	Pro	Leu	Pro	Asp	Leu 55	Leu	Met	His	Ile	Ile 60	Arg	Phe	Val	Met
Pro 65	Ser	Arg	Asn	Lys	Glu 70	Leu	Lys	Lys	Leu	Leu 75	Tyr	His	Tyr	Trp	Glu 80
Val	Cys	Pro	Lys	Met 85	Asp	Glu	Ser	Gly	Lys 90	Met	Arg	His	Glu	Met 95	Ile
Leu	Val	Cys	Asn 100	Ala	Ile	Gln	Arg	Asp 105	Leu	Gln	His	Pro	Asn 110	Glu	Tyr
Ile	Arg	Gly 115	Asn	Thr	Leu	Arg	Tyr 120	Leu	Thr	Lys	Leu 125	Lys	Glu	Pro	Glu
Leu	Leu 130	Glu	Thr	Leu	Val	Pro 135	Asn	Val	Arg	Gln	Cys 140	Leu	Glu	His	Arg
His 145	Ala	Tyr	Val	Arg	Lys 150	Asn	Ala	Val	Phe	Ala 155	Leu	Trp	Ser	Ile	His 160
Lys	Val	Ser	Asp	His 165	Leu	Ala	Pro	Asp 170	Ala	Asp	Glu	Leu	Ile	Tyr 175	Arg
Phe	Leu	Tyr	Glu 180	Glu	Asn	Asp	Ser	Val 185	Cys	Lys	Arg	Asn	Ala 190	Phe	Val
Cys	Leu 195	Gly	Asp	Leu	Asn	Arg	Glu 200	Ala	Ala	Leu	Gln 205	Tyr	Ile	Gln	Asp
Asn	Ile 210	Ser	Val	Ile	Glu	Thr 215	Leu	Asp	Pro	Leu	Ile 220	Gln	Leu	Ala	Phe
Ile 225	Glu	Phe	Ile	Lys	Lys 230	Asp	Ser	Ile	Gln	Asn 235	Pro	Ala	Leu	Lys	Gln 240
Gln	Tyr	Ala	Gln	Leu 245	Met	Thr	Glu	Ile	Ile 250	Glu	Ser	Ser	Ser	Asn 255	Val
Val	Met	Tyr	Glu 260	Ala	Ala	Asn	Thr	Leu 265	Thr	Val	Leu	Thr	Ser 270	Asn	Pro
Gln	Ser	Ile 275	Leu	Leu	Ala	Gly	Asn 280	Lys	Phe	Val	Glu	Leu 285	Ala	Thr	Arg

Val Ser Ile Leu Arg Val Gly Glu Ser Ser Leu Val Ser Lys Lys Ile
 595 600 605
 Asp Glu Asp Ser Ala Asp Arg Ile Leu Ser Tyr Ile Lys Ile Leu Asn
 610 615 620
 Asp Glu Glu Asp Leu Gln Glu Ile Lys Thr Ser Phe Leu Glu Asp Thr
 625 630 635 640
 Lys Asp Ala Phe Lys Ala Gln Ile Asn Asn Ala Glu Leu Lys Lys Ala
 645 650 655
 Glu Ala Leu Ala Lys Asp Leu His Asp Asn Ala Glu Gln Ile Asp Asp
 660 665 670
 Ala Ile Val Phe Arg Gln Leu Asp Lys Asp Asn Lys Lys Ser Lys Ala
 675 680 685
 Ser Val Asp Asp Val Ala Ala Ala Ser Gly Ser Asn Glu Leu Lys Lys
 690 695 700
 Glu Asn Leu Ser Ser Arg Leu Asn Lys Ile Ile Gln Leu Thr Gly Phe
 705 710 715 720
 Ser Asp Pro Ile Tyr Ala Glu Ala Phe Val Lys Val His Gln Tyr Asp
 725 730 735
 Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Thr Thr Thr Leu Arg
 740 745 750
 Asn Leu Ser Val Glu Phe Ala Thr Leu Gly Asp Leu Lys Val Val Asp
 755 760 765
 Lys Pro Thr Thr Ala Asn Ile Gly Pro His Gly Phe Tyr Lys Val Gln
 770 775 780
 Thr Thr Ile Lys Val Thr Ser Ala Asp Thr Gly Val Ile Phe Gly Asn
 785 790 795 800
 Ile Val Tyr Asp Gly Gln His Ser Asp Asp Ser Arg Ile Val Ile Leu
 805 810 815
 Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro Ala Thr Cys
 820 825 830
 Ser Glu Ser Gln Phe Arg Lys Met Trp Asn Glu Phe Glu Trp Glu Asn
 835 840 845
 Lys Ile Thr Ile Lys Ser Pro Ile Glu Thr Leu Lys Glu Tyr Leu Asp
 850 855 860
 Glu Leu Met Lys Gly Thr Asn Met Gln Cys Leu Thr Pro Gly Ala Val
 865 870 875 880
 Ile Gly Glu Glu Cys Gln Phe Leu Ser Ala Asn Leu Tyr Ser Arg Ser
 885 890 895

Val Thr Ile His Ala Gly Ile Glu Lys Ala Cys Phe Tyr Phe Gly Met
 260 265 270
 Lys Leu His Lys Val Asp Leu Asp Pro Val Thr Phe Gln Val Asp Val
 275 280 285
 Lys Lys Val Glu Arg Leu Ile Asn Ser Asn Thr Val Leu Ile Cys Gly
 290 295 300
 Ser Ala Pro Asn Tyr Pro His Gly Ile Ile Asp Asp Ile Glu Ser Leu
 305 310 315 320
 Ser Lys Leu Ala Val Lys Tyr Asn Ile Pro Leu His Val Asp Ala Cys
 325 330 335
 Leu Gly Ser Phe Ile Val Ser Phe Leu Glu Lys Ser Lys Val His Gly
 340 345 350
 Asp Arg Lys Leu Pro Ile Phe Asp Phe Arg Leu Pro Gly Val Thr Ser
 355 360 365
 Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala Pro Lys Gly Ser Ser
 370 375 380
 Ile Ile Met Tyr Arg Ser Pro Lys Leu Arg Glu Cys Gln Tyr Tyr Ile
 385 390 395 400
 Ala Ser Asp Trp Thr Gly Gly Met Tyr Gly Ser Pro Thr Leu Ala Gly
 405 410 415
 Ser Arg Pro Gly Ala Leu Val Val Gly Cys Trp Ala Thr Leu Ile Asn
 420 425 430
 Ile Gly Lys Gln Gly Tyr Thr Lys Phe Cys Tyr Asp Ile Val Ser Ala
 435 440 445
 Ser Met Lys Val Lys Arg Ala Ile Glu Thr Asp Pro Ile Leu Ser Lys
 450 455 460
 His Leu Gln Ile Ile Gly Asp Pro Ile Gly Ser Val Ile Ser Phe Gln
 465 470 475 480
 Leu Ala Pro Gln Gln Ser Gly Asn Leu Ser Ile Tyr Glu Ile Ser Asp
 485 490 495
 Leu Leu Thr Lys Lys Gly Trp His Phe Ala Thr Leu Gln Asn Pro Ser
 500 505 510
 Ala Leu His Phe Ala Phe Thr Arg Leu Thr Val Pro Val Val Asp Glu
 515 520 525
 Leu Ile Ala Asp Leu Val Glu Ala Thr Lys Glu Ala Val Ala Ile Ala
 530 535 540
 Glu Glu His Lys Lys Asn Gly Val Thr Lys Ala Pro Gly Asp Thr Ala
 545 550 555 560

<400>	327						
ttcaatttttt	ttaaaaaaat	agcaaaaaagg	tatttcttag	aaattgaaaa	aaaaaaatca	60	
caaaaaaatt	tataaaaccg	gatagggccg	ttatcgcagg	acgtgtccca	tgatcaatct	120	
acaatgaaat	gattcacatg	aaatatgtta	caattccaca	cttgctgcta	aaaagcaaca	180	
gttttgcaat	agagaaaagc	atgatatact	atcgataata	tctttcgata	agaacttaaa	240	
tgtagcaacg	ttgaatttta	aaataaaaact	tctttttcct	ggtgataaat	tttgactttg	300	
aagcataaag	aagacagagc	tgaaaaaaaa	ctactctcta	gacaaaatca	aaacctcgaa	360	
tatatTTTTg	gtgtttcttt	tttttttttt	ttgcctctcg	ttgaaatcat	ctccattctt	420	
cttttccacg	tctttgttga	aaactttgca	acctaaaaaa	ataagaatca	ctccaacaag	480	
tttaaactac	atttatcaatt	atgttgaaaa	ctagattaaa	acaaagcagg	gccataagtc	540	
gggttgtaag	aagatatgca	tgctcacacc	ccattttctc	caatcttgat	aagtaccagg	600	
ttggtctaaa	attgcatggt	tacgaagtta	cccaaactac	acctatacca	gaattttccc	660	
tcaatgctgt	atcataaaaa	cacacagaga	gtgggtgcaac	tcacttacat	ttggattccc	720	
ctaattgacag	taataatgta	tttctgattg	ctttcaaaac	aaatcctcca	gataatactg	780	
gggttcccca	tatttttagaa	catacaactt	tgtgtggtag	taaaaagttt	cgggtccgtg	840	
atccattttt	taaaatgacc	aacaggtcgt	tgagtaactt	tatgaatgca	atgacaggcc	900	
atgattacac	attttatcca	tttgctacca	ccaattcaaa	ggattttgaa	aacctaattg	960	
atgtgtattt	atcgtcagtg	tttgaaccgc	aattaaacca	taccgatttc	ttgcaagaag	1020	
gatggagaat	agaaaatcaa	aatgttcatg	acatatcgtc	caagcttgaa	ttcaagggag	1080	
ttgtatataa	tgaattgaag	ggccagtatt	cgaactctgc	atactacttt	tatatcaagt	1140	
tctctgagag	tatatatcca	tctctgaata	attcaggggg	tgatcccaag	aaaattgttg	1200	
atttgctgta	cgagggttta	ctagagtttc	acctgaaaaa	ttatcatcca	tcaaatgcaa	1260	
aaacattttac	ttatggaaaa	ttaccattgg	aagacagttt	aagtaaaata	agcaaatact	1320	
atgaatcatt	cgaaaaaaaag	gtgtcttcag	ttgacgtcaa	acaacctata	ttttctacag	1380	
ataaatcaga	aatctttgat	gtcaccatcc	cgggtccagt	tgatacaatg	aatggtaaa	1440	
agacttcaga	acagtactgc	acatctatca	cctggaactt	gggtaatcca	ttggatccaa	1500	
acatgcagta	tgatattttt	aaatggaaaa	tattgagctc	attattgttt	gatggacaca	1560	
actctccttt	ctatcaagag	ttaattgaaa	gtggatacgg	tgacgatttt	ctcgcataa	1620	
ctgggttgga	ctcaaccacc	gcgttgcttt	cgtttaactgt	tggtctcaac	tacttaacca	1680	
agcaaaaagt	tgataatttt	aatgaaaaag	ttatggaaat	cattaataat	aaaatcattc	1740	
ccgaattaag	taacgaagag	tctcttccat	atcatggtag	aattgatgct	atattgcatc	1800	
aaatagaaat	aggattcaaa	agacacaagc	ccgattttgg	atttggatta	ttgagctcta	1860	
ttgttccgct	atgggtgaat	ggagttgatc	caattgacac	cttgcaagtg	gaaaagatat	1920	
tgctgcattt	taaagaagat	tataaacaaa	atggtttaa	gatcttttaa	gaattattag	1980	
aaaagacatt	gtgtaaccct	cattgcgaaa	aattttaaag	caccattggag	ccaagagaag	2040	
attttaccaa	acaattggta	aaagatgaga	atttgatgat	cgagaaaaaga	gtaagtgaac	2100	
tcacagaaga	taacaagaag	gcaatctatg	agcaaaactt	ggaattagct	aaattacaat	2160	
tggaggatca	aaatacagaa	gttttaccba	cattgactat	tgatgacatt	caaagagag	2220	
gtgattttta	tgccattgat	ttggggccaa	taaataagaa	agttgtacat	gaaagggtag	2280	
ttgatacca	tggtctgggt	tatgccaaag	ctttaaaaga	tatttcttat	ttaccacaca	2340	
aaactttaca	gtaccttcca	ttgttttaaca	actgtttgac	gaaccttgct	ggaacagaaa	2400	
acacaccatt	tacggagttg	gaaactaaaa	tacaaatgct	aactggcggg	ataacattta	2460	
gttctaaaat	atcgactgac	ccctataata	ttgagcaact	aaaattacag	tatgtgttaa	2520	
gtggaatggc	tttgaaagaa	aagtcacctt	cagtttatga	tttatgggtg	gagattttta	2580	

770					775					780					
Gln	Lys	Tyr	Val	Leu	Gln	Gly	Glu	Phe	Arg	Tyr	Arg	Leu	Val	Gly	Asn
785					790					795				800	
Gln	Glu	Ile	Ile	Val	Glu	Asn	Glu	Lys	Leu	Ile	Glu	Lys	Phe	Asp	Lys
				805					810					815	
Asp	Ile	Ser	Ser	Asn	Arg	Pro	Thr	Leu	Ser	Leu	Thr	Val	Thr	Asp	Gly
			820					825					830		
Leu	Ser	Ala	Leu	Leu	Asn	Ser	Phe	Asn	Tyr	Asn	His	Thr	Ser	Glu	Asn
		835					840					845			
Val	Leu	Val	Asn	Leu	Pro	Phe	Gln	Val	Gly	Tyr	Ser	Ser	Leu	Gly	Lys
	850					855					860				
Ile	Gly	Ser	Ser	Tyr	Ser	Ser	Lys	Asp	Gly	Ala	Ser	Leu	Gln	Ile	Leu
865				870						875					880
Ser	Gln	Leu	Tyr	Ser	Phe	Lys	Asn	Leu	His	Ser	Lys	Ile	Arg	Glu	Ser
			885					890						895	
Asn	Gly	Ala	Tyr	Gly	Gly	Gly	Leu	Thr	Tyr	Asp	Gly	Leu	Asn	Gly	Thr
		900						905					910		
Leu	Asn	Phe	Tyr	Ser	Tyr	Arg	Asp	Pro	Asn	Pro	Val	Lys	Ser	Ile	Gln
		915					920					925			
Thr	Phe	Arg	Asp	Ser	Leu	Ser	Tyr	Gly	Leu	Asp	Ala	Asn	Trp	Asn	Asp
	930					935					940				
Lys	Asp	Leu	Gln	Glu	Ala	Lys	Leu	Arg	Val	Phe	Gln	Ser	Val	Asp	Ala
945				950						955					960
Pro	Ile	Asn	Ile	Ser	Ser	Gln	Gly	Ala	Ser	Ala	Phe	Phe	Glu	Asn	Ile
			965					970						975	
Asp	Asp	Tyr	Leu	Arg	Gln	Glu	Arg	Arg	Glu	Asn	Phe	Leu	Gly	Thr	Thr
		980					985						990		
Leu	Lys	Asp	Leu	Arg	Asp	Val	Thr	Glu	Lys	Tyr	Leu	Val	Asp	Asn	Gln
		995				1000					1005				
Asn	Asn	Leu	Val	Thr	Val	Ile	Gly	Asp	Asn	Glu	Ile	Leu	Asn	Val	Asp
1010					1015					1020					
Asn	Lys	Trp	Gln	Ile	Arg	Asn	Phe	Gln	Val						
1025				1030											

<210> 329

<211> 1366

<212> DNA

<213> Candida albicans

<400> 329

```

ttaagaacta gcagatgtaa aatgttttat gtcattatat aatttggttaa tacatgtata 60
tagatTTTTT aatgaatgta ttccctaaat agaacagaat tatgatgctg ttacagcaaa 120
aactggTTTT agtattggag aatgtttataa actgaaatttt gatttacaac caaaacccgt 180
gtcacgtgta agtaattagg gcttttaggg ctttctatat acaggcacca gaattttttt 240
ttatggggcg tagaaataat gtatgcgcgc gattcttcct gctagagggt tttctttttg 300
tatgtctgta acagtgcgac tcacatagtt aagtaatttt aaagccagag attgtgtaca 360
gtcgcacgcc ccctaatacac atagttaatt ctcaaacttt ctctctttct ctctttgctt 420
ttctcctaag gaaaaaaaaa atttattttca tttgttgaaa atttttgtat agttcagttt 480
aacaacacca gtaatcaaac atgccattag ttgtccaaga acaaggttca ttccaacaca 540
ttttacggta tgtgagtgtata ttataagatt atttgaatga gatagaaaag ggtaaggaa 600
ggaaagaaat tatccaacta ctgttttggg aaagattaat cagaaatttg aatgcaatga 660
aaaaactttt tcaagagatg gatatggaac aagattcgat tgttatcaac aaatataaag 720
aaaagcaatg atttactact gtttgggaaa gattttggat atgtgtatca acaatactac 780
tattttacttt ggagtaatat gttttcaata ttatcagaga cttatcaaaa tttatgagtt 840
tattattatt gaagttcaat accatcaagc ctttttttta accatcactc tattcaacaa 900
tcattttaat attaaagtct tttttttccc tgttttaaagt attcgattta ctaacattat 960
gaattattat tatagtttgt taaacaccaa cattgatggg agaatacaaga tcatgtacgc 1020
cttgaccaag atcagagggt tcggtagaag atatgccaac ttggtttgta aaaaagccga 1080
tgttgaatta accaaaagag ctggtgaatt gacccaagaa gaattggaaa gaattgtcac 1140
cattatgcaa aacccaacca actataaaat cccagcttgg ttcttgaaca gacaaaaaga 1200
tcaagttgat ggtaaagatt accatgtttt agctaacaac ttggaatcta aattgagaga 1260
tgatttggaa agattgaaga aaatcagatc tcacagaggt attagacact tctggggatt 1320
gaaagttaga ggtcaacata ctaaaactac ttctcgtggg cgtaa 1366

```

<210> 330

<211> 145

<212> PRT

<213> *Candida albicans*

<400> 330

```

Met Pro Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg
 1             5             10             15

Leu Leu Asn Thr Asn Ile Asp Gly Arg Ile Lys Ile Met Tyr Ala Leu
      20             25             30

Thr Lys Ile Arg Gly Val Gly Arg Tyr Ala Asn Leu Val Cys Lys
      35             40             45

Lys Ala Asp Val Glu Leu Thr Lys Arg Ala Gly Glu Leu Thr Gln Glu
      50             55             60

Glu Leu Glu Arg Ile Val Thr Ile Met Gln Asn Pro Thr Asn Tyr Lys
      65             70             75             80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Lys Asp Gln Val Asp Gly Lys
      85             90             95

Asp Tyr His Val Leu Ala Asn Asn Leu Glu Ser Lys Leu Arg Asp Asp
      100            105            110

Leu Glu Arg Leu Lys Lys Ile Arg Ser His Arg Gly Ile Arg His Phe
      115            120            125

Trp Gly Leu Lys Val Arg Gly Gln His Thr Lys Thr Thr Ser Arg Gly

```

130

135

140

Arg
145

<210> 331
<211> 1327
<212> DNA
<213> *Candida albicans*

<400> 331
 atagttatta caatataata aagcaaataa ataaaagaaa tgataaagaa ccatattaac 60
 aaagtttgaa cgtgctgtaa gtaaactcttg tatacgagaa tattcatctt ggaatatttc 120
 taaacgatac tggtaatacc taattctatt tgggtgtggtg catcacgtgc tagggctata 180
 gccctaatag tatatgcagt cgcatacatt aattgggtcat ctcataagta aattatataa 240
 tgtatagtgt gcgcgcactg taatttttca cactaagtta aggagagtgc gaaaaattta 300
 gtactaaca aattgtattg tgttgtgtgt ggctattggg cagagcgaaa atttcacccc 360
 tactgagagg aaactgtgag ggagagagat acacacaaac tctgtgcgca agaagaaaga 420
 caaaaaattt ttttgaaaaa aaaaaaagag acaaccaacc ttttattgta ttaacatttt 480
 aagatatcaa gaaactaaaa atgggctaagt tcatcaaadc tggtaaagtt ggtatgtaaa 540
 aatgagtacc tatatgggta gacaatgata gatttatttg ccaactatga atgggataga 600
 tatatatgat atgggagaga attttgaagg attgaaatat tttatataaa agagagaagc 660
 aaagagaaat aatgaacaat tgaaaagaag atacaaatc tgtaattta actagaatat 720
 gccattgaag atttaaatga ttaccatcgt aataaattta ttggaatttg ggagattctt 780
 ttggagttaa gaaaaaagca agtgattgat caatcactat ggagccgtca caagacatca 840
 acgaatccca caacattttt atttattcat atccatcata tggcagtaac aatcatgaat 900
 ctacaaatta catttaaaaa aagcattata ctaactaaat tttttagcta ttgttgtaag 960
 aggtcgttac gctggtaaaa aagtagtcat tgtgaaacca catgatgaag gtaccaaadc 1020
 tcaccatttc ccacatgcca ttgttgctgg tattgaaaga gctccattga aggttaccaa 1080
 gaagatggat gctaaaaaag ttaccaaaag aactaaagtc aagccatttg ttaaattagt 1140
 aaactacaac catttaaatgc caactagata ctcatagat gttgaatcat tcaaatctgc 1200
 tgtcacttct gaagcttttag aagaaccatc tcaaagagaa gaagctaaaa aagttgtcaa 1260
 gaaggctttt gaagaaaaac atcaagctgg taagaacaaa tggttcttcc aaaaattaca 1320
 cttttaa 1327

<210> 332
<211> 136
<212> PRT
<213> *Candida albicans*

<400> 332
 Met Ala Lys Phe Ile Lys Ser Gly Lys Val Ala Ile Val Val Arg Gly
 1 5 10 15
 Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
 20 25 30
 Thr Lys Ser His Pro Phe Pro His Ala Ile Val Ala Gly Ile Glu Arg
 35 40 45
 Ala Pro Leu Lys Val Thr Lys Lys Met Asp Ala Lys Lys Val Thr Lys
 50 55 60
 Arg Thr Lys Val Lys Pro Phe Val Lys Leu Val Asn Tyr Asn His Leu

65		70		75		80									
Met	Pro	Thr	Arg	Tyr	Ser	Leu	Asp	Val	Glu	Ser	Phe	Lys	Ser	Ala	Val
				85					90					95	
Thr	Ser	Glu	Ala	Leu	Glu	Glu	Pro	Ser	Gln	Arg	Glu	Glu	Ala	Lys	Lys
			100					105					110		
Val	Val	Lys	Lys	Ala	Phe	Glu	Glu	Lys	His	Gln	Ala	Gly	Lys	Asn	Lys
		115					120					125			
Trp	Phe	Phe	Gln	Lys	Leu	His	Phe								
	130					135									

<210> 333
 <211> 1157
 <212> DNA
 <213> Candida albicans

<400> 333
 ttccagtcac tccgaaatgc ataagcaaga cgtaggtgtg attgtggttg tttagtctaa 60
 tccaaaaata cttgccatga cgacccactg aagtaacaac tgcatttggt aaggcttttc 120
 tcatcttatt caattctttt tcagcatcat tcgtatcttt aagcacaggg aatagcaatg 180
 gatcatgtaa caaattcact ttcgtgattc gaaagcccaa aatgtttcgt tttacaacg 240
 cacacacatg tgaaacctaa accgagttag tcgtcaagaa aataattcag tggttaaagtc 300
 tgtaccttaa gcgtcaaacg tacttctgca acctctggca ttgagtgtaa tttaaatatt 360
 catgataatc tggaaactaca agctacgaaa aaaaaagaaa aagaaaaata gtacgagttc 420
 ttggtgagat aaataatgga gaacactttt ttttttctct ttggagggtt tagaaggcaa 480
 aaccaaattc agacaaggag atgaacagat tattcggaa gaaaagcact gcgccccaac 540
 catctttgaa tgatgcaatc aaggggaatc atgaaagagt ggggtctttg gatgttaaat 600
 taagcaagat caactcggaa ttatccacat accaacaaaa gataagcaga atgagagacg 660
 gacccgggaa gtcggcacta aaacaaaaag caatcaagtt actaagacag aggaagcaga 720
 tagaagctca aaaggatcag tttagagaatc aatcttggaa tatgacacaa gcttccatga 780
 caacagataa cttacaaaat accatgggtc caataaatgc aatgaaaaca gccataaac 840
 tggtgaaaca aacttatgga aaaattaata tcgatgaatt ggaagatctt caagatgaaa 900
 tggttgattt gattgataaa tcaaataaac tacaggaggc acttctgacg agctatgatg 960
 taccgatga catcagtgag ctggagttgg atgctgaatt agaagctctt ggcgaagaaa 1020
 ttgattttga aaatgaaatg gcagagagtg ggataggtgc acctagttac ttaaatgata 1080
 cagaacctac agcagcagat aaattgcta cattttattga cgaacaacca gaagaagctc 1140
 aaaaaatcgc aaactag 1157

<210> 334
 <211> 218
 <212> PRT
 <213> Candida albicans

<400> 334
 Met Asn Arg Leu Phe Gly Thr Lys Ser Thr Ala Pro Lys Pro Ser Leu
 1 5 10 15
 Asn Asp Ala Ile Lys Gly Ile Asp Glu Arg Val Gly Ser Leu Asp Val
 20 25 30
 Lys Leu Ser Lys Ile Asn Ser Glu Leu Ser Thr Tyr Gln Gln Lys Ile

acgttgaagg	tggagaatta	tttgatttat	tgggtgaacg	tgggtccatta	cctgaagtcg	900
aggctatcaa	gtatttccgt	caaatcatat	tgggtacggc	ttattgtcat	gctcttggtg	960
tatgtcacag	agatttaaaa	ccagagaatt	tgttactaga	ttctcaattg	aatgtaaaaa	1020
tagccgattt	tggaaatggca	gcttttagaaa	gtaacggcaa	attatttagag	acttcttgtg	1080
gttcacctca	ttatgctgct	ccagaaatcg	ttagtggatt	gaaatatcat	ggagctgctt	1140
ctgatgtttg	gtcttgtggg	gttatattat	ttgccttgtt	gacaggtaga	ttaccctttg	1200
atgatgaaaa	tattagaaat	ttacttctta	aagtccaggc	tggtaacttt	gaaatgcccg	1260
ttgatgaagt	tagcagagaa	gctagagatt	taattgctag	aatgttagag	gttgatccta	1320
tgagaagaat	atctactgaa	aaaatcttaa	gacacccatt	gttaaccaa	taccaatgt	1380
caaacgaaga	tttaatcagt	gaaaaatcat	taccacatcc	acatactggt	tacaaatctt	1440
tagggtcagt	tagaaacatt	gataaacaga	ttttatcaaa	cttgacaatt	ttatggaaatg	1500
atagacccga	agaggaaatt	gttgattgtc	ttttgaaaga	tggatccaat	ccagaaaaaa	1560
cattctatgc	attattgatg	agatacaagc	ataatcaaga	cgataacact	aataacaatt	1620
caccaaaaga	atcaacgagt	ttcaataata	aagtggtagc	cagtgggtcc	aaatacagtc	1680
ttaatggaac	ccctagaaga	aaaagagcca	gtcacataag	tgtgtcaaga	ccaacatctt	1740
tccaatacaa	gtctaactct	ggcgctgggtg	caacagcaaa	tagaaactcc	gttgccagac	1800
attctgtggc	ttctctggcc	aacaattctc	ctcgtaaatc	accatacaag	tcaccatata	1860
gatcacctta	tagatcacca	tataaatcgc	cttctaagag	atattcatat	aatcaatccc	1920
caactaaatc	tccttacgga	agaagatcaa	attcacaaag	acaatttgaa	aatgaaccat	1980
taagggcaaa	gccaagaaat	atttacaatg	agattgttga	tgacaaaagc	aacttttctc	2040
tacctccatc	gcttccacct	tccttacctt	caaaagattc	tcgttatatg	atcgatgaac	2100
ccaatcaacc	ccagttgcaa	caacctgctt	taagtcaagt	ccctgaaaaa	cctattgttg	2160
atgaatcccc	tgattttaatg	cagtcagcaa	aaatttctag	tggaaagaga	aattcaataa	2220
taggaaagaa	caacaacaac	agcaacagca	acaagagaat	gtctaagaga	aatcaattc	2280
gtgcatctat	gaccacggga	ttgaaaagaa	attccataac	catgaaattg	ttatctactt	2340
atgctaaatt	atcaggtgat	gacgactggg	aatacatgga	taaacaaaca	aaaagaacat	2400
cggctacttt	tgacgatttg	tgtgacaaaa	tatttaatca	agaagactat	gacgaagaag	2460
acgaacaatt	agttgatcct	gaagaaaagg	aagccaagga	atatgaaagg	ttaatggaat	2520
tggaaaagaaa	gaaacatgaa	gctgagttga	aagctagaag	agaattagaa	aagaagaaaa	2580
gaagacaaaa	gagacgttcc	attttgagtt	ctaagaaatt	aagtattatt	gtcaagaatg	2640
atgctgatcc	aaataataac	gaacaagagt	tggctgatga	aggtataaaa	caaccaaattc	2700
gtcaatccaa	aaacttgacc	gctttaagag	cattatctga	aggaaatcat	gcatctgaag	2760
aattgacatt	ggaagacgtt	gagaatttga	agagacgatc	agcatcacag	ccggttccaa	2820
aaagaagaca	aactccggtt	ttgacaagaa	gacctgtatc	aagattagat	ccattatggc	2880
aagcacacga	gaatgaacag	ttagatagag	caaaagatgc	cttggaaaca	gaatggaggg	2940
attcacaaaa	gagaagttct	actgttagtc	gtaaaaaagt	caacagagag	tcgatgatat	3000
cagttatgga	tgatattggt	gaagaggacc	aaggccgtgt	caacaggaga	tcaacacgaa	3060
acacttacta	tgaatgggaa	agagactatg	aaattccaga	accaactgtg	gaagattcca	3120
acttgactga	tgactacatg	acagaaatca	gaaaatcaag	acttttgaac	agtcagttaa	3180
atgttaggga	tccacttaat	gaaaaaagaa	aatctgaacc	caagactctt	attagcaatg	3240
ttcaaatacc	gagtgttact	agaaaatcaa	gaaatttcac	tacttccaac	aaaagggttg	3300
cggatttgtc	tatgtattca	acaaaggaat	cataccgtga	tttgaattct	ataattaact	3360
caccagatga	aaaccccgaa	cagcatcaaa	acatgaacaa	gccagcggtta	cgaaccagta	3420
ttgctgatcg	tttgataaaa	gctggattgg	ctgaaccaga	atatgaaact	gagactgatg	3480
gtgaagataa	agtgtctggt	attgatttgg	atgatcattt	agctgataga	aggacttcct	3540
attatgatgg	atctggaaag	agagcatcta	gagcttcaac	aactaaacgt	tacaatgttc	3600
attccagttc	agaaaaaaga	ccaaaatcca	aagttcctga	tttgccaaag	aatgattatg	3660
atgacacatt	tgtcagtaat	agtgatgaag	ttcataagcg	tcagtataaa	tcgatggttt	3720
ctgatgagtc	tagtgcattc	gatgatgtat	ttgataagat	taaattacca	gatggtaaat	3780
caactaaatc	ttccattgat	gaattggcta	acggcacgtc	tacaagtggg	catagaaaaa	3840
caaagataag	acattctcaa	ccggggcccg	aaatgttgat	tcctcatttg	aatggaggta	3900
ttgagtcgct	tcaaccaatg	tctaaagttc	tgggtaacaa	ttcaagtggg	catgatgata	3960
gtgttccacc	accaccgcca	gctcacaaag	tgaataaaaa	accattggat	gataagacga	4020
atttccctcc	accagaagtg	gatccaaaaa	gaaaagggtc	attttttaga	aaactttctt	4080
ggggatccaa	aaaaccatt	gaaaataata	caaacgccgc	cactaatacc	acgactcaac	4140
aacaattacc	aagtctgct	gaatcaaaag	aggagaaacc	aaaaagtcca	tttttcagat	4200
ggttttctgc	atctaatact	ccatctgctg	ctgaaattag	aaaattcaac	accatttttac	4260


```

ctggtgccaa aagagcccaa ttcagaaaga agagaaagtt tgaattaggt agacaaccag 600
ccaacaccaa gattggtcca aaaagaattc actctgtcag aaccagaggt ggtaaccaa 660
aattcagagc tttgagagtt gaaaccggta acttctcttg gggttccgaa ggtgtttcca 720
gaaaaaccag aattgctggt gtcgtttacc atccatctaa taacgaattg gttagaacca 780
acaccttgac caaatctgct gttgttcaaa ttgatgctac tccattcaga caatggtacg 840
aaaaccacta cgggtgctact ttaggtaaaa agaaggggtg tgctcatgct gctcacgctg 900
ctgaagttgc cgatgccaaag agatcaagaa aagtcgaaag aaaattggct gctagatctg 960
gtgctgctgc cattgaatcc gctgttgact ctcaattcgg ttctggtaga ttatacgctg 1020
tcatttcttc aagaccaggt caatctggta gatgtgatgg ttacatcttg gaaggtgaag 1080
aattagcctt ctacttgaga agattaactg ctaagaaata a 1121

```

<210> 338

<211> 206

<212> PRT

<213> Candida albicans

<400> 338

```

Met Gly Ile Ser Arg Asp Ser Arg His Lys Arg Ser Ala Thr Gly Ala
  1              5              10              15

Lys Arg Ala Gln Phe Arg Lys Lys Arg Lys Phe Glu Leu Gly Arg Gln
              20              25              30

Pro Ala Asn Thr Lys Ile Gly Pro Lys Arg Ile His Ser Val Arg Thr
      35              40              45

Arg Gly Gly Asn Gln Lys Phe Arg Ala Leu Arg Val Glu Thr Gly Asn
      50              55              60

Phe Ser Trp Gly Ser Glu Gly Val Ser Arg Lys Thr Arg Ile Ala Gly
      65              70              75              80

Val Val Tyr His Pro Ser Asn Asn Glu Leu Val Arg Thr Asn Thr Leu
              85              90              95

Thr Lys Ser Ala Val Val Gln Ile Asp Ala Thr Pro Phe Arg Gln Trp
      100              105              110

Tyr Glu Asn His Tyr Gly Ala Thr Leu Gly Lys Lys Lys Gly Gly Ala
      115              120              125

His Ala Ala His Ala Ala Glu Val Ala Asp Ala Lys Arg Ser Arg Lys
      130              135              140

Val Glu Arg Lys Leu Ala Ala Arg Ser Gly Ala Ala Ala Ile Glu Ser
      145              150              155              160

Ala Val Asp Ser Gln Phe Gly Ser Gly Arg Leu Tyr Ala Val Ile Ser
              165              170              175

Ser Arg Pro Gly Gln Ser Gly Arg Cys Asp Gly Tyr Ile Leu Glu Gly
      180              185              190

Glu Glu Leu Ala Phe Tyr Leu Arg Arg Leu Thr Ala Lys Lys
      195              200              205

```


<400> 343

```

<400> 344
Met Ser Asn Ser Ala Gly Phe Asp Arg His Ile Thr Ile Phe Ser Pro
  1          5          10          15
Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Phe Lys Ala Ile Asn Ser
      20          25          30
Ala Asn Ile Thr Ser Leu Gly Ile Thr Gly Gln Asp Ser Ala Val Ile
      35          40          45
Ile Ser Gln Lys Lys Ile Pro Asp Lys Leu Leu Asp Pro Lys Thr Val
      50          55          60
Ser Tyr Ile Phe Lys Ile Thr Pro Ser Ile Gly Met Val Ala Thr Gly
      65          70          75          80
Ser Ile Ala Asp Ala Arg Ala Gln Ala Met Arg Ala Arg Ser Glu Ala
      85          90          95
Thr Glu Phe Arg Tyr Lys Tyr Gly Tyr Glu Met Pro Val Glu Ser Leu
      100          105          110
Ser Arg Arg Met Ala Asn Ile Ser Gln Leu Tyr Thr Gln Arg Ala Tyr
      115          120          125
Met Arg Pro Leu Gly Val Ala Leu Thr Phe Ile Gln Val Asp Phe Ala
      130          135          140
Asp Glu Gly Arg Gly Pro Gln Ile Phe Lys Cys Asp Pro Ala Gly Tyr

```

352

145	150	155	160
Phe Thr Gly Val Lys Ala Val Ala Thr Gly Pro Lys Gln Gln Glu Ala			
	165	170	175
Thr Thr Tyr Leu Glu Lys Lys Phe Lys Lys Thr Asp Ala Val Lys Gly			
	180	185	190
Asp Trp Gln Lys Thr Val Glu Phe Ala Ile Ile Ala Leu Ser Ser Val			
	195	200	205
Ile Gly Thr Glu Phe Arg Lys Asn Asp Ile Glu Ile Gly Val Ala Thr			
	210	215	220
Glu Gly Glu Phe Arg Ile Leu Thr Pro Glu Glu Ile Asp Glu Arg Leu			
	225	230	235
Ile Ser Ile Ala Glu Gln Asp			
	245		

<210> 345
 <211> 968
 <212> DNA
 <213> Candida albicans

<400> 345
 cattgtaggt acacctgttt ttgctcaatg tacacacaca cgcaccagca gtaggaaaaa 60
 aaacaaaatt aaatgaaaaa tcatttttctg tcaatattaa gcttctttaag ataaccaacc 120
 aattaatatg tatgtgacat accatataaa taaagctaca aatggggata actatgtatt 180
 taatgataaa tgaatggaag accagaatgt ataatgttat aagatagtga tttatattga 240
 aaacaccctt aaaaaaatca accaccctc taaccgtcga attggaaatg tcaatttagt 300
 tagcatcgaa aatcaacaaa gacatgggga atcattttaca tataaaataa tgagagagaa 360
 ttacaaactg ctacgttatg ttttgttcat tatgtcttgt tcattatgtc ttgttcatta 420
 tgtcaaaaaa tctatagtta cctacctcta catcaattta tgggtctgaaa tactaacatt 480
 ttttttattt atagtgaata atgaagattg aagttgactc cttttcaggt tctaaaatct 540
 acccaggtag aggtacttta tttgtcagag gtgactctaa aatttttaga ttccaatcct 600
 caaaatctgc ttctttattc caacaaagaa agaaccctaa aagaatttct tggactgttt 660
 tgtacagaag acaccacaaa aaaggtattt ctgaagaagc tgctaaaaag agaaccagaa 720
 agaccgtcaa gcaccaaaga gctattgtcg gtgcttcttt ggaattgatc aaagaaagaa 780
 gaagtcaaaa accatctgac agaaaagctg ctagagactc taaattagct aaagacaaag 840
 aagctaaaaa agctgctaaa gctgccagaa aagctgaaaa ggctaaggct gttgcttctg 900
 gtgcttctgt tgtttctaaa caacaagcta aaggttcttt ccaaaaagtt aaagctacct 960
 cccgttaa 968

<210> 346
 <211> 155
 <212> PRT
 <213> Candida albicans

<400> 346
 Met Lys Ile Glu Val Asp Ser Phe Ser Gly Ser Lys Ile Tyr Pro Gly
 1 5 10 15
 Arg Gly Thr Leu Phe Val Arg Gly Asp Ser Lys Ile Phe Arg Phe Gln

20	25	30
Ser Ser Lys Ser Ala Ser Leu Phe Gln Gln Arg Lys Asn Pro Arg Arg		
35	40	45
Ile Ser Trp Thr Val Leu Tyr Arg Arg His His Lys Lys Gly Ile Ser		
50	55	60
Glu Glu Ala Ala Lys Lys Arg Thr Arg Lys Thr Val Lys His Gln Arg		
65	70	75
Ala Ile Val Gly Ala Ser Leu Glu Leu Ile Lys Glu Arg Arg Ser Gln		
85	90	95
Lys Pro Ser Asp Arg Lys Ala Ala Arg Asp Ser Lys Leu Ala Lys Asp		
100	105	110
Lys Glu Ala Lys Lys Ala Ala Lys Ala Ala Arg Lys Ala Glu Lys Ala		
115	120	125
Lys Ala Val Ala Ser Gly Ala Ser Val Val Ser Lys Gln Gln Ala Lys		
130	135	140
Gly Ser Phe Gln Lys Val Lys Ala Thr Ser Arg		
145	150	155

<210> 347

<211> 1418

<212> DNA

<213> Candida albicans

<400> 347

```

aatctaccat taggcaatgt catataatTT agattacgaa cagctgatga cgcagtttca 60
ttatctccat aattttataat ggcataccct ttggattttac ctgttaattc atcaaataat 120
aacttcacat ctaatactgg tccaactgat cttgcaatat cccgcacctg ttcttcagtg 180
taatcaaag gaaattttacc tattgaaaca caagtgtttt tactatccat atttagtttg 240
agctgcctag ttttctgtat tcttggtaac aaaaaactat aattatttaa caaattatcg 300
atagaatctc ttccaaagta caaccaatTT cgatacattt ttttctatga gatgtttttt 360
tcccctttgt ctttaactaa tgtatttggg tacactacct gaacctacca gttcagttca 420
gtctaaaaaa ttttttattt attgtgtttg tttatactac cctttgcata tattactaat 480
atztatctta ccttttcata atggatacaa aggaaataag atctaccgta tctaactctg 540
aaaaagcagt agatgacacc accattttta agttgttgaa tatcttgaat gatgggggta 600
aaccatccga aaaactcttg agagaaacca aagtaggtgt agctgtcaac aaattcagaa 660
gtcacgacag tgccgaaatc aacggtttag ttaaaaaaat gatcagaaat tggagagatg 720
ccgtgcaagc cgaaaagaac aacaaaaaga agttagcaat agcagctgga acaggaacag 780
gaacaccttc aagctcagca atttcgccat catcatcggg ttctggaagt acaacaccaa 840
aaccatcaga gtcaaccaca ccacggctg cccgtaaaagg tccaagaaat ccaaaaactg 900
acgggtgtaa tactcaatta tacgaaaatg ataccagaaa tgcacgggtt agtgctttat 960
acacgtcggt agcagttgat cgtgacgatt caccaaaaca cattttgaga atagctattg 1020
aaatcgaggc tgaagtatac aagagcgaat acctgaaagt aagtgcagat tatagaaata 1080
ggttaagaag ctttaccatg aatcttcgaa ataagaaaaa cccagaatta agagaaagaa 1140
tcttatcgaa acaaaatttta cctgctgcgt tcattaaaaa gaccctaata gaaatggctc 1200
ctgaggcatt gaaaaaggaa attgaaaaat tgcacaaaca aaacttggtt gatgctcaag 1260
gtgctactga aaagagagca gtgaccgata gattcacttg tggcaagtgt aagcacaaga 1320
aggtcagtta ttatcaaag caaaccagat cagcggatga gcctttaact acattttgta 1380

```

354

cttgtgaaaa ttgtggcaat agatggaagt tttcataa

1418

<210> 348

<211> 305

<212> PRT

<213> Candida albicans

<400> 348

Met Asp Thr Lys Glu Ile Arg Ser Thr Val Ser Asn Leu Glu Lys Ala
 1 5 10 15

Val Asp Asp Thr Thr Ile Leu Lys Leu Leu Asn Ile Leu Asn Asp Gly
 20 25 30

Val Lys Pro Ser Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val Ala
 35 40 45

Val Asn Lys Phe Arg Ser His Asp Ser Ala Glu Ile Asn Gly Leu Val
 50 55 60

Lys Lys Met Ile Arg Asn Trp Arg Asp Ala Val Gln Ala Glu Lys Asn
 65 70 75 80

Asn Lys Lys Lys Leu Ala Ile Ala Ala Gly Thr Gly Thr Gly Thr Pro
 85 90 95

Ser Ser Ser Ala Ile Ser Pro Ser Ser Ser Gly Ser Gly Ser Thr Thr
 100 105 110

Pro Lys Pro Ser Glu Ser Thr Thr Pro Ser Ala Ala Arg Lys Gly Pro
 115 120 125

Arg Asn Pro Lys Thr Asp Gly Val Asn Thr Gln Leu Tyr Glu Asn Asp
 130 135 140

Thr Arg Asn Ala Ser Val Ser Ala Leu Tyr Thr Ser Leu Ala Val Asp
 145 150 155 160

Arg Asp Asp Ser Pro Lys His Ile Leu Arg Ile Ala Ile Glu Ile Glu
 165 170 175

Ala Glu Val Tyr Lys Ser Glu Tyr Ser Lys Val Ser Asp Ser Tyr Arg
 180 185 190

Asn Arg Leu Arg Ser Phe Thr Met Asn Leu Arg Asn Lys Lys Asn Pro
 195 200 205

Glu Leu Arg Glu Arg Ile Leu Ser Lys Gln Ile Leu Pro Ala Ala Phe
 210 215 220

Ile Lys Met Thr Pro Asn Glu Met Ala Pro Glu Ala Leu Lys Lys Glu
 225 230 235 240

Ile Glu Lys Leu His Lys Gln Asn Leu Phe Asp Ala Gln Gly Ala Thr
 245 250 255

355

Glu Lys Arg Ala Val Thr Asp Arg Phe Thr Cys Gly Lys Cys Lys His
 260 265 270

Lys Lys Val Ser Tyr Tyr Gln Met Gln Thr Arg Ser Ala Asp Glu Pro
 275 280 285

Leu Thr Thr Phe Cys Thr Cys Glu Asn Cys Gly Asn Arg Trp Lys Phe
 290 295 300

Ser
 305

<210> 349
 <211> 1301
 <212> DNA
 <213> Candida albicans

<400> 349
 acatttattg ttggctatac tttcccagtt ttaaaggaat ggtaggcgg gtcagtctac 60
 tttattttta ctgtaatgtg ttgtgccagt gtatggttta tcaagactaa agttcctgag 120
 acaaagggta agcattcgta ccaggaagtc tggaattaaa cggtagttac ttccagtata 180
 tatggtgttc attgtgtttt gtgtctaaag ttgcgttagg gctaaagccc taatcaatag 240
 tagtgtactt tgtttgaaaa aaataatata tgcaaatata tgcatattag aattataagg 300
 gaatgaaaaat gaaaaaaaaa agaataattt tgtagatcgc atagtgtgag cgcgcacaca 360
 cacacaaaact ttgtagtgtt acagttttct tctttcccat acactctcgc agtcgcacgc 420
 ttgacaaaag ttaattagaa atagaaaaat ttctcattcc ttttgagttt tccaccataa 480
 tcaactagta ataaccaaca atgcoctacta gattaactaa aaccagaaaa cacagaggta 540
 atgtttcttg tatgtacaat ttactaaaag ttttaacgga tgaaagagta ttgaatgttc 600
 aaggacatat ggagatttag agaaaacatg gaaaactaat cgaaaatgaa taatgaatgg 660
 aaaatttttt aaactgaata tcagaataga cacaacacaa cagatccaga gtcattatca 720
 cattgatcat acaaccaaag caatgaatat gagtagtttg ggaaaccaca acatacgagt 780
 tatttttctag aacaatcaag tttatcattt acagaagaca gttccatcaa tatgtccaaa 840
 atactctttg aagtcaatta aagtc aaatg aacgaattac taacttattt ttttctttag 900
 ccgtaaggg tagaattggt aaacacagaa agcaccggg tggtagaggt aaagctggtg 960
 gtcaacatca tcacagaacc aacttgata aataccatcc aggttacttc ggtaaagttg 1020
 gtatgagata ctccacaaa caacaaaacc acttctggag accagaaatc aacttgaca 1080
 aattgtggac tttggttgat tctgaaaaga aagacgaata cttgagcaaa tcatctgctt 1140
 ctgctgctcc agtcatcgac accttggtc acggttacgg taaagttttg ggtaaaggta 1200
 gattaccaga agttccagtc attgtcaaag ccagatttgt ttctaaatta gctgaagaaa 1260
 aaatcagagc tgttggtggt gttgtcgaat tagttgctta a 1301

<210> 350
 <211> 149
 <212> PRT
 <213> Candida albicans

<400> 350
 Met Pro Thr Arg Leu Thr Lys Thr Arg Lys His Arg Gly Asn Val Ser
 1 5 10 15

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg
 20 25 30

Gly Lys Ala Gly Gly Gln His His His Arg Thr Asn Leu Asp Lys Tyr

<400> 352
Ala Ile Lys Ile Thr Val His Asn Gly Asp Arg Lys His Val Ala Ala
1 5 10 15
Leu Arg Thr Val Lys Ser Leu Ile Ala Asn Leu Ile Thr Gly Val Thr
20 25 30
Lys Gly Tyr Lys Tyr Lys Met Arg Phe Val Tyr Ala His Phe Pro Ile
35 40 45
Asn Val Asn Ile Ile Lys Lys Asp Gly Gln Asp Tyr Val Glu Ile Arg

Ser His Ser Ala Lys Ser Val Val Gly Gly Phe Ala His Gln Gly Trp
275 280 285

Ile Leu Gly Leu Ser Phe Asp Glu Glu Gly Lys His Leu Ala Ser Cys
 290 295 300

Gly Phe Asp Lys Cys Ile Arg Val Trp Asn Leu Glu Thr Ser Glu Arg
 305 310 315 320

Glu Ala Thr Ile Ser Ile Ser Ile Ser Asp Leu Asp Asp Thr Thr His
 325 330 335

Asn Asp Gln Asp Glu Ser Val Ala Ser Gly Val Ala Phe Ile Lys Lys
 340 345 350

Gly Val Arg Gly Gly Ser Gly Gly Asp Ser Asn Glu Gly Leu Cys Val
 355 360 365

Val Ser Phe Asp Arg Gly Ile Arg Trp Tyr Arg Glu Ala Gly Gly Ile
 370 375 380

<210> 355

<211> 1418

<212> DNA

<213> Candida albicans

<400> 355

atagagatgc ttattctggt ggttcagtta atttatatca tgtcactgaa caagggttga 60
 cttatcatgg taatttcaat gttggtgac tcttttggga agttaagaa aaggaacaat 120
 catttgtaaa ttagatgga taaagtaagt tgattgtata aaaaaagaat ggattcatta 180
 atataaattt acaaatctga taataaacta cagtaactat tatgcaacaa ttgaaagtat 240
 cctgtgtcac gtgattagg ctcaaaagcc ctaacagggt gcacgtgatg ttgattttatt 300
 tatccctgca cacattgagt tttttttcta tgggtgaaat tattagttag acgatgttgt 360
 tcgcatttta ccacacactc tcacactgag ttagtgcata ctaacaatct tctcacacta 420
 tacacaaaaa aaatctttcg tttgaaaagt tttgaaagg tctgtttctc aatagtatat 480
 ccatacaata actgccaaag atggtatgtt caagtgttta aagagatcga aatgttttgt 540
 ttttaattgga agtgatatca taatgagaaa atatgggaaa tagagatagg accgaattaa 600
 ttgaaagagt tttcttttgg ggaaatgggt tcaataagat ttttcaagat tggaatcaaa 660
 ttatgtcaga tgtgaagaag agtaaatata acaagaagtt caaatcatta aaaattttat 720
 gtaaatacaa cgattatcaa ttacagtcaa cgaatagaat aaaacaaaag ccagcatata 780
 acagatacca gtgattcatc ccagtgatat aaataatgat attcaattaa aaacaattat 840
 aagacatttt ttatttatgt atcaacaaaa tactaactta tctttctttt aattagtctg 900
 acaaatccca aaatgttatg cgtgaattac gtattgaaaa attagtttta aacatttgtg 960
 ttggtgaatc cgggtgata ttaaccagag ccgccaaagt tttagaacaa ttatctgggtc 1020
 aaaccccgat tcaatctaaa gctagatata ctgtcagaac tttcgggtatt agaagaaatg 1080
 aaaaaattgc cgtccacggt actgtcagag gtccaaaagc tgaagaaatc ttggaaagag 1140
 gtttgaaagt taaagaatat caattaagat ctaaaaactt ctctgctacc ggtaactttg 1200
 gtttcgggtat tgatgaacat attgatttag gtatcaaata tgatccatct attgggtattt 1260
 acggtatgga tttctacgtt gttatgggta gagccggtgc tagagtcacc agaagaaaga 1320
 gagctagatc cactattggt aactctcaca aaaccaacaa agaagatacc atccaatggg 1380
 tcaagaccag atacgatgct gaagttttgg ataaataa 1418

<210> 356

<400> 357						
tattgcgtaa	tcgttatcaa	tgtttggatt	gttgcaacgc	tgggttgtgt	gtatatgcga	60
gaaatgagta	attgtttaaa	aataatcgat	gcagcagtc	gccactaaat	aaataaaatg	120
tcatatgtgac	atgataagga	tttatcaata	ctgttaggtc	tatagcccta	actttaatca	180
tttacacgtg	atacaaaaaa	gttgtttgat	ccgcacgac	tatgagtacg	cactcactaa	240
ttatagcctg	aaaaaaaaaa	tttccacata	gtaaggggat	tttgtatggt	ggtgcgctcg	300
cctaagacgt	ctgcatacat	tttctaaaagt	cacactgata	taggggatgt	gtggtagtga	360
ttgtgtgttc	ccaccaaata	actttgcgga	cactctcata	tactcaattt	ttttcttaca	420
aaaatttttt	ttctttctact	tttttcaaga	attctttctt	tacaattcaa	caacatcaat	480
catggggtaaa	ggtaaacc aa	gagggcttaa	ctctgctaga	aaattaaag	ttcacagaag	540
aaacaacaga	tgggctgtatc	aagcttataa	agctagatta	ttaggtagcg	ctttcaaatc	600
ttctcaattt	ggtggttcat	ctcacgccaa	aggtatcggt	ttggaaaaaa	ttggtattga	660

361

```

atctaaacaa ccaaactctg ctatcagaaa atgtgtcaga gtccaattaa tcaaaaacgg 720
taagaaagtc actgctttcg ttccaaacga tggttgtttg aactttgttg acgaaaatga 780
cgaagtcttg ttggctgggt tcggtagaag aggtaaagct aagggggata ttccaggggt 840
tagattcaag gttgttaaag tttccggtgt ctctttatta gctttatgga aagaaaagaa 900
agaaaagcca agatcatag                                     919

```

<210> 358

<211> 145

<212> PRT

<213> Candida albicans

<400> 358

```

Met Gly Lys Gly Lys Pro Arg Gly Leu Asn Ser Ala Arg Lys Leu Arg
 1          5          10          15

Val His Arg Arg Asn Asn Arg Trp Ala Asp Gln Ala Tyr Lys Ala Arg
          20          25          30

Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His
          35          40          45

Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ser Lys Gln Pro
          50          55          60

Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly
          65          70          75          80

Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val
          85          90          95

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Arg Gly Lys
          100          105          110

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser
          115          120          125

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg
          130          135          140

Ser
145

```

<210> 359

<211> 1164

<212> DNA

<213> Candida albicans

<400> 359

```

aattcatttg atctctaaga agatgaacag gccttgaatg ggaggggttg gttcgacttc 60
cacgaaatgt gggttgaaaa acttgagtcc tcaaaaaggt tctctcgtaa aaggccagag 120
aaagaaaaaa ccaccaaaccc cccaccacca acctaacctt ttccttccat ccattcctct 180
ttccttactt tgcaaagtgt gaatccagtt atattcatta aagatcctat aaaatacagat 240
tattcacaat ttattatatc ttactcccgc aaattcatta attgtaatcg tattgattta 300
gttatacttt gtcaaatacac cgaatcaaata caattgaatg aaattttatg tttttattat 360

```

Gly His Lys Ile Leu Leu Ser Met Ala Ile Phe Leu Thr Ser Asn Lys
180 185 190

Leu Ile Ile Gly Ile Thr Gly Ser Asn Leu Leu Ile Asn Lys Lys Phe
 195 200 205
 Lys Ser Gln Leu Gln Thr Phe Asn Gln Arg Gln Asn Leu Val Ile Gln
 210 215 220
 Phe Ile Asn Leu Leu Leu Leu Ser Glu Thr Ser Val Ile Phe Phe Glu
 225 230 235 240
 Ile Tyr Glu Ile Asn Asp Val Cys Gly Pro Thr Gly Tyr Ile Asn Asp
 245 250 255
 Ile Asp Asn Leu Ile Ile Ser Gln Glu Thr Lys Ser Gly Gly Glu Phe
 260 265 270
 Val Asn Lys Phe Arg Lys Asp His Gly Phe Lys Leu Leu Asp Ile Thr
 275 280 285
 Ile Ile Lys Val Ile Gly Gly Asn Ile Glu Glu Asn Ser Trp Lys Gly
 290 295 300
 Lys Leu Ser Ser Thr Asp Ile Arg Glu Gln Glu Tyr Asn Arg Leu Leu
 305 310 315 320
 Asn Gln

<210> 361
 <211> 1427
 <212> DNA
 <213> Candida albicans

<400> 361
 caagagtaaa atctaaatcg ttccaatgat tttggacagc tcatagggtta agagggtctac 60
 atgtgttggg ggcagtagta ttggtattaa gtgggtgggt catggtatta gagagtgggt 120
 gttataaaaag aaggttgtga tttttttttt ccactggtgg tgggtggtgct gattgtactg 180
 ctgttcactt tattgtttcg tttcgttttt cctttgtttt gttgacgttg acattttttt 240
 tgctgttgtt gttgtatggg aatttttgta ttagttgttc ttttttgttt ttttttactt 300
 gttcaaagtt tcatataata ataataattct tgttttcata tttttttttt cagaacaaga 360
 acaaatacaa cttatataat ttgatcttac tcttatcccc aggtttttct atttgttttt 420
 gggtttgcca ttcatatata tatatctatt attcaaataca atttgaggag tatcattaat 480
 ttaaattata tcagttaaca atgtcgtatc gtggctcctaa tcaatttggt aatcaacctc 540
 cacatcatgg aataccttct caacctcaac cacatatagg tccaatatct tccagcaaaa 600
 gtcctttaga acaatttgaa gatgttgcta aaaaagttga agattggatc gatgattatt 660
 ttaaagtctt gaaaccatac gtcccagcaa ttggttagagc atttttggtg gccactttct 720
 atgaggatac ttaagaatc ttcactcaat ggaatgaaca agtttattac ttgcacaact 780
 atagactacta ttggcggttg ttgaccgttt tattcttgat caataatatg gtggttatga 840
 cagttgcac cacttttagta attgccagaa aaaagaataa cattgctact attgcattga 900
 tcgttggtgt tattatacaa ggtattgggt atggtttatt gtttgatgct caatttggtt 960
 tgagaaactt gtccgttggt ggagggttag tattagcatt ttccgatagt attgttagag 1020
 ataaaagatc cttaaacaatg ccagggtttac cgatgttgaa caatcaagac aacaaaaagt 1080
 atttcctttt agctggtaga attttgtagg tattattatt tttgggattc gtcttttctt 1140
 ctgattgggc attgggtaga gttttcatta ttataatcgg gttaacttct tgtgcttcaa 1200
 ttgttggttg ttacaagaca aagttttcag ctgctatcat gcttattggt ttattcttat 1260

364

acaatgtgtt cactaacc aa ttctgggctt atgcatctca agatgctaga cgtgactttt 1320
 tgagatatga attcttccaa gttttgtcaa ttgtgggagg attattgtta gtgggttaatg 1380
 caggtgctgg tgaattctcc atcgatgaaa agaaaaagat ttattaa 1427

<210> 362

<211> 308

<212> PRT

<213> Candida albicans

<400> 362

Met Ser Tyr Arg Gly Pro Asn Gln Phe Gly Asn Gln Pro Pro His His
 1 5 10 15

Gly Ile Pro Ser Gln Pro Gln Pro His Ile Gly Pro Ile Ser Ser Ser
 20 25 30

Lys Ser Pro Leu Glu Gln Phe Glu Asp Val Ala Lys Lys Val Glu Asp
 35 40 45

Trp Ile Asp Asp Tyr Phe Lys Val Leu Lys Pro Tyr Val Pro Ala Ile
 50 55 60

Gly Arg Ala Phe Leu Val Ala Thr Phe Tyr Glu Asp Thr Leu Arg Ile
 65 70 75 80

Phe Thr Gln Trp Asn Glu Gln Val Tyr Tyr Leu His Asn Tyr Arg His
 85 90 95

Tyr Trp Arg Trp Leu Thr Val Leu Phe Leu Ile Asn Asn Met Val Val
 100 105 110

Met Thr Val Ala Ser Thr Leu Val Ile Ala Arg Lys Lys Asn Asn Ile
 115 120 125

Ala Thr Ile Ala Leu Ile Val Val Val Ile Ile Gln Gly Ile Gly Tyr
 130 135 140

Gly Leu Leu Phe Asp Ala Gln Phe Val Leu Arg Asn Leu Ser Val Val
 145 150 155 160

Gly Gly Leu Val Leu Ala Phe Ser Asp Ser Ile Val Arg Asp Lys Arg
 165 170 175

Ser Leu Asn Met Pro Gly Leu Pro Met Leu Asn Asn Gln Asp Asn Lys
 180 185 190

Lys Tyr Phe Leu Leu Ala Gly Arg Ile Leu Leu Val Leu Leu Phe Leu
 195 200 205

Gly Phe Val Phe Ser Ser Asp Trp Ser Leu Gly Arg Val Phe Ile Ile
 210 215 220

Ile Ile Gly Leu Thr Ser Cys Ala Ser Ile Val Val Gly Tyr Lys Thr
 225 230 235 240

Lys Phe Ser Ala Ala Ile Met Leu Ile Val Leu Phe Leu Tyr Asn Val

275	280	285
Glu Lys Ala Ala Lys Lys Trp Glu Lys Glu Ser Gly Ser Arg Lys Ala		
290	295	300
Ala Glu Glu Ala Ala Ala Lys Lys Ala Ala Glu Glu Ala Ala Ala Lys		
305	310	315
Lys Ala Ala Glu Glu Ala Ala Ala Leu Lys Ala Asn Ser Lys Lys Ala		
	325	330
Lys Glu Ala Ala Lys Ala Ala Lys Lys Lys Asn Lys Arg Asn Ile Arg		
	340	345
Ala Ala Val Lys Asp Asn Asn Tyr Phe Gly Asp Ser Ala Lys Ser Ala		
355	360	365
Asp Ile Asp Ala Asp Val Asp Leu Leu Ile Glu Lys Phe Asp Asp Val		
370	375	380
Lys Leu Gly Glu Val Ala Asp Lys Val Lys Asp Ala Asp Ala Ala Ser		
385	390	395
Val Lys Ser Thr Phe Val Glu Val Ala Lys Glu Leu Val Gly Ala Gly		
	405	410
Ser Leu Asp Ala Ser Tyr Leu Lys Tyr Phe Asn		
420	425	

<210> 365
 <211> 1178
 <212> DNA
 <213> Candida albicans

<400> 365
 ttccatttgt aggcattgtg tagaatgtgg actgtaggaa ggtgcaaaat atatattcaa 60
 taagtcacat ctcaaattgg tagtagaaga attcaacctt gggacagtat tctctgctta 120
 aaatgagttt actgatcaaa taaaatattg gctcaacat tgaaaagcta ttcttgacac 180
 tttttgcagt tttagttttg gttgtttcac aattgaaaaa aaaaatgttg agccctaata 240
 gccctaattg tttgcacgtg atgtattgct ttgagtgaag agtgtacatt tgtacacaca 300
 caaacaacaa aaaactaact tcttccccca atatgctgcg tatagtgaga aatcttcttc 360
 tctcttgcca tactatcgca tttttttttt tggtaactca cgaaacctaa ttggaaagaa 420
 gaaaagagaa aaaaaaaaaa ttttcagttt tcaatagatt tcagtttttg aattatacat 480
 attagagaaa caagttaaca atggatgtt cattagattt accatgagtt atggagggat 540
 attcctggat gatcagaata tcataatata ggagtatact attttactgg aatcaagata 600
 taattgaatt gaaataaaaa ttgaataaga ggaagcatag aatacgggat gatgattaac 660
 aaatcagaaa acattgtact accgaataat gaattaggat caacatatta atatcaacta 720
 ctactttaa agaacaggaa aatgagaaga gaatcagcat gaaagttacc acctcagaaa 780
 acgtcaaaga aatatacttt tgggtgtggat ccatgtgtta ttactgaaat catcgaaacg 840
 aatataaccc tcctttttccc acattgacat aagtcagaca caatctttca aataaaacat 900
 gtaataactaa ctattatttt tttttcgtat aggttttagt tcaagattta ttacatccat 960
 ctccagccac tgaagctaaa caacacaaat tgaaaacttt agttcaacaa ccaagatctt 1020
 tctttatgga cgttaaatgt caaggatgtc ttaatatcac cactgttttc agtcacgctc 1080
 aaactgctgt cacttgtgac tcttgttcta ctgttttgtg taccaccaact ggtggttaaag 1140
 ctaaattgac tgaagggtgt tcattcagaa gaaagtaa 1178

368

<210> 366
 <211> 82
 <212> PRT
 <213> *Candida albicans*

<400> 366
 Met Val Leu Val Gln Asp Leu Leu His Pro Ser Pro Ala Thr Glu Ala
 1 5 10 15
 Lys Gln His Lys Leu Lys Thr Leu Val Gln Gln Pro Arg Ser Phe Phe
 20 25 30
 Met Asp Val Lys Cys Gln Gly Cys Leu Asn Ile Thr Thr Val Phe Ser
 35 40 45
 His Ala Gln Thr Ala Val Thr Cys Asp Ser Cys Ser Thr Val Leu Cys
 50 55 60
 Thr Pro Thr Gly Gly Lys Ala Lys Leu Thr Glu Gly Cys Ser Phe Arg
 65 70 75 80
 Arg Lys

<210> 367
 <211> 1179
 <212> DNA
 <213> *Candida albicans*

<400> 367
 tttatattgt tttttgtttc tatgtatagt aattatttaa tttgatgttc cattattcat 60
 gtaattgtga tgtatttttt ttgttggtcc ttctttgtgt tttgatattt tgcagctggt 120
 cggatcatatc aaatttgga ggagctacca aagcagaaat gatagcaaaa aaaaacagga 180
 gacttttgga atttcttggt ttagggctct agccctaata cctgtatata attgattgat 240
 gctttaaaat ttgtgcggtg aaaaacagaa gcgaaaaaaa aagagctgga aagtgtgatt 300
 aacaacaacg agggaagaaa aaaaacttaa ttaggtgaac aaaaattaat gtgtgagcgt 360
 gtacatgcac aattttcaat tggttattct cagcactaa caaactcaac ctccattgtg 420
 agaaaagaga tttttctttg aaaaaaaatt tacatacata tcttagttca ctagtaactt 480
 tcgaagacaa catagacaag atgggtatgt tccagtatag caatattcaa caatgagata 540
 caagatattc ctccaatata aagagattaa tgggtgtttt gatagagtgt aaagccatgt 600
 gtttaataag aatgatttgt caagggataa gatgaaaagt ggaaattgtc caaacaacat 660
 tgaaacgaat tttctgggat agcgttcaaa caatcaaacc tatccagggt tcttatgaca 720
 attaagaaaa caagtcaata ttatcaaaga tggagtttta taaggagaga tattgaaaca 780
 tcaaattggt gaaagaaata gccaaactatt tggcaccatt tcctgtgatc atagaaatac 840
 taacaatcct cttgtgttat agttaacggt ccaaaaacta gaaagaccta ctgtaaagggt 900
 aaagaatgcc gtaaacatac ccaacacaaa gttacccaat acaaagctgg taaagcttct 960
 ttgttcgctc aaggtaaaaa agatatgac agaaaacaat ccggttatgg tgggtcaaacc 1020
 aaacaaattt tccacaagaa agccaagact accaaaaaag ttgttttgag attggaatgt 1080
 gttgtctgta aaaccaaggc tcaattacca ttgaaaagat gtaaacattt cgaattgggt 1140
 ggtgacaaaa aacaaaaagg tcaagcttta caattttta 1179

<210> 368

<211> 106
<212> PRT
<213> *Candida albicans*

<400> 368

```
Met Val Asn Val Pro Lys Thr Arg Lys Thr Tyr Cys Lys Gly Lys Glu
  1              5              10              15

Cys Arg Lys His Thr Gln His Lys Val Thr Gln Tyr Lys Ala Gly Lys
      20              25              30

Ala Ser Leu Phe Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser
      35              40              45

Gly Tyr Gly Gly Gln Thr Lys Gln Ile Phe His Lys Lys Ala Lys Thr
      50              55              60

Thr Lys Lys Val Val Leu Arg Leu Glu Cys Val Val Cys Lys Thr Lys
      65              70              75              80

Ala Gln Leu Pro Leu Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp
      85              90              95

Lys Lys Gln Lys Gly Gln Ala Leu Gln Phe
      100              105
```

<210> 369
<211> 3583
<212> DNA
<213> *Candida albicans*

<400> 369

```
gtgcgaataa tacaagcgat cgtttgaata atccaatgat tagctctgat caacgaattc 60
aaaattttcc cctcaaggac gtagtacaac aagagatgag aaggggtttg aactgtttga 120
tttcagagga gatgacggtg caaaaagatc taccacccaaa gaagcacata attttttgaa 180
tgattcacga aagagttcca ttagtgatat ctcaagccaa aaattttcaa gggaaagttc 240
ccgtaatggt tcacgggaaa gcagcaggcg aagttcaata ataaaaattg atcatcatac 300
taatgtggac gtgtcaacga aaccggaaaa tataaatagc agagataaca aaactgagaa 360
gaatatgact ttgagttcag agtcaaccaa accgagtgtc gaagaagtta gtaaattctt 420
gaaaccaaca attaccaaga aaacttcatt cactgattac ttaaaatctg ccaaaactaa 480
ggctaaagaa gaaaaggtaa caatcgaaaa aagtgaacaa acgattaatt cagaagaacg 540
aaaaacggaa ccaattcaac aaagcgagca acttttaacg gacaaaaagg ataataaact 600
ggaacccaat agtgaagtaa atttgaaaga caataatgac gacctgaaag ctacagctgg 660
ctgtgccta ggacctgata agaatactgg aaaaaacgat tcagataaat cagaacgac 720
tcaacccaaa cttgcccgct cagaatcatt tgccgataca tcattattgt ctccagttaa 780
tgaaagtgat actgatttca atttcaatga gttagcagag ataccggaag caaaggatgg 840
ttcagttgtg gcagcaaatg tgctggagaa cattgatgag aatgaaaata tttcagaagc 900
tgaaactggt atagcagatg accttccacg tctcgatgaa ggaaagaaac ttttacgtga 960
acaaacagca gatgtaaaga gacataaatt gaagaaaaca aaattgaata ctatttttag 1020
ttccgatgaa gaggaggagg agattcaaga accagatttc aaactccaag aaccagaaaa 1080
actaccagaa gatgaccaac atcctgattt tcaaaattca aaagcaacaa cagaatcag 1140
taacgataaa acagaagtaa ataagccaga agtgaaagag gttggcgaga aagagagaaa 1200
tcaccaacta gaagatagat taccaattaa aaaagagaaa atgcgggtcg agaattgcaa 1260
gacatctgaa aacggtgtca gttcaaaatc agaatctaag atttcaaagt cgaagaaact 1320
accttacaaa gttaaactgt attcaagtgg tcgatcatta ttacaacgag cttgcaagaa 1380
```

```

gggtaatttt gcagatgtcc aagattacat agagaggggt gctagtgcc atgaaaagga 1440
tttctgtgga ttcacatgct tgcattgagg agcattggaa ggtcatacac aaattgtgaa 1500
atatctcatc gaaaatgggt ctaatgtaaa tgcgaaagct gatgaagctg gtgattccga 1560
gacaccattg atcgatgcag ctgaaaacaa acatcttgat tgtgttaaag tgttactaga 1620
aaatgatgct gatcctacta ttttcaatat tgatggattc accgctttta ctaagattta 1680
taatgaacat gaaggagaag aaggatatga tgaaattatt caagtcttag aagaagcaac 1740
tgcaaaactat aacagtcggt taccaagaga agttcagttt gtatcagatg ctctatttgg 1800
tagtggaacca atcatggagg atccaaatga caactatttt gcagagctaa ttaaaggtaa 1860
gggaatatat aaatacgctg cagagaattc aaaagagaaa acagcagaat attttgttgc 1920
tggtcataat ttagaaggaa aaccagatat tttaatttta gctgctagaa acggccacac 1980
agaacttggt gatattatac tagggctaaa ccctacacct tttaattattg ataccgagtc 2040
aagttgtggt gttactgcat tattggccag tattggacgc ggtcattttg aagttgtcga 2100
ttccttggtg tccaaagggt ctgatccatt caagacaaga aaaaaagatg ggttgaatgc 2160
tttagaaatt gcacaacact cgccacattt tgattcacgg gaagttagtg taataatgaa 2220
attcatggag aagaagagtg gaaccaaatt tttgtctggt attccgtcaa gggtagtatc 2280
tcgtgcaaca tctcgtgcac cttctgttcc cgtatcatca gacgaagatg acgtagtgga 2340
agaaaaagaa attacagcac acacagaaaa taaaagtgtc gaaaagaagc tggaggataa 2400
aatcacgaaa acagttaatg agcatgtcag caatcggaag cccacagagt ctacaggctg 2460
aaaacttgaa aagactcata gcaatgagga aagaaagcgg aaacgtgaat ggtcagacga 2520
tgaacctaaa gaaccacatc ttttgaagaa gtcaaagtct gatttgaaat tgaaatcact 2580
acatagagaa ttcacttctg atgatcacca caccagtga agccattcag attcttttgc 2640
agaaaaaaga aaacatttat cggcaacgcc acctgtctct ccgccaccac caccaccacc 2700
accttctcaa gcagttatca aggcacaaga agaacaaaaa atcaaagatg ctgaagaagc 2760
tagattgtgg caagaaaagg tcgaagctaa aaagaggggt cgaagagaaa tgttttttaa 2820
gtccgagaaa gagaaagagc agaaaacggaa agaagaagaa gaattgagag cacaagaaga 2880
aaaacgaatt gccaaagcaa aacaggaaga acaggagaga cttgctagag aagcagaaga 2940
gaaatcgaaa gaactagaag aaaagaaagt ggggttgaga caacagttga cattagatca 3000
ttatccggtt ggattgcgtt attgcaagtt tgatggaaac ccaaatatct cggctgttga 3060
taaatttttg cttttctatg tttttgtaat cgacgataaa aagtatgctg ttgatttgca 3120
agtctccttg atcacgtcaa cggttggtcag caagggttatc aatactgtac aacctcatca 3180
gaagagagaa ataaatgcaa ctgaaaaaag caaattgttg aagctctttt tcaagtttat 3240
tggtattgat cctaggaatc caaattgtga tcaaagaagc tcaataacaa atggtcaaaa 3300
acagtttcaa aatttggttg ttcattttgt ggaggtagat ttagctgaag aattttttaa 3360
ggaatttcca gaagtacact caaaagcaaa agataaccaa attgatgtta gtttagagtc 3420
tttgagtggg ttttctgatt gcgtcaagga tgatataata gttgatggaa atcttgaaat 3480
tgatattgat tccaagaaaa tcgaaaagtt tattcctcct catttgaata ctaggaaaga 3540
cattattagg actgtcagta ctttagcaca ccactatgg tga 3583

```

<210> 370

<211> 1072

<212> PRT

<213> Candida albicans

<400> 370

```

Met Thr Leu Ser Ser Glu Ser Thr Lys Pro Ser Val Glu Glu Val Ser
 1             5             10             15

Lys Ser Leu Lys Pro Thr Ile Thr Lys Lys Thr Ser Phe Thr Asp Tyr
          20             25             30

Leu Lys Ser Ala Lys Thr Lys Ala Lys Glu Glu Lys Val Thr Ile Glu
          35             40             45

Lys Ser Asp Lys Thr Ile Asn Ser Glu Glu Arg Lys Thr Glu Pro Ile
          50             55             60

```

371

Gln Gln Ser Glu Gln Leu Leu Thr Asp Lys Lys Asp Asn Lys Ser Glu
 65 70 75 80
 Pro Asn Ser Glu Val Asn Leu Lys Asp Asn Asn Asp Asp Ser Lys Ala
 85 90 95
 Thr Ala Gly Cys Ala Leu Gly Pro Asp Lys Asn Thr Gly Lys Asn Asp
 100 105 110
 Ser Asp Lys Ser Glu Thr Thr Gln Pro Lys Leu Ala Arg Ser Glu Ser
 115 120 125
 Phe Ala Asp Thr Ser Leu Leu Ser Pro Val Asn Glu Ser Asp Thr Asp
 130 135 140
 Phe Asn Phe Asn Glu Leu Ala Glu Ile Pro Glu Ala Lys Asp Gly Ser
 145 150 155 160
 Val Val Ala Ala Asn Val Ser Glu Asn Ile Asp Glu Asn Glu Asn Ile
 165 170 175
 Ser Glu Ala Glu Thr Val Ile Ala Asp Asp Leu Pro Arg Leu Asp Glu
 180 185 190
 Gly Lys Lys Leu Leu Arg Glu Gln Thr Ala Asp Val Lys Arg His Lys
 195 200 205
 Leu Lys Lys Thr Lys Leu Asn Thr Ile Phe Ser Ser Asp Glu Glu Glu
 210 215 220
 Glu Glu Ile Gln Glu Pro Asp Phe Lys Leu Gln Glu Pro Glu Lys Leu
 225 230 235 240
 Pro Glu Asp Asp Gln His Pro Asp Phe Gln Asn Ser Lys Ala Thr Thr
 245 250 255
 Glu Ile Ser Asn Asp Lys Thr Glu Val Asn Lys Pro Glu Val Lys Glu
 260 265 270
 Val Gly Glu Lys Glu Arg Asn His Gln Leu Glu Asp Arg Leu Pro Ile
 275 280 285
 Lys Lys Glu Lys Met Arg Ser Glu Asn Ala Lys Thr Ser Glu Asn Gly
 290 295 300
 Val Ser Ser Lys Ser Glu Ser Lys Ile Ser Lys Ser Lys Lys Leu Pro
 305 310 315 320
 Tyr Lys Val Lys Arg Asp Ser Ser Gly Arg Ser Leu Leu Gln Arg Ala
 325 330 335
 Cys Lys Lys Gly Asn Phe Ala Asp Val Gln Asp Tyr Ile Glu Arg Gly
 340 345 350
 Ala Ser Ala Asn Glu Lys Asp Phe Cys Gly Phe Thr Cys Leu His Glu
 355 360 365

Glu	Lys	Lys	Ser	Glu	Asp	Lys	Ile	Thr	Lys	Thr	Val	Asn	Glu	His	Val	675	680	685	
Ser	Asn	Arg	Lys	Pro	His	Glu	Ser	Thr	Gly	Arg	Lys	Leu	Glu	Lys	Thr	690	695	700	
His	Ser	Asn	Glu	Glu	Arg	Lys	Arg	Lys	Arg	Glu	Trp	Ser	Asp	Asp	Glu	705	710	715	720
Pro	Lys	Glu	Pro	His	Leu	Leu	Lys	Lys	Ser	Lys	Ser	Asp	Leu	Lys	Leu	725	730	735	
Lys	Ser	Leu	His	Arg	Glu	Phe	Thr	Ser	Asp	Asp	His	His	Thr	Ser	Glu	740	745	750	
Ser	His	Ser	Asp	Ser	Phe	Ala	Glu	Lys	Arg	Lys	His	Leu	Ser	Ala	Thr	755	760	765	
Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Gln	Ala	Val	770	775	780	
Ile	Lys	Ala	Gln	Glu	Glu	Gln	Lys	Ile	Lys	Asp	Ala	Glu	Glu	Ala	Arg	785	790	795	800
Leu	Trp	Gln	Glu	Lys	Val	Glu	Ala	Lys	Lys	Arg	Ala	Arg	Arg	Glu	Met	805	810	815	
Phe	Leu	Lys	Ser	Glu	Lys	Glu	Lys	Glu	Gln	Lys	Arg	Lys	Glu	Glu	Glu	820	825	830	
Glu	Leu	Arg	Ala	Gln	Glu	Glu	Lys	Arg	Ile	Ala	Lys	Ala	Lys	Gln	Glu	835	840	845	
Glu	Gln	Glu	Arg	Leu	Ala	Arg	Glu	Ala	Glu	Glu	Lys	Ser	Lys	Glu	Leu	850	855	860	
Glu	Glu	Lys	Lys	Val	Gly	Leu	Arg	Gln	Gln	Leu	Thr	Leu	Asp	His	Tyr	865	870	875	880
Pro	Val	Gly	Leu	Arg	Tyr	Cys	Lys	Phe	Asp	Gly	Asn	Pro	Asn	Ile	Ser	885	890	895	
Ala	Val	Asp	Lys	Phe	Leu	Pro	Phe	Tyr	Val	Phe	Val	Ile	Asp	Asp	Lys	900	905	910	
Lys	Tyr	Ala	Val	Asp	Leu	Gln	Val	Ser	Leu	Ile	Thr	Ser	Thr	Val	Val	915	920	925	
Ser	Lys	Val	Ile	Asn	Thr	Val	Gln	Pro	His	Gln	Lys	Arg	Glu	Ile	Asn	930	935	940	
Ala	Thr	Glu	Lys	Ser	Lys	Leu	Trp	Lys	Leu	Phe	Phe	Lys	Phe	Ile	Gly	945	950	955	960
Ile	Asp	Pro	Arg	Asn	Pro	Asn	Cys	Asp	Gln	Arg	Ser	Ser	Ile	Thr	Asn	965	970	975	

Gly Gln Lys Gln Phe Gln Asn Leu Leu Leu His Phe Val Glu Val Asp
 980 985 990

Leu Ala Glu Glu Phe Leu Lys Glu Phe Pro Glu Val His Ser Lys Ala
 995 1000 1005

Lys Asp Asn Gln Ile Asp Val Ser Leu Glu Ser Leu Ser Gly Phe Ser
 1010 1015 1020

Asp Cys Val Lys Asp Asp Ile Ile Val Asp Gly Asn Leu Glu Ile Asp
 1025 1030 1035 1040

Ile Asp Ser Lys Lys Ile Glu Lys Phe Ile Pro Pro His Leu Asn Thr
 1045 1050 1055

Arg Lys Asp Ile Ile Arg Thr Val Ser Thr Leu Ala His Pro Leu Trp
 1060 1065 1070

<210> 371
 <211> 659
 <212> DNA
 <213> Candida albicans

<400> 371
 tagtttcttt tggcgggtata tcctcactca tgattgatgt atttgccac taaaaagaaa 60
 accaatgaaa caataagatt gattgataga tttggttgta attaactga tgctttcaac 120
 atttggtttt gttcgtgtct cggtcattga gggtgggtaa attggttttc ttttgagaat 180
 tgtgagcatg caatgtcgca tgcaaatatg atgtcgctca attgacgacat actacttagg 240
 gctatagacc tattgcacgt gcgttagttt taaacctaaa aaaacaattt tgtgcagtcg 300
 tgcaccattc gttctatttt tctactgtga ttgacgtaca aaccttcaca gttcacgcac 360
 acttttgtcg attctcaaac ctctctcaca ggcttggtag gaatgaaaaa aattttggta 420
 aaggcgaaaa aaaaaaaaaa taaacttgaa tattttggaa tccccctttt gattactaca 480
 atagattaaa gtaactaaag atgattgaac catccttgaa agcttttagct tcaaaatata 540
 actgtgaaaa atccatttgt cgtaaatgtt acgctagatt gccaccaaga gccaccaact 600
 gtcgtaagag aaagtgtggt cacaccaatc aattgagacc aaagaagaaa ttgaagtag 659

<210> 372
 <211> 52
 <212> PRT
 <213> Candida albicans

<400> 372
 Met Ile Glu Pro Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Glu
 1 5 10 15

Lys Ser Ile Cys Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr
 20 25 30

Asn Cys Arg Lys Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys
 35 40 45

376

<400> 374

Met	Asn	Asp	Pro	Arg	Asp	Glu	Gln	Ile	Asp	Ser	Asp	Asp	Val	Leu	Thr
1				5					10					15	
Glu	Asp	Ser	Ser	Asp	Glu	Leu	Lys	Asp	Leu	Val	Gln	Glu	Phe	Glu	Leu
			20					25					30		
Lys	Tyr	Ala	Glu	Leu	Lys	Lys	Asn	Lys	Ala	Leu	Lys	Lys	Arg	Arg	Ser
		35					40					45			
Gln	Ser	Pro	Ser	Glu	Asp	Met	Ser	Asn	Lys	Gln	Lys	Pro	His	Gln	Pro
	50					55					60				
Glu	Val	Pro	Arg	Thr	Pro	Glu	Lys	Ala	Lys	Val	His	Leu	Asp	Lys	Val
65					70					75					80
Val	Glu	Glu	Pro	Lys	Gln	Arg	Ile	Phe	Thr	Lys	Lys	Glu	Pro	Arg	Asp
				85					90					95	
Ser	Lys	Ile	Lys	Glu	Ser	Asn	Phe	Leu	Asn	Lys	Leu	Tyr	Glu	Thr	Ser
			100					105					110		
Asn	Lys	His	Asp	Lys	Glu	Asp	Ala	His	Lys	Ile	Asp	Phe	Ser	Lys	Arg
		115					120					125			
Arg	Phe	Glu	Phe	Gln	Leu	Asp	Lys	Tyr	Thr	Phe	Thr	Pro	Lys	Asp	Val
	130					135					140				
Val	Asp	Asp	Leu	Glu	Pro	Ile	Ser	Lys	Leu	Tyr	Leu	Arg	Arg	Arg	Tyr
145					150					155					160
Leu	Ala	Gln	Ser	Gln	Ile	Ala	Asp	Ile	Ile	Ala	Glu	Thr	Asp	Ser	Asn
				165					170					175	
Met	Lys	Phe	Leu	Lys	Ile	Asp	Lys	Phe	Leu	Ala	Lys	Thr	His	Lys	Ser
			180					185					190		
Asn	Asn	Tyr	Ala	Glu	Pro	Lys	Tyr	Cys	Asn	Trp	Cys	Leu	Val	Ala	Phe
		195					200					205			
Val	Val	Arg	Lys	Asp	Pro	Val	Gln	Val	Ala	Ala	Asn	Asn	Ser	Lys	Tyr
	210					215					220				
Ile	Lys	Leu	Lys	Val	Gly	Asn	Phe	Met	Asn	Ser	Val	Asp	Leu	Met	Leu
225					230					235				240	
Phe	Asp	Lys	Ala	Phe	Gln	Lys	Asn	Gly	Lys	Ile	Gln	Pro	Gly	Asp	Leu
			245						250					255	
Leu	Phe	Ile	Leu	Asn	Pro	Leu	Ile	Asn	Lys	Tyr	Glu	Ile	Gln	Val	Gly
			260					265					270		
Lys	Gly	Gln	Phe	Gln	Ser	Gly	Phe	Asn	Leu	Lys	Val	Glu	Asn	Thr	Asn
		275					280					285			
Val	Ser	Ser	Ile	Leu	Glu	Ile	Gly	Ser	Leu	Arg	Asp	Phe	Gly	Phe	Cys
	290					295					300				

[illegible]

<210> 375
 <211> 1499
 <212> DNA
 <213> Candida albicans

<400> 375
 tttcttcac aacttgctca aatgtctttg aaagtgaag cttacttttt tggtttcgtt 60
 taggtggcat caaggtaaag gagggagttt tggatatagt aggtttttga cttatttcct 120
 tttttgagta gatataacag aactaccaaa agtgagccca catctgttaa tcttgaaaag 180
 caaaattgag aaaaccattt atgcaagtcg tgtactgggt atattcttgg tcaattgcta 240
 cacttttgta atgaatactg taatgtagcc gacgtgggtt gaanaatata tatttaagta 300
 tatagaatca ggtcaatata aaatgtttga aatataacaa aatgtttcaa tgtaaaactga 360
 tgggttaaggg attataaaatc aaactgagta gtgcttttgt tcctaaaaaa cccatcgtgg 420
 tggtaacgtc aggagaccgc gacatcaaat ggaattcaca caatcagtct ccgaatttat 480
 tacccttgaa acttaactta atgaaagagc cttccatcac tactaccttt gttgaggtta 540
 cagacaaaact tcctacaaaag cctccgtgca ggggtgtttt caagaatgag tatgagcagc 600
 cctccggcag tgtcaaatta agaggcatgg gacacttggg tggccagtct atagatgtgg 660
 ccagaaaact tggcaaactg aacgtagcag ttttttcgtc atctgggtgg aatgcaggat 720
 tagcagctgc ttatgccagc cagttttttg gagtatcgtg cactgtgggt ttgcctgaaa 780
 gttcgaagcc aactgttata gaaaagttga aatccttggg tgcagatgtc attattcatg 840
 ggaaacattg gggagaggcc gataactatt taactgattt tgttattaaa aatcttgaca 900
 aaacagtcta tccggtctat tgtcacccct ttgatgacct attgttgtgg gagggtcata 960
 gtaagatcat cacggaaatc atcgatcaaa agcaattacc caactttgat aaagttaagg 1020
 gggtcatttg ttcggtagga gggggtggct tatacaacgg aatagttgaa ggtttgga 1080
 atcataagga gataccagtg ttggcaattg aaactaaaca agcggccacg tttcacgagg 1140
 cggtcaaaaga aggtaaaagt gtccatttac aaaaagtgca aactttggcc acttcttttg 1200
 cttcgccgta cttttcttcc aaggcattag caaactatat tgagcgtcct acagttcttg 1260
 ctgaaattga tgacttgac gctgttaaaag gtgttgttga tgtatacgac catttcggat 1320
 atatggttga gcctgcatgt ggtgcatccg ttgcatcagt gatgcacagg caagatttat 1380
 tgaataaatt tggtagatta agtccagatg atattatcat tgttgtcata tgtgggtggat 1440
 cggctatcaa caagtatatt atagacgaat atagaagttt attagaaaaa gactcttga 1499

<210> 376
 <211> 332
 <212> PRT
 <213> Candida albicans

<400> 376
 Met Lys Glu Pro Ser Ile Thr Thr Thr Phe Val Glu Val Thr Asp Lys
 1 5 10 15
 Leu Pro Thr Lys Pro Pro Cys Arg Val Phe Phe Lys Asn Glu Tyr Glu
 20 25 30
 Gln Pro Ser Gly Ser Val Lys Leu Arg Gly Met Gly His Leu Val Gly
 35 40 45
 Gln Ser Ile Asp Val Ala Arg Lys Leu Gly Lys Ser Asn Val Ala Val
 50 55 60
 Phe Ser Ser Ser Gly Gly Asn Ala Gly Leu Ala Ala Tyr Ala Ser
 65 70 75 80

379

Gln Phe Phe Gly Val Ser Cys Thr Val Val Leu Pro Glu Ser Ser Lys
85 90 95

Pro Thr Val Ile Glu Lys Leu Lys Ser Leu Gly Ala Asp Val Ile Ile
100 105 110

His Gly Lys His Trp Gly Glu Ala Asp Asn Tyr Leu Thr Asp Phe Val
115 120 125

Ile Lys Asn Leu Asp Lys Thr Val Tyr Pro Val Tyr Cys His Pro Phe
130 135 140

Asp Asp Pro Leu Leu Trp Glu Gly His Ser Lys Ile Ile Thr Glu Ile
145 150 155 160

Ile Asp Gln Lys Gln Leu Pro Asn Phe Asp Lys Val Lys Gly Val Ile
165 170 175

Cys Ser Val Gly Gly Gly Gly Leu Tyr Asn Gly Ile Val Glu Gly Leu
180 185 190

Glu Asn His Lys Glu Ile Pro Val Leu Ala Ile Glu Thr Lys Gln Ala
195 200 205

Ala Thr Phe His Glu Ala Val Lys Glu Gly Lys Val Val His Leu Gln
210 215 220

Lys Val Gln Thr Leu Ala Thr Ser Leu Ala Ser Pro Tyr Leu Ser Ser
225 230 235 240

Lys Ala Leu Ala Asn Tyr Ile Glu Arg Pro Thr Val Leu Ala Glu Ile
245 250 255

Asp Asp Leu Asp Ala Val Lys Gly Val Val Asp Val Tyr Asp His Phe
260 265 270

Gly Tyr Met Val Glu Pro Ala Cys Gly Ala Ser Val Ala Ser Val Met
275 280 285

His Arg Gln Asp Leu Leu Asn Lys Phe Gly Thr Leu Ser Pro Asp Asp
290 295 300

Ile Ile Ile Val Val Ile Cys Gly Gly Ser Ala Ile Asn Lys Tyr Ile
305 310 315 320

Ile Asp Glu Tyr Arg Ser Leu Leu Glu Lys Asp Ser
325 330

<210> 377

<211> 2564

<212> DNA

<213> Candida albicans

<400> 377

tttttgaaaa cagagaatga atgaacaatt gatgaccata gaaatgaagt gagaacacat 60

```

aaatctgcga cacttcacgt gataacaaca aagtgcacatg aacaacaaat gtcgtttgta 120
taatttgcga catttgttgt tcaagccaaa aaaagaaaga cagaaacaga aaaaagaaaa 180
atctcaaagt tgccacgtaa gcacaattaa tctttttatg gttgtaacta tttctagtat 240
attctacgta ataggtgagg tcctatatgc agtacacaca ggtttttttc acagatgttg 300
acacagtgtt gaaaattatt cacgttgatt tataaatata caacttacct tccacggttt 360
tttttttgat ttttgatttt ttgaattctt ctttcttttt tttgtcattt atttattaaa 420
acattctctt gtaatacttt atttgataaa ttttacaaga ttttaattaga tcaattagat 480
tatagaatca tttcaatata atgagatcat cacaatcttc ttgggttacca cgtattgggt 540
tatttatatg ggcgttagtt atactttatac catttttggg ttcaccgaag cacgcatttg 600
cggttgctgc agtgagcgat gatgaatcct cgacagataa ttatggtaca gtcattggta 660
tagatttggg taccacttat tcctgtgttg gtgttatgaa aaacggtaag gttgaaattt 720
tggccaacga tcaaggtaat agaatcactc catcatacgt gtcgttcaat ggcgatgaaa 780
gattgggttg agacgctgcc aagaatcaag ctctctctaa tgtcaacaac actgttttcg 840
atattaaaag attgattggg ttgaaatata atgatgacac tgtgcaaaag gaacttaaac 900
atttgcctta caaaattgaa aataagggtg acaaaccagt tgttaaagtt gaataccaag 960
gtgaagaaaa aactttctcc cctgaagaaa tttcatctat ggttttgggt aaaatgaaga 1020
gtattgctga agattacctt ggcaaaaaag ttactcatgc cgttgtcact gttccagctt 1080
atttcaacga tgctcaaaag caagctacta aagatgccgg tactattgct ggtttgaacg 1140
ttttgagaat tgtcaatgaa cctactgctg ccgctattgc ctatggatta gacaaaggcg 1200
accaagaaaa acaaattatt gtttacgatt tgggtggtgg tacttttgat gtttctttat 1260
tgtccattga aggtggtgtt ttcgaagtct tggctactgc tgggtgatac cacttgggtg 1320
gtgaagatth tgatttcaag attgtcagat acttggccaa acaattcaag aagaagcaca 1380
atattgatat cactgccaat tctaaagcca tttccaaatt gaagagagaa gccgaaaagg 1440
ccaagagaac tttatcttct caaatgagta ctagagttag aatcgactcc tttgttgatg 1500
gtattgactt ttctgaaact ctttcaagag ccaagtttga agaattgaac attgctgctt 1560
tcagaaagac tttgaaacca gttgaacaag tgttgaagga tgggtggtgc aagaaatccg 1620
atattgatga tattgttttg gttggtggtt ccaccagaat tccaaaagtt caagaattat 1680
tggaaggatt ctttgatggg aaaaaggctt ctaaagggtat taaccagat gaagctgttg 1740
cttatgggtc cgctgttcaa gcagggtgtt tgagtggtga agaaggtgtt gatgacattg 1800
ttttgttgga tgtaaccca ttgactttag gtattgaaac ttctgggtggg gttatgacca 1860
ctttgatcaa gagaaacact gccatcccaa ccaagaaatc tcaaactctc tcaactgctg 1920
ctgatcaacca accaactggt ttgatccaag tctatgaagg tgaaagaacc atggctaaag 1980
acaacaacag attgggcaaa ttcgaattga ctgggtattcc accagctcca agaggtgtcc 2040
cacaaattga agtcactttc tcattggatg ccaatggtat cttgaaagtt gaagctgctg 2100
ataagggaac tggtaaattc gaatccatta ctatcaccaa cgaaaagggt agattatcca 2160
aggatgaaat tgatagaatg gttgaagaag ctgaaaaata cgctcaacaa gatcaagaat 2220
tgaaagaaaa gattgaagct agaaactcat tagaaaacta tgctcatgtc ttgagaggtc 2280
aattgagtga tacttctgaa accggtttag gttctaaatt ggatgacgat gacaaggaaa 2340
ctttggatga cgctatcaag gaaaactttg aatttattga agataacttt gatactgcta 2400
ctgctgaaga atttgaagaa caaaaacaaa aattaattga cgttgctaac ccaatcacag 2460
caaaattata cggtggagct gctggtgaag gtgctggtgg cgctggggat gccaaattcg 2520
gtgatgatga ttcagatgat gaattcgatc acgatgaatt gtag 2564

```

<210> 378

<211> 687

<212> PRT

<213> Candida albicans

<400> 378

Met Arg Ser Ser Gln Ser Ser Trp Leu Pro Arg Ile Gly Leu Leu Tyr
1 5 10 15

Val Ala Leu Val Ile Leu Ile Pro Phe Leu Val Ser Pro Lys His Ala
20 25 30

Phe Ala Val Ala Ala Val Ser Asp Asp Glu Ser Ser Thr Asp Asn Tyr

[illegible]

340				345				350							
Ala	Phe	Arg	Lys	Thr	Leu	Lys	Pro	Val	Glu	Gln	Val	Leu	Lys	Asp	Gly
		355					360							365	
Gly	Val	Lys	Lys	Ser	Asp	Ile	Asp	Asp	Ile	Val	Leu	Val	Gly	Gly	Ser
		370				375					380				
Thr	Arg	Ile	Pro	Lys	Val	Gln	Glu	Leu	Leu	Glu	Gly	Phe	Phe	Asp	Gly
385					390					395					400
Lys	Lys	Ala	Ser	Lys	Gly	Ile	Asn	Pro	Asp	Glu	Ala	Val	Ala	Tyr	Gly
				405					410					415	
Ala	Ala	Val	Gln	Ala	Gly	Val	Leu	Ser	Gly	Glu	Glu	Gly	Val	Asp	Asp
			420						425					430	
Ile	Val	Leu	Leu	Asp	Val	Asn	Pro	Leu	Thr	Leu	Gly	Ile	Glu	Thr	Ser
		435					440						445		
Gly	Gly	Val	Met	Thr	Thr	Leu	Ile	Lys	Arg	Asn	Thr	Ala	Ile	Pro	Thr
		450				455					460				
Lys	Lys	Ser	Gln	Ile	Phe	Ser	Thr	Ala	Ala	Asp	Asn	Gln	Pro	Thr	Val
465					470					475					480
Leu	Ile	Gln	Val	Tyr	Glu	Gly	Glu	Arg	Thr	Met	Ala	Lys	Asp	Asn	Asn
				485					490					495	
Arg	Leu	Gly	Lys	Phe	Glu	Leu	Thr	Gly	Ile	Pro	Pro	Ala	Pro	Arg	Gly
			500						505				510		
Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Ser	Leu	Asp	Ala	Asn	Gly	Ile	Leu
		515					520						525		
Lys	Val	Glu	Ala	Ala	Asp	Lys	Gly	Thr	Gly	Lys	Ser	Glu	Ser	Ile	Thr
		530				535					540				
Ile	Thr	Asn	Glu	Lys	Gly	Arg	Leu	Ser	Lys	Asp	Glu	Ile	Asp	Arg	Met
545					550					555					560
Val	Glu	Glu	Ala	Glu	Lys	Tyr	Ala	Gln	Gln	Asp	Gln	Glu	Leu	Lys	Glu
				565					570					575	
Lys	Ile	Glu	Ala	Arg	Asn	Ser	Leu	Glu	Asn	Tyr	Ala	His	Val	Leu	Arg
			580						585				590		
Gly	Gln	Leu	Ser	Asp	Thr	Ser	Glu	Thr	Gly	Leu	Gly	Ser	Lys	Leu	Asp
		595					600						605		
Asp	Asp	Asp	Lys	Glu	Thr	Leu	Asp	Asp	Ala	Ile	Lys	Glu	Thr	Leu	Glu
						615					620				
Phe	Ile	Glu	Asp	Asn	Phe	Asp	Thr	Ala	Thr	Ala	Glu	Glu	Phe	Glu	Glu
625					630					635					640
Gln	Lys	Gln	Lys	Leu	Ile	Asp	Val	Ala	Asn	Pro	Ile	Thr	Ala	Lys	Leu

645 650 655
 Tyr Gly Gly Ala Ala Gly Glu Gly Ala Gly Gly Ala Gly Asp Ala Lys
 660 665 670
 Phe Gly Asp Asp Asp Ser Asp Asp Glu Phe Asp His Asp Glu Leu
 675 680 685

<210> 379
 <211> 1346
 <212> DNA
 <213> Candida albicans

<400> 379
 gccccatggg gacagaaaag tattgatcca ggtttctttg aaggtttgta atacgtttta 60
 aacttggtgac ctaactcatt ttcataaaat tcttgataaa aattgggttc tttgaattgt 120
 ttgtaatctc ttaagattgt ctctgtctca gtgtttgcag tggagctgct attgccagtc 180
 ggcggcataa cagcagggtc tggatgtgca tcttcactca ctaagccgga caatcccaaa 240
 gccgtctctt gttcttttat tcttctaagg aatgctttat gtagttctga cattcttgcg 300
 taaaaggaag tacagtatta aagctcgaaa ctcaattgca acaaaagtct taattttttc 360
 ttctataagt aattgatctt ggtcccccaa acaaaaagat acagaggaga aaggagggcc 420
 ttaggctgac agaaaaaaaa aatttagtac ctgccacacc agtagctcca aaccatata 480
 tgatttgata gagttgaagt atgctgacag atcttacttc acactttcag tacatggcta 540
 taagcttggt tgtcgggttac aaagccttac taaataatga gacaccagtg tcatgtatag 600
 tcgtggattc aaaatcagat aaaatcatta gcataggcta caattatacc aaccactctc 660
 taaatggtac acaacacgca gaatttattg ctttacaacg atttggggaa caaaaactga 720
 gtattgacta taatgattta attttgtatg tgacagtggg gccttgattt atgtgtgcat 780
 cttattttac tcagttgggc atcaaaaaag taatatttgg ttgtgggaat gatagattcg 840
 gaggaaatgg taccatttta tcaatacata gtgacatcac cttgcctaac gcagcttatt 900
 ccagtatcgg gggtatatgt aggacagaag gaatccaact attacgaaat ttttatattc 960
 aacaaaatga gtcggcacca aatccaaaaa tcaaaaagaa cacagatatt gagagtaagg 1020
 aataccaga gaatcagttt ttagcatttt caaaggatga atttatagag ttttacggaa 1080
 atgaaagagt gcatattttac gatgggaaga tttttgaaat cactccatta caaaacaagg 1140
 gttatgatat aaaagaattg atatcgttgg atatgatgca aaaagttcca tttctagagg 1200
 atgagttggg acaaattaca gatgagcaaa taattgaatt tcacaactta tttttcaaca 1260
 taaatgatga tggaacggtt aattataaaa aaccaatagg caaatataac agtaaaaaa 1320
 gacactttgc aaacgatgaa gaatag 1346

<210> 380
 <211> 281
 <212> PRT
 <213> Candida albicans

<400> 380
 Met Ser Thr Asp Leu Thr Ser His Phe Gln Tyr Met Ala Ile Ser Leu
 1 5 10 15
 Phe Val Gly Tyr Lys Ala Leu Leu Asn Asn Glu Thr Pro Val Ser Cys
 20 25 30
 Ile Val Val Asp Ser Lys Ser Asp Lys Ile Ile Ser Ile Gly Tyr Asn
 35 40 45
 Tyr Thr Asn His Ser Leu Asn Gly Thr Gln His Ala Glu Phe Ile Ala

atgtggtgtc tataagagta atttgatgtg aaaaatatac aatctataat cagtatgttc 360
 agtttttgaa tggaaagccc aagaagaaca acagggaaat taaaaataaa aaggtgttgg 420
 agaaaaaaaa aaaaattgaa cagaaagatt catcctttta gatcaaacga aatataatctt 480
 accatccccc cccctccaaa atgcttagat ttactaggac tactgcttgg aaattaagat 540
 ctattccaat tgccactatt caatatagac aatttactta ttccactata tgttatcaat 600
 taaaaaccct tactccatct ttaggaataa ataataccat tgaatccaat ataccttcag 660
 aaactaatag attagctaaa actggtacta gatttttgaa aaaaggtgaa gttaaattca 720
 ataatgaaac tcaaaaatat gaaattcaat tagatgggaa aactctacgc acaccacttg 780
 gattcccatt agaattacca atcaataaaa aacaattggc atatttaatt gctcatgaat 840
 ggactcattt acctgatatt aaagtgaat caagtacttt accattaaca gcttttagcca 900
 ctagagctat agatttgagt caacaacatt tgagtgatat gaagacagaa aaagctgaag 960
 aaatgttagc attggaagat attaaattac aaatgttaag atatcttgat actgatactt 1020
 gtcttatatt tgctaccaac aaagaatgtg atggtaaatt aagaaaaaga caagaagaaa 1080
 tttatcgtcc attaattaat gaatttaatt aatttttcac aatttatgct cataataaaa 1140
 atttaatccc tcgacaaaaa tctattgaat tgaaatatat agattgtgaa actgatggat 1200
 taagaggtaa taaacaagat gaaaccactc aattagttgt attggattgg ttaaatcaat 1260
 taccaattta tgatttaatt gccttgagaa aaacaatctt aactactaaa tcatttttat 1320
 gtggaattac tttattaaga tcaaatgtta atgatattga aacttttaaaa gaattatatc 1380
 aatttaataa aaattccatt gatgaagatt attatcataa aacttttagaa gaattagttg 1440
 aattaggaaa tttagaaact atttatcaaa ctgaagaatg ggggtgaagta gaagatactc 1500
 atga 1504

<210> 382

<211> 334

<212> PRT

<213> Candida albicans

<400> 382

Met Leu Arg Phe Thr Arg Thr Thr Ala Trp Lys Leu Arg Ser Ile Pro
 1 5 10 15
 Ile Ala Thr Ile Gln Tyr Arg Gln Phe Thr Tyr Ser Thr Ile Cys Tyr
 20 25 30
 Gln Leu Lys Thr Leu Thr Pro Ser Leu Gly Ile Asn Asn Thr Ile Glu
 35 40 45
 Ser Asn Ile Pro Ser Glu Thr Asn Arg Leu Ala Lys Thr Gly Thr Arg
 50 55 60
 Phe Trp Lys Lys Gly Glu Val Lys Phe Asn Asn Glu Thr Gln Lys Tyr
 65 70 75 80
 Glu Ile Gln Leu Asp Gly Lys Thr Leu Arg Thr Pro Leu Gly Phe Pro
 85 90 95
 Leu Glu Leu Pro Ile Asn Lys Lys Gln Leu Ala Tyr Leu Ile Ala His
 100 105 110
 Glu Trp Thr His Leu Pro Asp Ile Lys Val Lys Ser Ser Thr Leu Pro
 115 120 125
 Leu Thr Ala Leu Ala Thr Arg Ala Ile Asp Leu Ser Gln Gln His Leu
 130 135 140
 Ser Asp Met Lys Thr Glu Lys Ala Glu Glu Met Leu Ala Leu Glu Asp

145 150 155 160
 Ile Lys Leu Gln Met Leu Arg Tyr Leu Asp Thr Asp Thr Cys Leu Ile
 165 170 175
 Phe Ala Thr Asn Lys Glu Cys Asp Gly Lys Leu Arg Lys Arg Gln Glu
 180 185 190
 Glu Ile Tyr Arg Pro Leu Ile Asn Glu Phe Asn Glu Phe Phe Thr Ile
 195 200 205
 Tyr Ala His Asn Lys Asn Leu Ile Pro Arg Gln Lys Ser Ile Glu Leu
 210 215 220
 Lys Tyr Leu Asp Cys Glu Thr Asp Gly Leu Arg Gly Asn Lys Gln Asp
 225 230 235 240
 Glu Thr Thr Gln Leu Val Val Leu Asp Trp Leu Asn Gln Leu Pro Ile
 245 250 255
 Tyr Asp Leu Ile Ala Leu Glu Lys Thr Ile Leu Thr Thr Lys Ser Phe
 260 265 270
 Leu Cys Gly Ile Thr Leu Leu Arg Ser Asn Val Asn Asp Ile Glu Thr
 275 280 285
 Leu Lys Glu Leu Tyr Gln Phe Asn Lys Asn Ser Ile Asp Glu Asp Tyr
 290 295 300
 Tyr His Lys Thr Leu Glu Glu Leu Val Glu Leu Gly Asn Leu Glu Thr
 305 310 315 320
 Ile Tyr Gln Thr Glu Glu Trp Gly Glu Val Glu Asp Thr His
 325 330

<210> 383

<211> 3689

<212> DNA

<213> Candida albicans

<400> 383

tatttatata taatctaaca acaagtacta tcccttaacc tattagctca atgtcattct 60
 tcattaaaca agagatatgg taattgttga ttagacaaca gttgggtatc catttgtatt 120
 ggaacgcttt ttttaaactg ctgttttatt gtaaaaatta ttgtcgtctt tcttcataac 180
 attatttga acagtctcta actgtattgt tgggctgaca gtagagtatt gcggtcattt 240
 ttaggagtga ttataattct ctgtgagaaa cgcaagcaac aaaaaaagaa caaaggaaac 300
 acaatcatga ttaattatat taatagtaga aactcaaggg tgagctagat gactgagcgt 360
 gcgagaaaaa aaaaaaaaca tcatccaaag tttaaacaaa gtattctttt tttttttcaa 420
 ttttacaacc aaagataaat aactacacaa caccacacat tacagccaaa accacatatc 480
 tgtgcaatat ttacgctcca atggattcaa acccgtgtca agacgtatcg ggtgatacca 540
 gtagcacacc aatggccaac aataatccca ctaatgacag cacaatctcc tctcagaacc 600
 attctaaaac tggcttgaga aaacaccaac aacaacacta ccaccaacac ctgcacctgc 660
 aaatgcattc tcattcacag cagtcacctt atattaatca attggaatac tttaccaata 720
 accagttttc acgctctttc aatagtttaa ttttggagga tgccaatgat gccaacacca 780
 acaatagttc aacaacaacc ttaaataaga aaaccattaa caagtcacca ccattcaata 840

tcaagcagga	cttattaaac	gatagtatcg	acacgtttct	tgataactcc	aacacggaaa	900
cgatagaaga	tggagacgtc	acaacaacag	acgacgatca	cgattttgat	gatgaagata	960
ttgaagatcc	tgaagcagtg	cagtacaccc	caactttgaa	tatcttgaaa	tccaaaaaag	1020
tcgatagctt	caatattata	tctagcaagc	atagaaagag	caatagtcag	attacctaca	1080
atctgcacgt	acggaagcca	tccgaagaag	atacgtcatc	atcgatggct	acaataagggt	1140
tatctaacaa	ctcacaaagt	tcaattaaga	gatcggtcaa	gtatttgaat	ttatctattg	1200
attccaattt	gaaaacgggt	gatggaggta	aaattcccga	tgaaatagat	gacattagtt	1260
tgaacgaaat	agatgttgca	gtggcaccta	acgatttttc	atcaccacta	tcagcaagaa	1320
agccggacat	atttgctgct	ataactgcag	caaacgggaa	ttccaataat	caatttaaaa	1380
ggccacacaa	gttggttagt	caatcgctt	ccccgtcgtc	aaagaataag	tttcgcatat	1440
catcatcaac	cacatcttcg	ccacagtcta	acttgcattc	accttccaag	ttgggactga	1500
aaggattcaa	aatgttttaa	aatgcaataa	gagacgcgat	aatgtcgctc	agcagagtta	1560
tgactccaga	aaaaccgaaa	atggtatcta	aaatatattg	caagtcagca	aaaataaggc	1620
gagcttatac	cccaacccat	acatctaccc	caatggctgt	ctcatcactc	aaccctcctt	1680
catcatctac	actgaattca	acaacggcag	caataacatc	tacaagtcca	gcagctgatg	1740
agcattatga	tattgacaat	gactgtgaca	gtccgtcaaa	aaatagaaaa	ctgtctaata	1800
tttctgcata	ttcaattatt	atztatcaag	atgaaaatca	tatcaagtca	aatcatgcta	1860
gaaaatctag	taatccaata	ccataccctc	cgaccgaacc	actaccgaca	aatatttctg	1920
cttctgtggc	tgaaccaggg	aaaggggtcaa	ctacaactaa	aagcaacctc	tctaagggtt	1980
gtcccttatt	tgatgataaa	gagaataaag	cttcttatca	gtttgtttaa	ccattgcaaa	2040
cagctttcaa	ttcctcgggg	ttggtcaaaa	agaatagcat	aagtgggtctg	ctggacagga	2100
aactacctcc	agaaacacca	atcaaaaagaa	atccattaat	gatttttaaat	accaacaaag	2160
ttgtacctcc	atatagcagt	ggatttgctg	aaggaaaaga	tgtaatgggt	gatcaacatg	2220
atatatatct	ccatattcca	tgtcaaaatc	aacgttttcc	tggcagcgtg	aatcccaaca	2280
ctactacgaa	caacaacaac	actcaacagc	atcatgatag	tgatctttct	attgaagtgt	2340
gaaggaataa	ttcttatgat	gccagtagta	gcactatcaa	taacacaagt	tatatcaaaa	2400
ttttcccttc	ttcgggaattg	aaaaaggagc	aggtgcttca	gcgaccacaa	gaagatttag	2460
aattagtttt	caattctgac	attgaactag	atgataacat	aataccagaa	acaccaacaa	2520
agaaactgct	actaccgaat	cagcaccatc	aacatcactt	acccctttac	acgcaatcca	2580
agagtcattt	gttgaagttt	gacactgaga	aagatggaag	aaggaatttg	tcaatagtct	2640
tagataaate	aaatgcaact	aaacgagaaa	ttagcgaacc	accttcaaca	ccaatcaata	2700
tgctatttgc	aaagaatagt	tttaagaaac	ctatgaataa	tgctgaaaga	ggtgatgacc	2760
ctgatagtat	aattgctcaa	cgcatagata	ttatgccatc	gttagatgaa	gttgactcag	2820
tgtctgttta	tccttcaaag	atagatgaac	atttaattga	aaagtttgga	atgaagaata	2880
tcaagtatat	tggatcggga	gcattttcca	ttgcttttga	atggtttatt	aataacgaaa	2940
agtttgctat	caaaaagaact	aaaaaaccac	ttattggaaa	attggagaaa	caaactataa	3000
aacgagaaat	tgaagcattg	agagtgttga	caagcattaa	agaagatgaa	gcaactaata	3060
tgaagaaca	agaagaaggg	aaagagtatc	tagtttattt	cattgaggcc	tgggatttta	3120
ataattacta	ctatataatg	acagaattct	gtgaagggtg	tacattattt	gatttcttag	3180
aggaaaataa	acattacaaa	attgatgaat	ttagaatttg	gaagatccta	attgaaattc	3240
taaatgggtt	aaaattttatt	catctgaaaa	attattttaca	tttggattta	aaaccagcaa	3300
acatttttat	cacttttgaa	gggtcattga	aaattgggtga	tttcggattg	gctactaaat	3360
tgcttatact	agaaaaggac	tttgatcttg	aaggagatcg	taattatatt	gccccggaat	3420
tgattaatga	caaaaatttat	actccgtttg	cagatatttt	cagtcttgga	ttgattatat	3480
tggagatcgc	tgctaataata	attttaccag	ataatggaac	gccatggcgt	aaattgagaa	3540
gtggagactt	gagtgatgct	ggccgattat	caagtgataa	tatttcaatg	tttttacaac	3600
acaatccaaa	taccaatagc	aatatcagtg	gcagtggaag	tagaagtggg	agtggcagta	3660
caggaggcaa	tggtagtgc	ggtgattga				3689

<210> 384

<211> 1062

<212> PRT

<213> Candida albicans

<400> 384

Met Asp Ser Asn Pro Cys Gln Asp Val Ser Gly Asp Thr Ser Ser Thr

610					615					620					
Thr	Ile	Asn	Asn	Thr	Ser	Tyr	Ile	Lys	Ile	Phe	Pro	Ser	Ser	Glu	Leu
625					630					635					640
Lys	Lys	Glu	Gln	Val	Leu	Gln	Arg	Pro	Gln	Glu	Asp	Leu	Glu	Leu	Val
				645					650					655	
Phe	Asn	Ser	Asp	Ile	Glu	Leu	Asp	Asp	Asn	Ile	Ile	Pro	Glu	Thr	Pro
			660					665					670		
Thr	Lys	Lys	Ser	Leu	Leu	Pro	Asn	Gln	His	His	Gln	His	His	Leu	Pro
		675					680					685			
Leu	Tyr	Thr	Gln	Ser	Lys	Ser	Pro	Leu	Leu	Lys	Phe	Asp	Thr	Glu	Lys
	690					695					700				
Asp	Gly	Arg	Arg	Asn	Leu	Ser	Ile	Val	Leu	Asp	Lys	Ser	Asn	Ala	Thr
705					710					715					720
Lys	Arg	Glu	Ile	Ser	Glu	Pro	Pro	Ser	Thr	Pro	Ile	Asn	Met	Ser	Phe
				725					730					735	
Ala	Lys	Asn	Ser	Phe	Lys	Lys	Pro	Met	Asn	Asn	Ala	Glu	Arg	Gly	Asp
			740					745					750		
Asp	Pro	Asp	Ser	Ile	Ile	Ala	Gln	Arg	Ile	Asp	Ile	Met	Pro	Ser	Leu
		755					760					765			
Asp	Glu	Val	Asp	Ser	Val	Ser	Val	Tyr	Pro	Ser	Lys	Ile	Asp	Glu	His
	770					775					780				
Leu	Ile	Glu	Lys	Phe	Gly	Met	Lys	Asn	Ile	Lys	Tyr	Ile	Gly	Ser	Gly
785					790					795					800
Ala	Phe	Ser	Ile	Ala	Phe	Glu	Cys	Leu	Phe	Asn	Asn	Glu	Lys	Phe	Ala
				805					810					815	
Ile	Lys	Arg	Thr	Lys	Lys	Pro	Leu	Ile	Gly	Lys	Leu	Glu	Lys	Gln	Thr
			820					825						830	
Ile	Lys	Arg	Glu	Ile	Glu	Ala	Leu	Arg	Val	Leu	Thr	Ser	Ile	Lys	Glu
		835					840					845			
Asp	Glu	Ala	Thr	Asn	Met	Gln	Glu	Gln	Glu	Glu	Gly	Lys	Glu	Tyr	Leu
	850					855					860				
Val	Tyr	Phe	Ile	Glu	Ala	Trp	Asp	Phe	Asn	Asn	Tyr	Tyr	Tyr	Ile	Met
865					870					875					880
Thr	Glu	Phe	Cys	Glu	Gly	Gly	Thr	Leu	Phe	Asp	Phe	Leu	Glu	Glu	Asn
				885					890					895	
Lys	His	Tyr	Lys	Ile	Asp	Glu	Phe	Arg	Ile	Trp	Lys	Ile	Leu	Ile	Glu
			900					905					910		
Ile	Leu	Asn	Gly	Leu	Lys	Phe	Ile	His	Ser	Lys	Asn	Tyr	Leu	His	Leu

915 920 925
 Asp Leu Lys Pro Ala Asn Ile Phe Ile Thr Phe Glu Gly Ser Leu Lys
 930 935 940
 Ile Gly Asp Phe Gly Leu Ala Thr Lys Leu Pro Ile Leu Glu Lys Asp
 945 950 955 960
 Phe Asp Leu Glu Gly Asp Arg Asn Tyr Ile Ala Pro Glu Leu Ile Asn
 965 970 975
 Asp Lys Ile Tyr Thr Pro Phe Ala Asp Ile Phe Ser Leu Gly Leu Ile
 980 985 990
 Ile Leu Glu Ile Ala Ala Asn Ile Ile Leu Pro Asp Asn Gly Thr Pro
 995 1000 1005
 Trp Arg Lys Leu Arg Ser Gly Asp Leu Ser Asp Ala Gly Arg Leu Ser
 1010 1015 1020
 Ser Asp Asn Ile Ser Met Phe Leu Gln His Asn Pro Asn Thr Asn Ser
 1025 1030 1035 1040
 Asn Ile Ser Gly Ser Gly Ser Arg Ser Gly Ser Gly Ser Thr Gly Gly
 1045 1050 1055
 Asn Gly Ser Ala Gly Asp
 1060

<210> 385
 <211> 887
 <212> DNA
 <213> Candida albicans

<400> 385
 agtcaagaat tttatgatga ctttgaggga tggctctgatt aagacttggtc ttttaccagt 60
 tttttcagca ttgttgatgg cgtttaaagc atcagctaag acggagggtc tagtcatggt 120
 tgaattgtct gttgataaaa agaaaccgtg aaaaggaagt attgtgaaaa atcgattgat 180
 attttttttt ttctctcttc ctactgtaa cagtagtaaa cacactagtt acaactgatg 240
 acctgcatat tataaatctt tctgaaaaaa tttttttccc tgtatttttg taattctttc 300
 gctctttctc actcactcac acttattaat gaatgaaagg tttggtgtct acaaactcca 360
 ctaacaaaat ctactcctg tgcctaaaca cacacagacc cacacgcaaa cttttctctc 420
 agaaacagaa aaaaaaaatt tcaagcaaaa attttttcca tctagatttt ctttcttcag 480
 aatatcaagt aactttaaag atgcctgtat gtacaataac agtggtataa tgatgtcttt 540
 cagtctttta ttgggtgatt attataataa atggcagatg agaaatatat tggataataa 600
 accttgcaaa tgaaatcagt tgaccatttt gaaataatgg accattagca ataccagat 660
 tgctggaaca aagacgagag aactagacaa ctacagatata atagaacatc catactaact 720
 tcaatcattt cttatagtct caaaaatcat tcagaactaa acaaaagtta gctaaggctc 780
 aaaagcaaaa cagaccattg ccacaatgga tcagattgag aactgacaac aaaatcagat 840
 acaatgctaa aagaagacac tggagaagaa ctaagttggg tatctaa 887

<210> 386
 <211> 51
 <212> PRT

392

<213> *Candida albicans*

<400> 386

Met Pro Ser Gln Lys Ser Phe Arg Thr Lys Gln Lys Leu Ala Lys Ala
 1 5 10 15

Gln Lys Gln Asn Arg Pro Leu Pro Gln Trp Ile Arg Leu Arg Thr Asp
 20 25 30

Asn Lys Ile Arg Tyr Asn Ala Lys Arg Arg His Trp Arg Arg Thr Lys
 35 40 45

Leu Gly Ile
 50

<210> 387

<211> 893

<212> DNA

<213> *Candida albicans*

<400> 387

gatttcattt gcaagggttta ttatccaata tattttctcat ctgccatttta ttataataat 60
 caccaataa aagactgaaa gacatcatta taacactgtt attgtacata caggcatctt 120
 taaagttact tgatattctg aagaaagaaa atctagatgg aaaaaatttt tgcttgaaat 180
 tttttttttc tgtttctgag agaaagggtt gcgtgtgggt ctgtgtgtgt ttaggcacag 240
 gagtgagatt ttgttagtgag agtttgtaga caccaaacct ttcattcatt aataagtgtg 300
 agtgagtgag aaagagcgaa agaattacaa aaatacaggg aaaaaaattt tttcagaaaag 360
 atttataata tgcagggtcat cagttgtaac tagtgtgttt actactgtta cagtggaggaa 420
 ggaggaaaaa aaaaaatatc aatcgatttt tcacaatact tccttttcac ggtttctttt 480
 tatcaacaga caattcaacc atgactagaa cctccgtctt agctgatgct ttaaaccgca 540
 tcaacaatgc tgaaaaaact ggtaaaagac aagtcttaac cagaccatcc tccaaagtca 600
 tcataaaatt cttgactgtc atgcaaaaac acggttacat tgggtgaattc gaatacattg 660
 atgatcacag atccggtaaa attgttggtc aattaaatgg tagattaaac aaatgtgggtg 720
 tcattcaacc aagattcaac gtcaaaatca acgacattga aagatggact gacaacttgt 780
 tgccagctag acaattcggg tacgttatct taaccacttc tgctgggtatc atggaccacg 840
 aagaagctag aagaaagcac gtttctggtg aaatcttagg tttcgtttac tag 893

<210> 388

<211> 130

<212> PRT

<213> *Candida albicans*

<400> 388

Met Thr Arg Thr Ser Val Leu Ala Asp Ala Leu Asn Ala Ile Asn Asn
 1 5 10 15

Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Ile Arg Pro Ser Ser Lys
 20 25 30

Val Ile Ile Lys Phe Leu Thr Val Met Gln Lys His Gly Tyr Ile Gly
 35 40 45

Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln
 50 55 60

Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Gln Pro Arg Phe Asn
 65 70 75 80
 Val Lys Ile Asn Asp Ile Glu Arg Trp Thr Asp Asn Leu Leu Pro Ala
 85 90 95
 Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp
 100 105 110
 His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe
 115 120 125
 Val Tyr
 130

<210> 389
 <211> 4619
 <212> DNA
 <213> Candida albicans

<400> 389
 caacgacaac aacaataaga agaatotttt ccagatatgt taaaatcctt atattaaatg 60
 ttaatagaag cctaaaaatt gcttgaattg atagatttgc tgattctttt gctagaaaca 120
 cgcgttatat tacttatcct ttctgtaatt tcttgatctc tgtttgaatc aacaacgcct 180
 ttgttttctc tttctgcctc cctctgccac cccagttta tttgtttgct tgtcgacgtg 240
 ctgccaaaaa aaaaaattga gttctctctc tcttttttac aacagagaag agacaaaaga 300
 aaaaaaaaaac atcaaaatta agattcaagc tttttttttt agttttttta acaacaaaat 360
 tgaaattaca atccttgaat ttacaacttc atattcagct ctaaaacta ataattataa 420
 caataattaa ttgaattatt ctataaacca ctgatatttg attttatctt tttatttttg 480
 tttgttccca taattgtgtc atgcctgaca atatagaaga tcgatccgag ataccttctg 540
 atgcaaagga aattgtgact acaaatgaaa ttgaagcaac agattcagaa catacaacaa 600
 atgtcgataa tgaactccct caaggtgaat ccaatgaaca aacaggagat gactcaaattg 660
 acaaccttgc atccaaacgt caattaatca atgatttatt acacaatgat cattttgaag 720
 aaggaacaga acgttacatc atccctcaaa atttcttaca tgaatttttg aatttaccaa 780
 tcgataattt tagtgatttg aaagatcaac ttggctccat tgatttccac tcattactta 840
 atgaacaagg taatttatat cccgagaatg aagaaccagt cactttttgt catgtatcgc 900
 cagaagtatt tcaacatttg ggtgaatggg ttggaatatt gggccaacca attattagag 960
 ctatcattat taatccagac accaaagaaa aacagattga aagattcccg ccattatttt 1020
 ggggttcatca attaggtaaa aagacgcaac caacatactt gcgacaccgt cataatggaa 1080
 gcaaccacaa tcatcatcac catgggtcatc acgattcacc aataccagta ttgctttcca 1140
 aaacaagcac ttttcataga ttaatggatg ttatacgtta taatgttctt aaagcaccac 1200
 gaaaatcgac gaaagatttt aggatgttgg ttattgtccc acaagataaa ggcttacagt 1260
 atttgatttc aatacaaaact tttatgtttg atatctccaa aaaaactttg gtttcaccaa 1320
 atatgcttga ggatgctttg aaagatcacg gtattgtggc cagttcctat aatataatgg 1380
 tagaagcaaa agaaaaacat caaacagaat ttcctattga tcaatttatt ttatctcatt 1440
 ctaacgcata tgaagaagta tcacaggggtg gtggacacct tggattatca aacatgggga 1500
 acacatgtta tatgaactcg gctttacaat gtttattaca cgttcttgaa atcaactatt 1560
 atttttttta caacatttat aaaaaagaat tgaattttga caacccttg ggatatcatg 1620
 gagatgttgc caatgcattt gggttcactt taaaacaagc atttgatcac gtgaaaaata 1680
 gttctagat atctcctcga gaattcaaact caactattgg gagatattcc tcgatgtttt 1740
 ctgggtatct tcaacaagat tctcaagagt tgttgagttg gctattagat gctcttcatg 1800
 aggatgtgaa tagaattcac caaaaacat attgtgaaaa gcccgattg aaagatgacg 1860
 aaattgatga ccccaagcc atcaccaaac ttgccaatac ttgctggaat caacataagg 1920
 caagaaacga ctcggtgata attgatttat ttactgggtt gtatcaatct acattaatct 1980

```

gtcctgattg  tggttaagaaa  tccataactt  ttgatccctt  taatgattta  actttacctt  2040
taccatcag  taagaaatgg  tatcacacat  ttacaattgt  tgatttgtcc  aatcaaggcg  2100
ttataccgga  aaggataatg  aagttggaag  ttgagttgaa  taaaacatcc  aatttcgatg  2160
atttacttag  ctatttgagt  aatttcttga  atgttccatc  tactgagttg  tttgcttatg  2220
agatttttca  aaatgcaatc  tatagtgact  tccaattaga  ttacaccaag  aacaagtttt  2280
tacctatcag  tgatattatc  agagatacag  atgatgttat  agtgtagatt  gttccacata  2340
accctgccgt  tgacatcatt  gtgccagtgt  tcaatgccgt  tgaagatgct  gatagttcat  2400
atcaaaggt  taattttttt  ggaatcccat  tatttgtggt  gatgaataaa  gaagtcgatg  2460
tcaatagttt  tggtttttatt  agaaagaaat  tatttagaac  agtttcttta  ttgagtataa  2520
ttgatttggg  tgatgaatat  gaaaaaataa  aaaggagtaa  tgaagattac  gttgaaaaag  2580
tattttacaa  aaaactggat  ttccctgcat  tgtcacagcc  attagaaacc  tccgattgtg  2640
aaaaaaaaca  caataatact  agcgacaacg  acgacgatga  ggatgctgac  aacgatgaag  2700
gctatgatag  tgaagtgtct  ttggctaacc  cataccttgg  agctaatttt  ggggttcaaaa  2760
tcatgtatgt  tcatgactat  agccctaaat  tgaattctaa  ccttcgtagc  aggtacaatc  2820
atgaccaaac  aaccaaattc  aaacaaacag  agagagttat  taatgttctc  acacacaaac  2880
ctacttttag  cgattttcaa  cctttatcgg  accaattatc  agaatacaaa  cgcaactatt  2940
attttttacc  tgattataaa  aagatggatg  atgagatgga  ccaattgggtg  gaggaagtga  3000
accaaaattt  ggcagagcaa  ngagaagcga  gatcatcggt  gtcagaaaat  agtagtagag  3060
cactggaaga  acaagatgga  tttgtattaa  taaataaaga  ggatactctc  aagcaacaat  3120
caactgtacc  tgctgctgct  gaaacgggtac  ctccaccatt  acctgttaga  aataatactg  3180
gagttcacat  cccgtcatcc  gatgaagaaa  cagaaagtga  agctaatttg  ggaagtttgt  3240
ttgattcaac  atcaaacttg  ccgttgccct  caccatctac  atattccgaa  tcaacaaaac  3300
cttcgaatgt  aaactccctc  atggaaagta  actttgaaag  ttcatacagc  gacttgaatt  3360
ctggtacaac  attgatatcg  aaggacacag  ttttgttatg  tgattgggat  aaggaaattt  3420
atcaaaaatg  ctttgggtgat  aaagaattac  aagcatggga  aaacatatcg  aatttaccga  3480
atccagaatt  ggagaaaaat  agagctcatt  ttgaaagaca  aagaaaagct  aaaattacat  3540
tatctgattg  tcttaagagt  ttcagtaccc  ctgaaatttt  aggtgaacat  gatttatggt  3600
attgtccacg  ttgtactgaa  cataaacgtg  ccacaaagac  aatccaactt  tggccaacgg  3660
gtgatatect  cactattcat  ttgaaaagat  ttcatagtgc  tcgtgcattt  agtgataaga  3720
ttgatgtttt  ggttgatttc  ccaattgaag  gtttagatat  aagttcgtat  gttgccaata  3780
ctgatttgag  acctgaagat  tgtttatacg  acttgattgc  cgttgataat  cattatggtg  3840
ggttaggagg  tggtcattac  actgcctcgg  taaagaattt  cagagatgat  aaatggtatt  3900
attttaatga  tagtcgagtc  actgaaatta  ataactctca  agaagtcgta  gctaattctg  3960
cgtacctttt  attttaccgt  cgaagaagtt  cgaaaggagc  tggatttttg  ggaggagaaa  4020
actttatcga  cttgcttcaa  aaaggctcag  aggaatactc  tgagagtttg  caaaagaaaa  4080
gattggttct  tcaaaatggt  ggccaaatag  tcaatacgtg  tgccaaaatt  gaacaagata  4140
taattgataa  agaaacagag  aaacagaaaag  aggaacaaga  acaggaacag  gaacaggaac  4200
aggaacagga  acaagagcaa  gagcaagagc  cagttcaaga  gccagatcaa  gaacaagagc  4260
cagatcaaga  gccagatcaa  gatcaagatc  aagagccaga  tcaagagcca  gatcaagatc  4320
aagagcagaa  tgaacaataa  aaaaaatcta  gaccattcga  tgaactcaaa  ccatcaacta  4380
gtgaaacaaa  taaccaacaa  caaacaactc  agttcaactt  tgatgatgaa  gataatgatt  4440
acgattatga  agcagaagta  gaagattcca  atattcgcaa  acaaagatta  ctttcaaaaag  4500
aaaataacag  caataaattg  gtgcatatta  aaagcaatgg  tcgccaagaa  gtcacttcat  4560
caccagtacc  aattgaaact  gatggtgaca  ctgatgtaac  tgattccaat  tcaacatag  4619

```

<210> 390

<211> 1372

<212> PRT

<213> Candida albicans

<400> 390

Met Pro Asp Asn Ile Glu Asp Arg Ser Glu Ile Pro Ser Asp Ala Lys
1 5 10 15

Glu Ile Val Thr Thr Asn Glu Ile Glu Ala Thr Asp Ser Glu His Thr
20 25 30

Gly Ile Pro Leu Phe Val Val Met Asn Lys Glu Val Asp Val Asn Ser
 645 650 655
 Phe Gly Phe Ile Arg Lys Lys Leu Leu Glu Thr Val Ser Leu Leu Ser
 660 665 670
 Lys Ile Asp Leu Val Asp Glu Tyr Glu Lys Ile Lys Arg Ser Asn Glu
 675 680 685
 Asp Tyr Val Glu Lys Val Phe Tyr Lys Lys Ser Asp Phe Pro Ala Leu
 690 695 700
 Ser Gln Pro Leu Glu Thr Ser Asp Cys Glu Lys Asn Asn Asn Asn Thr
 705 710 715 720
 Ser Asp Asn Asp Asp Asp Glu Asp Ala Asp Asn Asp Glu Gly Tyr Asp
 725 730 735
 Ser Glu Val Ser Leu Ala Asn Pro Tyr Leu Gly Ala Asn Phe Gly Phe
 740 745 750
 Lys Ile Met Tyr Val His Asp Tyr Ser Pro Lys Leu Asn Ser Asn Leu
 755 760 765
 Arg Ser Arg Tyr Asn His Asp Gln Thr Thr Lys Phe Lys Gln Thr Glu
 770 775 780
 Arg Val Ile Asn Val Pro Thr His Lys Pro Thr Phe Ser Asp Phe Lys
 785 790 795 800
 Pro Leu Ser Asp Gln Leu Ser Glu Ser Lys Arg Asn Tyr Tyr Phe Tyr
 805 810 815
 Pro Asp Tyr Lys Lys Met Asp Asp Glu Met Asp Gln Leu Val Glu Glu
 820 825 830
 Val Asn Gln Asn Leu Ala Glu Gln Xaa Glu Ala Arg Ser Ser Gly Ser
 835 840 845
 Glu Asn Ser Ser Arg Ala Ser Glu Glu Gln Asp Gly Phe Val Leu Ile
 850 855 860
 Asn Lys Glu Asp Thr Leu Lys Gln Gln Ser Thr Val Pro Ala Ala Ala
 865 870 875 880
 Glu Thr Val Pro Pro Pro Leu Pro Val Arg Asn Asn Thr Gly Val His
 885 890 895
 Ile Pro Ser Ser Asp Glu Glu Thr Glu Ser Glu Ala Asn Leu Gly Ser
 900 905 910
 Leu Phe Asp Ser Thr Ser Asn Leu Pro Leu Pro Pro Pro Ser Thr Tyr
 915 920 925
 Ser Glu Ser Thr Lys Pro Ser Asn Val Asn Ser Pro Met Glu Ser Asn
 930 935 940

Phe Glu Ser Ser Ser Ala Asp Leu Asn Ser Gly Thr Thr Leu Ile Ser
 945 950 955 960
 Lys Asp Thr Val Leu Leu Cys Asp Trp Asp Lys Glu Ile Tyr Gln Lys
 965 970 975
 Cys Phe Gly Asp Lys Glu Leu Gln Ala Trp Glu Asn Ile Ser Asn Leu
 980 985 990
 Pro Asn Pro Glu Leu Glu Lys Asn Arg Ala His Phe Glu Arg Gln Arg
 995 1000 1005
 Lys Ala Lys Ile Thr Leu Ser Asp Cys Leu Lys Ser Phe Ser Thr Pro
 1010 1015 1020
 Glu Ile Leu Gly Glu His Asp Leu Trp Tyr Cys Pro Arg Cys Thr Glu
 1025 1030 1035 1040
 His Lys Arg Ala Thr Lys Thr Ile Gln Leu Trp Ser Thr Gly Asp Ile
 1045 1050 1055
 Leu Thr Ile His Leu Lys Arg Phe His Ser Ala Arg Ala Phe Ser Asp
 1060 1065 1070
 Lys Ile Asp Val Leu Val Asp Phe Pro Ile Glu Gly Leu Asp Ile Ser
 1075 1080 1085
 Ser Tyr Val Ala Asn Thr Asp Leu Thr Pro Glu Asp Cys Leu Tyr Asp
 1090 1095 1100
 Leu Ile Ala Val Asp Asn His Tyr Gly Gly Leu Gly Gly Gly His Tyr
 1105 1110 1115 1120
 Thr Ala Ser Val Lys Asn Phe Arg Asp Asp Lys Trp Tyr Tyr Phe Asn
 1125 1130 1135
 Asp Ser Arg Val Thr Glu Ile Asn Asn Pro Gln Glu Val Val Ala Asn
 1140 1145 1150
 Ser Ala Tyr Leu Leu Phe Tyr Arg Arg Arg Ser Ser Lys Gly Ala Gly
 1155 1160 1165
 Ile Leu Gly Gly Glu Asn Phe Ile Asp Leu Leu Gln Lys Gly Arg Glu
 1170 1175 1180
 Glu Tyr Ser Glu Ser Leu Gln Lys Lys Arg Leu Val Leu Gln Asn Val
 1185 1190 1195 1200
 Gly Gln Ile Val Asn Thr Tyr Ala Lys Ile Glu Gln Asp Ile Ile Asp
 1205 1210 1215
 Lys Glu Thr Glu Lys Gln Lys Glu Glu Gln Glu Gln Glu Gln Glu
 1220 1225 1230
 Glu Gln Glu Gln Glu Gln Glu Gln Glu Glu Pro Val Gln Glu Pro
 1235 1240 1245

399

Asp Gln Glu Gln Glu Pro Asp Gln Glu Pro Asp Gln Asp Gln Asp Gln
 1250 1255 1260

Glu Pro Asp Gln Glu Pro Asp Gln Asp Gln Glu Gln Asn Glu Thr Ile
 1265 1270 1275 1280

Lys Lys Ser Arg Pro Phe Asp Glu Leu Lys Pro Ser Thr Ser Glu Thr
 1285 1290 1295

Asn Asn Gln Gln Gln Thr Thr Gln Phe Asn Phe Asp Asp Glu Asp Asn
 1300 1305 1310

Asp Tyr Asp Tyr Glu Ala Glu Val Glu Asp Ser Asn Ile Arg Lys Gln
 1315 1320 1325

Arg Leu Leu Ser Lys Glu Asn Asn Ser Asn Lys Leu Val His Ile Lys
 1330 1335 1340

Ser Asn Gly Arg Gln Glu Val Thr Ser Ser Pro Val Pro Ile Glu Thr
 1345 1350 1355 1360

Asp Gly Asp Thr Asp Val Thr Asp Ser Asn Ser Thr
 1365 1370

<210> 391

<211> 2693

<212> DNA

<213> Candida albicans

<400> 391

```

ttcatttcct aaattcaa at gaattatcat caccaatgcc accatcattt tctattaact 60
atggtagtga atgggattta gaaatcattc aaactagttt agataatgaa aaagaatcag 120
aaactaaatc atttactggg gaattagaat atacttcaac ttcttccaat ggtgaacatg 180
acaccaccac cactgccact aaacatgaat tgatattaca acaaattttg aatttcta atg 240
atgaatcata tattaatcct aaatcattaa catttgatcc attaaaaatt ttcactaaac 300
aattaattgg tgaattaatt aaaattaatc aattttacaa ttcaaaagaa tctggaaattt 360
tcaaaattta taataattta attcatgatt taaaaaatca aaatattaat attgatgatg 420
tatttaaat cactcaagct tataattatt ccatcctaaa tataataaat actgatgatc 480
atcatcaata tcattttaaaa tcaactttat caagaacagt tactaatgct agtgtatttg 540
ataccattaa tcatattgat aatgattatg ataataataa taacaaccaa agaataatt 600
atgatttgga gaaacaaaat aatactacag ttgcaattca tgatgatgat gattcagaag 660
acgatgaaga agaagaggaa gaagaaactc atagtcatga ttcagtatta cttaatcata 720
cacattttta tggttaacaa caattaaaaa tcacattaaa acgtaaagcc attacattat 780
ttataaatct ttctgaatta aaatcattta ttgaattgaa tagaattgga ttcacgaaaa 840
tttgtaaaaa atttgataaa acttggtggtt attcaattaa acaagatttt attaatgaat 900
ttttacctca atattctcga gtatttgaaa atgataccat tgaagaatta gattataaat 960
tgaatcaa at tattaataat tatgcctttt tatcaataa attaatct caatcaacaa 1020
ctaaagaaga tttggataat ataaaaattg aattaagatc ttatttacgt gatcatattg 1080
tatttgaaag aaataccggt tggaaagatt tattatcatt agaaaagaaa tcttataata 1140
ttgatttaga taattctgtg gttcaaaata ataaaatggg tgatgaagg catataatta 1200
ttcaatgat gaatttatcc atgaaaagaa ttaatttacc acaatgcctt aaaaaattga 1260
ttaaatatga tcatattgat attccacaat ttttattaac tactcaaatg cttaaaatta 1320
ttattattgt cattgttttc atttatattat tagcagttaa aacttttaat gatccagttc 1380
aaggctcgtt tttagcagta ttagttgctg ctgccatgct ttgggcttca gaagcattac 1440

```

400

```

ctttatacac tacagcttta ttaatcccac ttttggttgt tacttgtaaa gtttgtaaaa 1500
ctccgggaac cgatgatcca atggatgcca ccaaggcatc acaatatatt tttgggacaa 1560
tgtggaattc cacaattatg atattaattg gtgggtttac attagctgct gcattatcaa 1620
aatataatct tgccaaaata ttatcatcat atatttttagc attagcaggt acaaatccaa 1680
gaaatgtatt attggcaatc atgtgtgtat cattatttct ttccatgtgg atttctaata 1740
ttgctgcccc cgttttatgt ttttcattaa ttcaaccagt ttttaagaagt atccccacag 1800
attccccgtg tgctaaagca ttagtggttag ggatcgcttt ggcgtctgat gttgctggta 1860
tggcttcacc aattgcatct ccacaaaatg ttattgctct tgaatcaatg aatcctaata 1920
cagggtgggg gaaatgggtt gctgtggcat tacctgtggc aatcattagt ttaattttta 1980
tttgggtgga attattcatg acgtttaaaa tcaataatgt taaaatcaaa caattcaaac 2040
caattaaaga aaaattaacc atgaaacaat ggtttgattt tgccgtcact ataactacta 2100
ttcttttatg gtgtgttatg caaaaaattg atggaacatt tggatgaatca ggtataatca 2160
cttgatcccc aattgtatta tttttcggta ccggtttatt aaaagttgat gatttaaata 2220
attatccttg gtcaattggt atggttagcca tgggtgggtat tgcattaggg aaagccggtt 2280
cttcttcagg tttattgaaa actattgctt tagcattaca aaaacgaatt atgcattatg 2340
atgccattgt tgtattaatc atttttggag cattaatttt ggtggtagct acatttgtaa 2400
gtcatactgt atcagcactt attattatcc ccttggttaa agaagttgga gattcattac 2460
ctaaacctca tccattaatg cttattatgg gtgtagcttt aattgcttca ggggcaatgg 2520
gattaccaac ttcaggattc cctaattgtg cggcaattgg tatgagagat gaagttggta 2580
aaccttattt gacgggttaat ttatttatta ctagaggggt tccggcaagt ataattgttt 2640
atgtttgtat tatcaccatt gggtatggta ttatgtcatc attgaacttt taa 2693

```

<210> 392

<211> 896

<212> PRT

<213> Candida albicans

<400> 392

```

His Phe Leu Asn Ser Asn Glu Leu Ser Ser Pro Met Pro Pro Ser Phe
 1          5          10         15

Ser Ile Asn Tyr Gly Ser Glu Trp Asp Leu Glu Ile Ile Gln Thr Ser
          20          25          30

Leu Asp Asn Glu Lys Glu Ser Glu Thr Lys Ser Phe Thr Gly Glu Leu
          35          40          45

Glu Tyr Thr Ser Thr Ser Ser Asn Gly Glu His Asp Thr Thr Thr Thr
          50          55          60

Ala Thr Lys His Glu Leu Ile Leu Gln Gln Ile Leu Asn Ser Asn Asp
          65          70          75          80

Glu Ser Tyr Ile Asn Pro Lys Ser Leu Thr Phe Asp Pro Leu Lys Ile
          85          90          95

Phe Thr Lys Gln Leu Ile Gly Glu Leu Ile Lys Ile Asn Gln Phe Tyr
          100         105         110

Asn Ser Lys Glu Ser Glu Ile Phe Lys Ile Tyr Asn Asn Leu Ile His
          115         120         125

Asp Leu Gln Asn Gln Asn Ile Asn Ile Asp Asp Val Phe Lys Phe Thr
          130         135         140

Gln Ala Tyr Asn Tyr Ser Asp Pro Asn Ile Ile Asn Thr Asp Asp His

```


755	760	765
Ala Leu Ala Leu Gln Lys Arg Ile Met His Tyr Asp Ala Ile Val Val		
770	775	780
Leu Ile Ile Phe Gly Ala Leu Ile Leu Val Val Ala Thr Phe Val Ser		
785	790	795 800
His Thr Val Ser Ala Leu Ile Ile Ile Pro Leu Val Lys Glu Val Gly		
	805	810 815
Asp Ser Leu Pro Lys Pro His Pro Leu Met Leu Ile Met Gly Val Ala		
	820	825 830
Leu Ile Ala Ser Gly Ala Met Gly Leu Pro Thr Ser Gly Phe Pro Asn		
	835	840 845
Val Thr Ala Ile Gly Met Arg Asp Glu Val Gly Lys Pro Tyr Leu Thr		
	850	855 860
Val Asn Leu Phe Ile Thr Arg Gly Val Pro Ala Ser Ile Ile Val Tyr		
	865	870 875 880
Val Cys Ile Ile Thr Ile Gly Tyr Gly Ile Met Ser Ser Leu Asn Phe		
	885	890 895

<210> 393

<211> 2279

<212> DNA

<213> Candida albicans

<400> 393

tataaaagttt	caagtataaa	aaggcggttta	aaattaattc	ttgtgattta	aataagttaa	60
attctttttt	tttttctttg	ttagtttttc	gctttatccg	ttttacccaa	gaaaggagca	120
atactgtttc	acccctcccc	ccttcccagt	tccatggccc	gcccccccc	tctcaacagt	180
tgctgtcggt	cctgcctcat	tttccacgcc	cattacatta	tatgactaat	atccgttgcc	240
ttattattaa	agtcacaata	cattgaaaga	tagaatagca	agcaagggtg	aaaaaaattt	300
ttttttttat	cacattcaat	acttatatcc	taaattgata	aacaatagag	taattgatac	360
tttcgaagga	caataaaaacg	atatatatatt	atatattaga	gtgaacaata	gcgattgcca	420
atcacagaca	acagataatt	tatctttctc	ctatttcattt	gcacaattaa	atccaaaaaa	480
aaaaaagaat	cgaattccat	atgtcgcata	agactcagag	ccaattatct	tcacaaatga	540
aaaacttgaa	tactccacca	atagacttca	actcaacttc	aagtaacaat	accatgcctt	600
ctgaacccaa	tctgcaaccg	caacaacaac	aatcacaaac	agaagcaaaa	acggagccac	660
aaaccatacg	ccctgctact	tttacaacta	gtggcaattc	atcatcttcg	tcgatatcta	720
ccttatcagc	agatatcatt	caaccacttc	atcaactact	gataaataac	aacaattcaa	780
ctgtgacgca	accagcgcca	caaagctcat	cgtttcaacg	ccgaaacaat	ccacaacggt	840
tcaatcgga	tcaactcaat	gtatacactg	acttcaatag	tactacttca	tctgcttcaa	900
gcattagtag	ttcaccaaaa	gatttcttca	ccagagagcc	accacggatc	catagtaa	960
tgatatgtga	agagattgcc	tctgccaata	atcgagctgc	ttaaagaggtt	ttatcacggt	1020
tatctactga	tgaattgcgt	tcagttaa	cacatactga	attagctgaa	actgcta	1080
gagtgagaat	gtagccaaa	aatttatccc	gagcaaccat	tcaattagac	gtagagcta	1140
ttatgattat	cactaaagct	agagataatg	gacttattta	tttaacaaaa	gaagttggtg	1200

404

```

aatggatttt ggatcaacat cctcatataa caatttatgc tgatgagaaa ttagcaaagt 1260
cgaaaagatt caatccggaa agtattattg ccaattatcc aaatggttgt aagaaattaa 1320
aatattggaa taaaaaatta actacgaaaa atccagaaat ttctgattta gtacttacat 1380
taggtggtga tggtagtgta ttatttgctt caaacttatt tcaaaaaatt gttccaccta 1440
tactttcatt ttcattgggc tcattagggt ttttaaccaa ttttgaattc agtgcattta 1500
gaacagtatt gagcaaatgt tttgattctg gagttaaagc aaatttgctg atgcgattca 1560
cttgctgagt acacactgat gaaggggaagt tgatttgtga acaacaagtg ttgaatgaat 1620
tggtagtga tagaggacct agcccatatg ttactcattt ggaattatac ggcgatggat 1680
cattgttaac ggttgcccaa gctgatgggt tgattattgc aactccaact ggctcgactg 1740
cttattcatt atctgctggt gggctcttag ttcacctggg tgtgagtgcc attagtgtta 1800
ctccaatttg tcctcacacc ttatcggtca gacctatact attacctgat gggatgtttt 1860
tgaagggttaa agtcccactg agcagtagag ccactgcgtg gtgttcattc gatggtaaa 1920
tgcgtagtga attgaagaaa gggtattatg tcactattca agcttcacca ttccccttac 1980
ctacagtaat gtcttccaaa acagaatata ttgattctgt cagtagaaat ttacattgga 2040
acatcagaga gcaacaaaaa ccatttagtt catatttgaa accagaaacg cgacaaagta 2100
ttgctgaaaag tgaaagattg gataatttac atatttcaag tgaacaagat gaatcgaatc 2160
atgaggaacc tgaaataact gaagattttg atattaatta tactgacaat gaacgtgatt 2220
cttctagttc cactcctagt gaagaaagca acgaagaatg tgctaatacc acgacataa 2279

```

<210> 394

<211> 592

<212> PRT

<213> Candida albicans

<400> 394

```

Met Ser His Lys Thr Gln Ser Gln Leu Ser Ser Gln Met Lys Asn Leu
 1              5              10              15

Asn Thr Pro Pro Ile Asp Phe Asn Ser Thr Ser Ser Asn Asn Thr Met
      20              25              30

Pro Ser Glu Pro Asn Ser Gln Pro Gln Gln Gln Gln Ser Gln Pro Glu
      35              40              45

Ala Lys Thr Glu Pro Gln Thr Ile Arg Pro Ala Thr Phe Thr Thr Ser
      50              55              60

Gly Asn Ser Ser Ser Ser Ser Ile Ser Thr Leu Ser Ala Asp Ile Ile
      65              70              75              80

Gln Pro Leu His Gln Leu Ser Ile Asn Asn Asn Asn Ser Thr Val Thr
      85              90              95

Gln Pro Ala Pro Gln Ser Ser Ser Phe Gln Arg Arg Asn Asn Pro Gln
      100              105              110

Arg Phe Asn Arg Asn Gln Leu Asn Val Tyr Thr Asp Phe Asn Ser Thr
      115              120              125

Thr Ser Ser Ala Ser Ser Ile Ser Ser Ser Pro Lys Asp Phe Phe Thr
      130              135              140

Arg Glu Pro Pro Arg Ile His Ser Lys Leu Ile Cys Glu Glu Ile Ala
      145              150              155              160

Ser Ala Asn Asn Arg Ala Ala Lys Glu Val Leu Ser Arg Leu Ser Thr

```


165										170					175						
Asp	Glu	Leu	Arg	Ser	Val	Lys	Ser	His	Thr	Glu	Leu	Ala	Glu	Thr	Ala						
			180					185					190								
Asn	Gly	Val	Arg	Met	Leu	Ala	Lys	Asn	Leu	Ser	Arg	Ala	Thr	Ile	Gln						
		195					200					205									
Leu	Asp	Val	Arg	Ala	Ile	Met	Ile	Ile	Thr	Lys	Ala	Arg	Asp	Asn	Gly						
	210					215					220										
Leu	Ile	Tyr	Leu	Thr	Lys	Glu	Val	Val	Glu	Trp	Ile	Leu	Asp	Gln	His						
225					230					235					240						
Pro	His	Ile	Thr	Ile	Tyr	Ala	Asp	Glu	Lys	Leu	Ala	Lys	Ser	Lys	Arg						
				245					250					255							
Phe	Asn	Pro	Glu	Ser	Ile	Ile	Ala	Asn	Tyr	Pro	Asn	Gly	Cys	Lys	Lys						
			260					265					270								
Leu	Lys	Tyr	Trp	Asn	Lys	Lys	Leu	Thr	Thr	Lys	Asn	Pro	Glu	Ile	Phe						
		275					280					285									
Asp	Leu	Val	Leu	Thr	Leu	Gly	Gly	Asp	Gly	Thr	Val	Leu	Phe	Ala	Ser						
	290					295					300										
Asn	Leu	Phe	Gln	Lys	Ile	Val	Pro	Pro	Ile	Leu	Ser	Phe	Ser	Leu	Gly						
305					310					315					320						
Ser	Leu	Gly	Phe	Leu	Thr	Asn	Phe	Glu	Phe	Ser	Ala	Phe	Arg	Thr	Val						
				325					330					335							
Leu	Ser	Lys	Cys	Phe	Asp	Ser	Gly	Val	Lys	Ala	Asn	Leu	Arg	Met	Arg						
			340					345					350								
Phe	Thr	Cys	Arg	Val	His	Thr	Asp	Glu	Gly	Lys	Leu	Ile	Cys	Glu	Gln						
		355					360					365									
Gln	Val	Leu	Asn	Glu	Leu	Val	Val	Asp	Arg	Gly	Pro	Ser	Pro	Tyr	Val						
	370					375					380										
Thr	His	Leu	Glu	Leu	Tyr	Gly	Asp	Gly	Ser	Leu	Leu	Thr	Val	Ala	Gln						
385					390					395					400						
Ala	Asp	Gly	Leu	Ile	Ile	Ala	Thr	Pro	Thr	Gly	Ser	Thr	Ala	Tyr	Ser						
				405					410					415							
Leu	Ser	Ala	Gly	Gly	Ser	Leu	Val	His	Pro	Gly	Val	Ser	Ala	Ile	Ser						
			420					425					430								
Val	Thr	Pro	Ile	Cys	Pro	His	Thr	Leu	Ser	Phe	Arg	Pro	Ile	Leu	Leu						
		435																			

406

465		470		475		480
Gly Tyr Tyr Val Thr Ile Gln Ala Ser Pro Phe Pro Leu Pro Thr Val						
	485			490		495
Met Ser Ser Lys Thr Glu Tyr Ile Asp Ser Val Ser Arg Asn Leu His						
	500			505		510
Trp Asn Ile Arg Glu Gln Gln Lys Pro Phe Ser Ser Tyr Leu Lys Pro						
	515			520		525
Glu Thr Arg Gln Ser Ile Ala Glu Ser Glu Arg Leu Asp Asn Leu His						
	530			535		540
Ile Ser Ser Glu Gln Asp Glu Ser Asn His Glu Glu Pro Glu Ile Thr						
	545			550		555
Glu Asp Phe Asp Ile Asn Tyr Thr Asp Asn Glu Arg Asp Ser Ser Ser						
	565			570		575
Ser Thr Pro Ser Glu Glu Ser Asn Glu Glu Cys Ala Asn Thr Thr Thr						
	580			585		590

<210> 395

<211> 1042

<212> DNA

<213> Candida albicans

<400> 395

```

atagcggccg cgcatataat agagaatatg tcattaccag cttcatttga cttaactcca 60
gaagatgcta aattgttatt agctgccaac gtccatttgg gtgctaagaa cgttcaagtt 120
cacaacaaac catatgttta caaaaccaga ccagatggta tgaacatcat caacattggt 180
aaaacttggg aaaaaattgt tttggctgcc agaattattg ctgctgttcc aaacgcttct 240
gatgttgctg tttgttcttc aagaactttc ggtcaaagag ctgttttgaa atttgctgct 300
cacactgggt ctactgccat tgctggtaga ttcactccag gtaactttac caattatatc 360
actcgttcat tcaaagaacc aagattagtt gttgttactg acccaagaac cgatgctcaa 420
gccatcaaag aatcatctta tgtaaacatt ccagttattg ccttgactga catgcagtct 480
ccatctgaat acgttgatgt tgccattcca tgtaacaaca aaggtaaaca ctgtattggt 540
ttaatctggt gggtgcttgc tagagaagtc ttgagattaa gaggtattat cccagacaga 600
actaccgaat ggtcagttat gccagatttg tacttctaca gagaccaga agaaattgaa 660
caaaatgccg tcgaagaagc taaaactgaa ggagttgaag gagctccagt tgctgaagct 720
gaaaccgaat ggactgggtg aactgaagat gttgattggg ctgattctgg tgctaccccc 780
agctgctgaa gatgctgctg cttctatctg gtaaacactg aaatctacca ataagaagta 840
gaagtagaag tagaagaaga aacaataaca acaataacaa ccaaaataaa aaaaagggtt 900
aatgatgtat attatcgata aggagaaaga agagattttc ttttttaata atgaggatgc 960
cattttatac aaatccaaaa ttgtaattaa gaaagattaa taaatataaa atatatatat 1020
ataagtaaaa aaaaaaaaaa aa                                     1042

```

<210> 396

<211> 253

<212> PRT

<213> Candida albicans

<400> 396

```

Met Ser Leu Pro Ala Ser Phe Asp Leu Thr Pro Glu Asp Ala Lys Leu
 1          5          10          15

Leu Leu Ala Ala Asn Val His Leu Gly Ala Lys Asn Val Gln Val His
          20          25          30

Asn Lys Pro Tyr Val Tyr Lys Thr Arg Pro Asp Gly Met Asn Ile Ile
          35          40          45

Asn Ile Gly Lys Thr Trp Glu Lys Ile Val Leu Ala Ala Arg Ile Ile
          50          55          60

Ala Ala Val Pro Asn Ala Ser Asp Val Ala Val Cys Ser Ser Arg Thr
          65          70          75          80

Phe Gly Gln Arg Ala Val Leu Lys Phe Ala Ala His Thr Gly Ala Thr
          85          90          95

Ala Ile Ala Gly Arg Phe Thr Pro Gly Asn Phe Thr Asn Tyr Ile Thr
          100          105          110

Arg Ser Phe Lys Glu Pro Arg Leu Val Val Val Thr Asp Pro Arg Thr
          115          120          125

Asp Ala Gln Ala Ile Lys Glu Ser Ser Tyr Val Asn Ile Pro Val Ile
          130          135          140

Ala Leu Thr Asp Met Gln Ser Pro Ser Glu Tyr Val Asp Val Ala Ile
          145          150          155          160

Pro Cys Asn Asn Lys Gly Lys His Cys Ile Gly Leu Ile Trp Trp Leu
          165          170          175

Leu Ala Arg Glu Val Leu Arg Leu Arg Gly Ile Ile Pro Asp Arg Thr
          180          185          190

Thr Glu Trp Ser Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
          195          200          205

Glu Ile Glu Gln Asn Ala Val Glu Glu Ala Lys Thr Glu Gly Val Glu
          210          215          220

Gly Ala Pro Val Ala Glu Ala Glu Thr Glu Trp Thr Gly Glu Thr Glu
          225          230          235          240

Asp Val Asp Trp Ala Asp Ser Gly Ala Thr Pro Ser Cys
          245          250

```

<210> 397

<211> 1335

<212> DNA

<213> Candida albicans

Asp Tyr Phe Glu Tyr Tyr Asp Met Phe Tyr Glu Gly Leu Asn Gly Gln
115 120 125

Leu	Pro	Asn	Leu	Asp	Leu	Leu	Asn	Thr	Ala	Asn	Val	Met	Thr	Tyr	His
130						135					140				
Glu	Gln	Ile	Pro	Cys	Ala	Met	Gln	Gly	Met	Ser	Asp	Arg	Val	Ile	Asn
145					150					155					160
Tyr	Ser	Thr	Arg	Leu	Gln	Thr	Leu	Phe	Arg	Gly	Ile	Leu	Lys	Leu	Thr
				165					170					175	
Leu	Val	Gly	Leu	Thr	Asp	Glu	Val	His	Gly	Cys	Glu	Ala	Phe	Ser	Gly
			180					185					190		
Trp	Gln	Ile	Gln	Ala	Phe	Thr	Ile	Lys	Val	Arg	Gly	Thr	Glu	Gly	Lys
		195					200					205			
Asp	Val	Thr	Gln	Phe	Gly	Arg	Ile	Val	Asp	Ser	Thr	Phe	Arg	Ser	Val
	210					215					220				
Asn	Asn	Leu	Leu	Glu	Lys	Phe	His	Gln	Ser	Phe	Phe	Phe	Tyr	Leu	Met
225					230					235					240
Leu	Ser	Pro	Lys	His	Phe	Val	Ser	Ile	Gly	Thr	Tyr	Leu	Pro	Ser	Ala
				245					250					255	
Ile	Leu	Leu	Ala	Val	Ser	Tyr	Ala	Leu	Ser	Ser	Val	Ser	Ala	Val	Val
			260					265					270		
Val	Ala	Gly	Phe	Asp	Phe	Arg	Lys	Leu	Tyr	Phe	Val	Val	Val	Val	Glu
		275					280					285			
Ile	Ala	Cys	Ala	Ile	Leu	Ala	Phe	Val	Pro	Val	Asn	Gln	Val	Met	Leu
	290					295					300				
Val	Ala	Ile	Ser	Ala	Val	Val	Leu	Leu	Pro	Arg	Gln	Ala	Ile	Phe	Ser
305					310					315					320
Lys	Gln	Ala	Ala	Phe	Ser	Leu	Ile	Ser	Ile	Ala	Leu	Leu	Ala	Val	Ala
				325					330					335	
Leu	Leu	Ile	Thr	Ala	Leu	Leu	Ile	Val	His	Phe	Ala	Leu	Ala	Phe	Ser
			340					345					350		
Ile	Gly	Ile	Leu	Ala	Leu	Pro	Leu	Thr	Phe	Val	Pro	Thr	Leu	Met	Lys
		355					360					365			
Asn	Lys	Ser	Arg	Leu	Thr	Ala	Phe	Cys	Leu	Ala	Val	Ser	Asn	Pro	Phe
	370					375					380				
Phe	Val	Ile	Phe	Val	Ala	Gly	Lys	Val	Leu	Gly	His	Pro	Glu	Leu	Phe
385					390					395					400
Asp	Arg	Leu	Val	Thr	Ala	Trp	Ser	Asp	Ile	Gln	Cys	Trp	Thr	Trp	Phe
				405					410					415	
Ile	Val	Val	Leu	Gly	Trp	Phe	Pro	Ala	Trp	Val	Ile	Ile	Thr	Leu	Ser
			420					425					430		

Tyr Cys Gly Tyr Lys Pro Val Lys Glu Lys Ser Glu
 435 440

<210> 399
 <211> 1190
 <212> DNA
 <213> Candida albicans

<400> 399
 taggtcattc ataacaattg atagatgcaa gctaattgga atgaaaaatc catcttgtat 60
 caaaaccctt tgttcctcat agttaatccg actaaagaag tgtttttttt ttcttttctt 120
 ttttgcata tcctagttag cttaacgaca gtaatagtta aagcgttggg aagtaatggg 180
 gaactcgaac catttggttg acgctgacga ttaataatgt gaatttcttt ttcttttttg 240
 gttgtagtaa ttgctttggt ttggtgtcta aattaggaaa atgtcgtgac cttacgtaca 300
 gcacacacat accactgtcg tgcactgacc aacaacaatg cgggtgtaat cgataacca 360
 aagattataa ataggggggtg gaagggtcgcc actggttgaa atgaatcaac acagtttttt 420
 ttcttcttgc tttttctttc tattttacat taaaaattct gacaatcgtc aactaacata 480
 tatatacaaa tctacaagca atgcaaattt tcgttaaaac tttgactggg aaaaccatta 540
 ccttagaagt cgaatcttct gacaccatcg ataacgtcaa atccaagatc caagacaaag 600
 aaggatttcc accagaccaa caaagattga ttttcgccgg taaacaatta gaagatggca 660
 gaaccttggtc tgactacaac atccaaaaag aatctacttt acatttggtt ttaagattga 720
 gaggtgggtat gcaaattctt gttaaaactt taactggtaa gactatcact ttggaagtcg 780
 aatcttctga caccatcgat aacgtcaaat ccaagatcca agacaaagaa ggtattccac 840
 cagaccaaca aagattgatt ttcgccggtg aacaattgga agacggtaga accttgtctg 900
 actacaacat ccaaaaagaa tctactttac atttggtttt aagattgaga ggtgggtatgc 960
 aaatctttgt taaaacttta actggtaaga ctatcacttt ggaagtcgaa tcttctgaca 1020
 ccacgataa cgtcaaattc aagatccaag acaaagaagg tattccacca gatcaacaaa 1080
 gattgatttt tgctggtaaa caattagaag atggcagaac cttgtctgac tacaacatcc 1140
 aaaaagaatc taccttgcac ttggtcttga gattgagagg tggtttctaa 1190

<210> 400
 <211> 229
 <212> PRT
 <213> Candida albicans

<400> 400
 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1 5 10 15
 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp
 20 25 30
 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
 35 40 45
 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 50 55 60
 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
 65 70 75 80
 Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
 85 90 95

Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140

Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
145 150 155 160

Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp
165 170 175

Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln
180 185 190

Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu
195 200 205

Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg
210 215 220

Leu Arg Gly Gly Phe
225

<210> 401

<211> 2390

<212> DNA

<213> Candida albicans

<400> 401

```
tccagaatag taattagga ctttaatttt attaggagtg gattgcatag aatatgctat 60
ctaatagata catcttatta tattcttatt catgggaaag caccagtata tggaaatgct 120
gcccaaggta gtgcacacaa caaactagtt tacaaagtaa aattcgaagt tacgtcaaag 180
cttagaatgg ttcttatagt agttgtctac tctatcaaaa aaccataat ttgtctatat 240
aacgtaagga tcaactatag ctggttgagta agaaatatgt tgcgagccgt accgacaatg 300
gattggctga aacttgttct catcaaactt gcaaaacact tggagacgcg cgcgcgtttc 360
aacacacaat aaacaacacg aaaaataagg tagaaaacaa aaaaaaata aaaggaactt 420
taaacaagaa gtaatcccca ttaaaacttg atcaacactt ttagggtttc cgatttcccc 480
attttcttga ctaaaataat atgagaatac tatgtgttgc cgaaaaacca tcgatttcaa 540
aagaggtggc aaacattttg ggaggagggc gaaaaaaagt aagaaactca cgagaaaaat 600
tcatcaaaaa ctacgatttc accttcactt tcaactctga agatgggcca tgtcaagtaa 660
ccatgacttc ggtggctgga catatcacag gacttgattt tgggtctgcc ttttcgtggg 720
gaaatttgtt tcccgggcga ctatttgaag cagacatcaa gaccattatc accaagaaat 780
ctatttatga aaatattgca gaagaggcaa gaaacgctga taagttgatg atctggacag 840
attgtgatag agaaggagaa tacattggat ttgaaattat gaatgctgca agaaaataca 900
ataggaacct tgggttaaac aatatttggc gagctagggt ttcacatctt gaacgaaatc 960
acattattcg agcagcaaaa aatcccgtga atttgatat gagtgcagtt tctgcagttt 1020
cttgctgat ggaaatcgat cttcgagtgg gtaccagttt tacacgtttg ttgactgatc 1080
aattgagaca aaaggggata attgaaaaga atgaactagc ttcttatggg acatgtcaat 1140
tcccgacatt ggggtttgtt gttgatcgat acaaacgagt caagagtttt acaccggaac 1200
cattctggta tattgagatt gaaactagga aagagaataa aaagacaatt ttcaattggg 1260
ttcgagggtca ttttttcgac aagatgtatg tggttatgct ttatgatcga tgctgcaaaa 1320
```

```

gtggagaatt tggaaccata tcaaaaatag aatcaaaacg gaaaccaaat ttccgtccat 1380
tcccattgac aaccgtggag ttacaaaaag attgtgctag attttttaag atgtctgcta 1440
agacggcggtt ggcagctgct gaaagacttt ataacctagg gtatttgtcg taccctagaa 1500
ctgaaactga caggtttgcc aaagaaaccg atttcaagag cttactagag gtgcacaaac 1560
aagatccgcg atgggggaagc tataacaaca agcttttgaa cgaagggttc gaaactcctc 1620
gaagcgggttc tcatgatgat aaggcgcac cccaatcca tcctatcaaa tatgtttctt 1680
tggaaccctt aaacaccctc gatgaaaaga aagtgtatga atacgttgtg cgacgcttta 1740
ttgcctgttg ctccaaagat gctgttggtt cgcaaaccgt ggtgacttta aaatggggag 1800
atgaattctt caccgcaagt ggattaatgg tgcataaaaa aaattatttg gaagtgtata 1860
cttacaaaaa atggggaagc tctaaacaac taccgaaatt tacagaggga gaacagggtc 1920
agttgtcgag tggaatattg aaagacggta aaacaagtcc acccaatcat atgaccgagc 1980
ccgagctaatt tgcattgatg gatgccaacg gtattggaac cgatgctact atcgctgaac 2040
atattaacaa aatagagact aggcactata ttaataaatt gaaaaagggg aaaaatgaat 2100
atattcttcc tactccttta ggaatggggc ttatagaagg ccttgaaaaa atggaatttg 2160
aagatgtatc actatcgaaa ccatttttgc ggaagtcggt ggaacgatca cttgaggaca 2220
tagcaaccgg gtcccggcca aaagtggatg ttttgaatac aacaataggc gtatatgttg 2280
acgcttatag tgtttgttct catcagatac ttgttttgtg caatgaatgt aggagaatta 2340
tacttggaag tagcagtaac aacaacaaca acaataataa taatacgtaa 2390

```

<210> 402

<211> 629

<212> PRT

<213> Candida albicans

<400> 402

```

Met Arg Ile Leu Cys Val Ala Glu Lys Pro Ser Ile Ser Lys Glu Val
  1             5             10             15

```

```

Ala Asn Ile Leu Gly Gly Gly Arg Lys Lys Val Arg Asn Ser Arg Glu
          20             25             30

```

```

Lys Phe Ile Lys Asn Tyr Asp Phe Thr Phe Thr Phe Asn Ser Glu Asp
          35             40             45

```

```

Gly Pro Cys Gln Val Thr Met Thr Ser Val Ala Gly His Ile Thr Gly
          50             55             60

```

```

Leu Asp Phe Gly Ser Ala Phe Ser Trp Gly Asn Cys Val Pro Gly Arg
          65             70             75             80

```

```

Leu Phe Glu Ala Asp Ile Lys Thr Ile Ile Thr Lys Lys Ser Ile Tyr
          85             90             95

```

```

Glu Asn Ile Ala Glu Glu Ala Arg Asn Ala Asp Lys Leu Met Ile Trp
          100             105             110

```

```

Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile Gly Phe Glu Ile Met Asn
          115             120             125

```

```

Ala Ala Arg Lys Tyr Asn Arg Asn Leu Gly Leu Asn Asn Ile Trp Arg
          130             135             140

```

```

Ala Arg Phe Ser His Leu Glu Arg Asn His Ile Ile Arg Ala Ala Lys
          145             150             155             160

```

```

Asn Pro Val Asn Leu Asp Met Ser Ala Val Ser Ala Val Ser Cys Arg

```


165					170					175					
Met	Glu	Ile	Asp	Leu	Arg	Val	Gly	Thr	Ser	Phe	Thr	Arg	Leu	Leu	Thr
			180					185					190		
Asp	Gln	Leu	Arg	Gln	Lys	Gly	Ile	Ile	Glu	Lys	Asn	Glu	Leu	Ala	Ser
		195					200					205			
Tyr	Gly	Thr	Cys	Gln	Phe	Pro	Thr	Leu	Gly	Phe	Val	Val	Asp	Arg	Tyr
	210					215					220				
Lys	Arg	Val	Lys	Ser	Phe	Thr	Pro	Glu	Pro	Phe	Trp	Tyr	Ile	Glu	Ile
225						230					235				240
Glu	Thr	Arg	Lys	Glu	Asn	Lys	Lys	Thr	Ile	Phe	Asn	Trp	Val	Arg	Gly
				245					250					255	
His	Phe	Phe	Asp	Lys	Met	Tyr	Val	Val	Met	Leu	Tyr	Asp	Arg	Cys	Cys
			260					265					270		
Lys	Ser	Gly	Glu	Phe	Gly	Thr	Ile	Ser	Lys	Ile	Glu	Ser	Lys	Arg	Lys
		275					280					285			
Pro	Asn	Phe	Arg	Pro	Phe	Pro	Leu	Thr	Thr	Val	Glu	Leu	Gln	Lys	Asp
	290					295					300				
Cys	Ala	Arg	Phe	Phe	Lys	Met	Ser	Ala	Lys	Thr	Ala	Leu	Ala	Ala	Ala
305						310					315				320
Glu	Arg	Leu	Tyr	Asn	Leu	Gly	Tyr	Leu	Ser	Tyr	Pro	Arg	Thr	Glu	Thr
				325					330					335	
Asp	Arg	Phe	Ala	Lys	Glu	Thr	Asp	Phe	Lys	Ser	Leu	Leu	Glu	Val	His
			340					345					350		
Lys	Gln	Asp	Pro	Arg	Trp	Gly	Ser	Tyr	Thr	Thr	Lys	Leu	Leu	Asn	Glu
		355					360					365			
Gly	Phe	Glu	Thr	Pro	Arg	Ser	Gly	Ser	His	Asp	Asp	Lys	Ala	His	Pro
	370					375					380				
Pro	Ile	His	Pro	Ile	Lys	Tyr	Val	Ser	Leu	Asp	Thr	Leu	Asn	Thr	Leu
385						390					395				400
Asp	Glu	Lys	Lys	Val	Tyr	Glu	Tyr	Val	Val	Arg	Arg	Phe	Ile	Ala	Cys
				405					410					415	
Cys	Ser	Lys	Asp	Ala	Val	Gly	Thr	Gln	Thr	Val	Val	Thr	Leu	Lys	Trp
			420					425					430		
Gly	Asp	Glu	Phe	Phe	Thr	Ala	Ser	Gly	Leu	Met	Val	His	Glu	Lys	Asn
		435					440					445			
Tyr	Leu	Glu	Val	Tyr	Thr	Tyr	Lys	Lys	Trp	Glu	Ser	Ser	Lys	Gln	Leu
	450					455					460				
Pro	Lys	Phe	Thr	Glu	Gly	Glu	Gln	Val	Lys	Leu	Ser	Ser	Gly	Ile	Leu

414

465 470 475 480
 Lys Asp Gly Lys Thr Ser Pro Pro Asn His Met Thr Glu Pro Glu Leu
 485 490 495
 Ile Ala Leu Met Asp Ala Asn Gly Ile Gly Thr Asp Ala Thr Ile Ala
 500 505 510
 Glu His Ile Asn Lys Ile Glu Thr Arg His Tyr Ile Asn Lys Leu Lys
 515 520 525
 Lys Gly Lys Asn Glu Tyr Ile Leu Pro Thr Pro Leu Gly Met Gly Leu
 530 535 540
 Ile Glu Gly Leu Glu Lys Met Glu Phe Glu Asp Val Ser Leu Ser Lys
 545 550 555 560
 Pro Phe Leu Arg Lys Ser Leu Glu Arg Ser Leu Glu Asp Ile Ala Thr
 565 570 575
 Gly Ser Arg Pro Lys Val Asp Val Leu Asn Thr Thr Ile Gly Val Tyr
 580 585 590
 Val Asp Ala Tyr Ser Val Cys Ser His Gln Ile Leu Val Leu Cys Asn
 595 600 605
 Glu Cys Arg Arg Ile Ile Leu Gly Asn Ser Ser Asn Asn Asn Asn Asn
 610 615 620
 Asn Asn Asn Asn Thr
 625

<210> 403
 <211> 3098
 <212> DNA
 <213> Candida albicans

<400> 403
 atatataaaa ttatggctta gtgcccttta ttaactaaat tagaggttac attaatacaa 60
 ctttaacaaac aaggaaacta acatccacgt atagggcttc ttatattaat atacctaatt 120
 caacctgatt atattgcctt atatacagct tgtaaaaaaa cacataagaa agtttacatc 180
 tcaagatgaa ttatccccct attgtaaaaa gtacatcgcc taatgataga catcatagag 240
 tactggcgac tccttacatg atggtaacga caacaactac aacaaaaaaa aaacattatc 300
 ttgacgggat aattagtagt gtgcgagagg cacacgataa gatttatcag tttccttttc 360
 tcggttgacc ttaactgtgt tttgtataga ctttattttt tttgtttttg accacacca 420
 ctttttaata tcacaagata ttttaactgat tatagaaaac aacaacaata acccaaatac 480
 gttaaccact tttattacat atgatagaca atataatcaa taatttgcaa atcactactac 540
 agcaaaatga tgataatttt acatccccctc acgacgatgt gatatatoga ccacattctg 600
 ctctgttagc acgatatcaa gtaataattg catctacatt gggactcact gccctattac 660
 tattttctat cttacgatta aaatatccca aaatatatgt ggcaaaacttt aatcatttga 720
 atttcagtct acattcgacc tcaagaagga atttacctga attgccttca aattcattat 780
 ttggttgagt tcctacagtt tacaaaatta ctgagcaaga aattttggaa catgctggat 840
 tagatgcagt tgtgtttttg gaatttttta aaatgtgcat tcgaataata agcatatgtt 900
 tagtatttgc cattattatc atatctccta tcagatacaa gtttacaggg agagtagatg 960
 aagattatcc cgacgatgat agtgacaacg atgacgatga tggaagtaat aataatggta 1020

```

ccacaataat taagcatata gtgtcagctg gaattctggt ggcaagtaaa aataacgatg 1080
gagaacagta tcaacaattt ctttggttat acactatttt cacctatgta tttacatttg 1140
ttactgttta ctttctattc aaacaaacca ataggattat ttctatgcgt cagaagtatc 1200
ttggatcgca aaattcagtc accgatagaa cggtaaaaat atctgggata ccaggatcat 1260
tacgagatga agtggcactc gcacggcaca ttgaccgttt gaatattggt gaagtggatt 1320
ctgtgttgat tgtcaaggag tggcaaaatc taaacaaact attcaaaaga aggagaagaa 1380
tagttcgaaa attagaggaa agttgggttg aatattttga aaaaaatggg ataaccaata 1440
agagcgattt gatatcggtg catccccaag ttggcgaaact gtatcgtttt tccaatagggt 1500
atactgatga tgcagaagaa tcaccagact ggggatctca aaattcgaac tctgcacaag 1560
cttcaataat agatcaagac tcagaatctg ttgaaggaga ttcttctgac actttgaatc 1620
gcttggtgaa tgatgaactg agaacaagac caagtcttcg gaaagggttg ttcggattgt 1680
ttggacctaa aatgatttca ataaactact acaccgataa attggagggtc atagataaag 1740
agattaccag ggccagaact agagaatatc ccgccacttc gactgcattt ctactatga 1800
aaaccgtggc tgaagcacaa atgttggcac aggcagctct ggatccaaaa gtcaatcatc 1860
ttatcaccaa cttggccctt gctcctcatg atatccgatg ggataatttg tcatctaacta 1920
gacaagacag aaatacaaaag atccttgctg tcacgatatt tatttggtata atgagtttgt 1980
tgttgggttta tccagtcaga tttatggcta gttttttaa cactaaaagc atttctaaaa 2040
tatggccatc attggggaaa gctattgaat cgcataaatg ggccgaaact ttgattactg 2100
gattattgcc aacttattta tttacaattt taaatattgt gattccgttt ttttatgtat 2160
ggatttctga aaagcaaggt tatttatctc atagtgatga agagttgtca tcggtatcca 2220
agaacttttt ctatatattt gtgaacttat ttttggtttt cacaactttt ggtaccgcct 2280
cttttggtga tacgaccaa attgcatttg atttagcaag atcactcaga gatttgtcaa 2340
tgttctatgt tgacttaata attctacaag gattgggtat attcccattc aaattattat 2400
tggtaggggaa cttacttcgc tttttagtga attcattatt taggtgcaag accccaagag 2460
attacttgaa tttgtacaaa ccgccagttt tcaatttttg tctacaatta ccacaacca 2520
tattgatatt tattattacg ttggtatact cggtaatgtc ttcgaagata ttaactgcag 2580
ggttactata ttttattatt gggtattttg tgagcaaata ccaattgctt tatgcttgtg 2640
ttcatcctcc acactcaacg ggcaaagttt ggccaataat tttccgaaga atcatattag 2700
ggttatttct ttttcaaate acaatgggtg gcacattagc attacaagat gcaatcacat 2760
gtgctacttt cttggcacca ttgccgtttt tgacacttta cttttggttg agtttccata 2820
aacaatatat tcccttgcca acattcattg ccttgagagc aattgaaagc aatgaaaata 2880
tcaaccctac tgatttggag caaatcattg aaaacaacaa taataaaact cttgacgaaa 2940
gaagggaatt gaactactaa tacgaatacc ccaatctagt taatgattta gacgggcca 3000
tgattgcatt ggatggtgaa gatgtattga tagttaatcg agatggtaca actgtacgga 3060
aaccacctca atatttcagt tcagaatggg actattaa 3098

```

<210> 404

<211> 865

<212> PRT

<213> Candida albicans

<400> 404

```

Met Ile Asp Asn Ile Ile Asn Asn Leu Gln Ile Ile Leu Gln Gln Asn
  1                      5                      10                      15

```

```

Asp Asp Asn Phe Thr Ser Pro His Asp Asp Val Ile Tyr Arg Pro His
      20                      25                      30

```

```

Ser Ala Arg Val Ala Arg Tyr Gln Val Ile Ile Ala Ser Thr Leu Gly
      35                      40                      45

```

```

Leu Thr Ala Leu Leu Leu Phe Ser Ile Leu Arg Leu Lys Tyr Pro Lys
      50                      55                      60

```

```

Ile Tyr Val Ala Asn Phe Asn His Leu Asn Phe Ser Leu His Ser Thr
      65                      70                      75                      80

```


Ser Leu Arg Lys Gly Trp Phe Gly Leu Phe Gly Pro Lys Val Asp Ser
 385 390 395 400
 Ile Asn Tyr Tyr Thr Asp Lys Leu Glu Val Ile Asp Lys Glu Ile Thr
 405 410 415
 Arg Ala Arg Thr Arg Glu Tyr Pro Ala Thr Ser Thr Ala Phe Leu Thr
 420 425 430
 Met Lys Thr Val Ala Glu Ala Gln Met Leu Ala Gln Ala Val Leu Asp
 435 440 445
 Pro Lys Val Asn His Leu Ile Thr Asn Leu Ala Pro Ala Pro His Asp
 450 455 460
 Ile Arg Trp Asp Asn Leu Ser Leu Thr Arg Gln Asp Arg Asn Thr Lys
 465 470 475 480
 Ile Leu Ala Val Thr Ile Phe Ile Gly Ile Met Ser Leu Leu Leu Val
 485 490 495
 Tyr Pro Val Arg Phe Met Ala Ser Phe Leu Asn Thr Lys Ser Ile Ser
 500 505 510
 Lys Ile Trp Pro Ser Leu Gly Lys Ala Ile Glu Ser His Lys Trp Ala
 515 520 525
 Glu Thr Leu Ile Thr Gly Leu Leu Pro Thr Tyr Leu Phe Thr Ile Leu
 530 535 540
 Asn Ile Val Ile Pro Phe Phe Tyr Val Trp Ile Ser Glu Lys Gln Gly
 545 550 555 560
 Tyr Leu Ser His Ser Asp Glu Glu Leu Ser Ser Val Ser Lys Asn Phe
 565 570 575
 Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Thr Phe Gly Thr
 580 585 590
 Ala Ser Phe Val Asp Thr Thr Lys Ile Ala Phe Asp Leu Ala Arg Ser
 595 600 605
 Leu Arg Asp Leu Ser Met Phe Tyr Val Asp Leu Ile Ile Leu Gln Gly
 610 615 620
 Leu Gly Ile Phe Pro Phe Lys Leu Leu Leu Val Gly Asn Leu Leu Arg
 625 630 635 640
 Phe Leu Val Asn Ser Leu Phe Arg Cys Lys Thr Pro Arg Asp Tyr Leu
 645 650 655
 Asn Leu Tyr Lys Pro Pro Val Phe Asn Phe Gly Leu Gln Leu Pro Gln
 660 665 670
 Pro Ile Leu Ile Phe Ile Ile Thr Leu Val Tyr Ser Val Met Ser Ser
 675 680 685

Thr Ile Asp Leu Ser Val Asn Leu Asn Lys Gln Leu Tyr Gln Asp Arg
 195 200 205
 Phe Glu Trp Asp Met Asn Gln Asn Glu Val Thr Pro Glu Ile Phe Ala
 210 215 220
 Glu Ile Val Val Ala Asp Leu Gly Leu Ser Leu Glu Phe Lys Asn Ala
 225 230 235 240
 Ile Ser His Ala Leu His Glu Ile Ile Ile Arg Val Lys Lys Glu Val
 245 250 255
 Ile Asp Gly Thr Phe Asp Asn Glu Met His Asn Leu His Leu Val Lys
 260 265 270
 Gly Ile Met Phe Glu Gln Gly Ile Arg Ile Phe Thr Glu Asn Ser Val
 275 280 285
 Gln Asn Gly Asn Asp Arg Trp Glu Pro Leu Val Glu Val Leu Thr Ser
 290 295 300
 Ser Glu Ile Glu Arg Arg Glu Asn Glu Arg Val Arg Asn Leu Arg Arg
 305 310 315 320
 Leu Lys Arg Glu Asn Met Arg Arg Asp Tyr Asp Asp His Ser Arg Arg
 325 330 335
 Arg Gln Ala Gly Lys Arg Arg Tyr Asp Glu Leu Glu Gly Ala Trp Val
 340 345 350

<210> 407

<211> 737

<212> DNA

<213> Candida albicans

<400> 407

aagaaaagta tagtcaaatt gttatacaag ctaaggagcc ataaactttc tttggacatg 60
 ctaatatcgc tcttgaccat tgtttactat attcaacaaa acgaattcaa caaggcaaac 120
 gaaagctaca tgaaactaag tatcggcaac gtctgttggc caattggggg ggtcaatgta 180
 ggtattcatg caagaagtgc agcactgaaa ataaccgggtg cctctaacgt cagtaacata 240
 atgctaagcg agtctacacg aagatggatt ataagtataa agaggttgat tagttttaaa 300
 gagagagtat ataataatgc acgtgattag tttagtaatt ttttgcgagt tagggctata 360
 gccctaagac attcacacaa ctaacaaaaa ggaagttctc acgcacataa cgtgtaaccc 420
 acataaagaa agaaaaaaaa atttctcttg aaaaaattca catcacgctt taaccacttc 480
 aacctataac aactccaacc atggctagag aaatcaagga tatcaaagaa ttcgtcgaat 540
 tggctagaag atcagacatc aaatctgcta ttgtcaaagt taacgccaag gtcaatgcta 600
 acggtaaaaa attcaaacaa accaaattca aggtcagagg ttcaagatac caatacactt 660
 tagttgtcaa cgatgcttct aaagctaaaa aattacaaca atctttacca ccaaccttaa 720
 aaatcaccaa cttgtaa 737


```
<210> 410
<211> 127
<212> PRT
```

<400> 410

Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Ala Glu
115 120 125

<210> 411

<211> 1631

<212> DNA

<213> Candida albicans

<400> 411

tctcatcttttc	gaaatctttcc	ctcttggaag	cgaccaagag	ttggatttcgg	tgcccttgac	60
tagcacaact	ttgttcaa	ctttattgaa	taatgcaaca	ccacgaaccg	gtatggtcga	120
tttatatttt	ccgaatttag	ataatgcttc	ctgtgggtca	ccccatttcc	aaataagcgg	180
gcattttctct	aaaatctttg	tactgaacgt	cttcatcttc	atgcttttgca	aatcggggatt	240
caactgacga	acaaagtcag	cataaaacca	ttgtgctttcc	tcaattctgaa	acattattct	300
ttcaatggaa	gataaatctc	cttcgggaac	attcaccaca	aatctaacta	acaaattctc	360
caacaccgca	tctagagttt	gattagctaa	accattgcgt	aattggatcg	acatatcttg	420
ttattttcta	tgattaactc	ttcttttttc	ttcttttttc	actgaatatt	cgtaattaaa	480
attgattcaa	aattgtattg	atgtttgtat	actggataaa	caacttgtgt	gagatcattc	540
aatgtatttg	ctggcgagga	aggaggcaag	gacgaacttt	ttttccttca	tacttttttt	600
tttctctctc	tcttttcttt	cagtcacatt	gtctgagtg	taaaggctgg	cttttctgtg	660
ctgaaccttg	tggactggta	aacgcacgac	atagagtaat	atttggagaa	accaaagaa	720
ttttgaaaaa	ccgtggtttg	aattcgacca	cagattgggt	ggacgacaaa	atgcaaagt	780
tattcatccg	gactttttgt	acctcaagaa	tagagttcca	gcggtaccag	ccgcgttttg	840
ttaataccat	taagaaacg	gtcaaactcg	cacaagaaaa	gtcgtacagt	attactagac	900
cattgggggt	gtcaaaacca	gttttggttaa	atcataaatt	gtcagacaca	tactcattgt	960
ccaatatata	cgaggagttg	tttgggtcaaa	aatccaaaga	agaagacag	aaacaactag	1020
actacgattt	gaaacactcg	ccaatttatg	aagtcaagtc	atttgagaat	acaaagggga	1080
aaatattttac	tctctctgtt	tctgtacttc	gacaagacaa	atctttgtat	ttcccgatt	1140
ttatagcgaa	aacattggca	ggtaatcaga	gaagtttgta	cgactcatta	gacaatagat	1200
taagcatagt	caaatgtgtt	tcttctgttg	ctggtgagca	gtgtaccctg	tctgtacttta	1260
aqgttqaaaa	caaagattac	tattcccagg	attatgatac	ctttgtggag	gaatatcccc	1320

```

ataccagat acttgatgtg aatatgccgc aaagttggat caaggggttt gtgacaaact 1380
tgagcacagg aaatttaaga aagactttga agccagctct gagatacgag aattatttca 1440
tcttgcttg ccacataatg tcagcggaaa ttagagaaca gttgtactgt gataatcaat 1500
gttccgggta tatttatatt gttgattcga tggggaagat aagatgggcg acaagtgggt 1560
atgcaactcc tgaggatttg aaattgatgt ggaagggtgt gaaaggggtg caaagagaaa 1620
tgaccaagta a                                     1631

```

<210> 412

<211> 376

<212> PRT

<213> Candida albicans

<400> 412

```

Met Phe Val Tyr Trp Ile Asn Asn Leu Cys Glu Ile Ile Gln Cys Ile
  1           5           10           15

Cys Trp Arg Arg Arg Arg Gln Gly Arg Thr Phe Phe Pro Ser Tyr Phe
          20           25           30

Phe Phe Ser Leu Ser Leu Phe Phe Gln Ser His Cys Ser Ser Val Lys
          35           40           45

Gly Trp Leu Phe Cys Ala Glu Pro Cys Gly Ser Val Asn Ala Arg His
          50           55           60

Arg Val Ile Phe Gly Glu Thr Lys Arg Ile Leu Lys Asn Arg Gly Leu
          65           70           75           80

Asn Ser Thr Thr Asp Trp Leu Asp Asp Lys Met Gln Ser Val Phe Ile
          85           90           95

Arg Thr Phe Ala Thr Ser Arg Ile Glu Phe Gln Arg Tyr Gln Pro Arg
          100          105          110

Phe Val Asn Thr Ile Lys Glu Thr Val Lys Ser Ala Gln Glu Lys Ser
          115          120          125

Tyr Ser Ile Thr Arg Pro Leu Gly Leu Ser Lys Pro Val Leu Leu Asn
          130          135          140

His Lys Leu Ser Asp Thr Tyr Ser Leu Ser Asn Ile Tyr Glu Glu Leu
          145          150          155          160

Phe Gly Gln Lys Ser Lys Glu Arg Arg Gln Lys Gln Leu Asp Tyr Asp
          165          170          175

Leu Lys His Ser Pro Ile Tyr Glu Val Lys Ser Phe Glu Asn Thr Lys
          180          185          190

Gly Lys Ile Phe Thr Pro Pro Val Ser Tyr Phe Arg Gln Asp Lys Ser
          195          200          205

Leu Tyr Phe Pro Asp Phe Ile Ala Lys Thr Leu Ala Gly Asn Gln Arg
          210          215          220

Ser Leu Tyr Asp Ser Leu Asp Asn Arg Leu Ser Ile Val Lys Leu Phe

```

<400> 413						
ccagtgcggtt	ttgtttgttt	ccacatcata	cacttcactg	aaactaaata	agttttgttta	60
catttttgaga	cttcaggtac	gacccagggg	tgcgacaaag	tttaggtagt	ttgtcgtctg	120
aatgtcgcaa	caaaataggg	ctgtagccct	agtcatgtga	tgtgaattaa	cataacaaga	180
agaattgctg	gtgcgcacaaa	agattatgtg	tattttatgt	gcgttggtat	cctgcacact	240
aaaattgagc	agtgtacaca	cacacatat	gggctgtatt	tttattcttg	ttttttctgt	300
gtctctcac	gtttaagctc	taagtgaatt	tgtgtgtgct	gtaatagtgt	gtgtgttcca	360
agtcccagct	ctcacagata	ctcacgcacg	cccatactac	tgaaaatttc	ctgactttct	420
gtatctaaaa	attttttact	aggaattttt	ttcttttaag	tttttactt	gtttcatata	480
atcaccaact	caagtacaac	atggctgtcg	gtaaaaacaa	gagattgtcc	aaaggaaaga	540
aaggattaaa	aaagaagggtc	gttgaccct	tcaccagaaa	agattgggtt	gacatcaaag	600
ctccaaccac	ttttgaaaaac	agaaatgttg	gtaaaaactt	gatcaacaga	tctaccggtt	660
taagaatgac	cgctgatggc	ttgaaaggta	gagttttcga	agtttgtttg	gccgacttac	720
aagggttcga	agaccactct	tacagaaaaa	tcaaatgtgag	agttgatgaa	gttcaaggta	780
aaaacttggt	gaccaacttc	catgggtttg	atttcacttc	tgacaaatta	agatcattgg	840
tcagaaaatg	gcaatcatta	gttgaagcta	atgtcactgt	taaaacttcc	gacgattacg	900
ttttgagagt	ttttgccatt	gctttcacca	aaagacaacc	aaaccaaata	aagaaaacta	960
cttacgctca	atcctctaaa	ttgagagaag	tcagaaaagaa	gatgatgtaa	attatgcaaa	1020
ggaagtttca	caactgtact	ttagctcaat	taactttccaa	attgattcca	gaagtcattg	1080
ggcgtgaaat	tgaaaaatcc	acccaaccca	ttttcccat	acaaaatgtc	cacatcagaa	1140
aagtcaaat	gttgaacaaa	ccaaaattcg	acttggggtc	attattgggt	ttgcacgggt	1200

425

aaggttcaac cgaagaaaaa ggtaagaaag tttcttctgg tttcaaagat gttgttttag 1260
aatctgttta a 1271

<210> 414

<211> 256

<212> PRT

<213> Candida albicans

<400> 414

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Leu
1 5 10 15

Lys Lys Lys Val Val Asp Pro Phe Thr Arg Lys Asp Trp Phe Asp Ile
20 25 30

Lys Ala Pro Thr Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Ile
35 40 45

Asn Arg Ser Thr Gly Leu Lys Asn Ala Ala Asp Gly Leu Lys Gly Arg
50 55 60

Val Phe Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser
65 70 75 80

Tyr Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu
85 90 95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Ser Asp Lys Leu Arg Ser
100 105 110

Leu Val Arg Lys Trp Gln Ser Leu Val Glu Ala Asn Val Thr Val Lys
115 120 125

Thr Ser Asp Asp Tyr Val Leu Arg Val Phe Ala Ile Ala Phe Thr Lys
130 135 140

Arg Gln Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Gln Ser Ser Lys
145 150 155 160

Leu Arg Glu Val Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Val
165 170 175

Ser Asn Cys Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val
180 185 190

Ile Gly Arg Glu Ile Glu Lys Ser Thr Gln Thr Ile Phe Pro Leu Gln
195 200 205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp
210 215 220

Leu Gly Ser Leu Leu Ala Leu His Gly Glu Gly Ser Thr Glu Glu Lys
225 230 235 240

Gly Lys Lys Val Ser Ser Gly Phe Lys Asp Val Val Leu Glu Ser Val
245 250 255

<210> 415
<211> 1517
<212> DNA
<213> *Candida albicans*

<400> 415
tgatatggat ttttcaaaac taagaaacaa taccaactac aacaacaaga aacataagtg 60
tttgcttaat tcaatgacct cgagtcatat tcccacgttt taagtatgag tgttttacga 120
agttgtggat cctattttta ataaaacaat aatagtaata aaaaaaaaaa ccttctttgc 180
ttttcgagaa tttgtaacac attgtttctt tcttcccaca gcaaccaaatt tttattttat 240
tttttctttt gggacttacc cacagttgct caattatgta taacaagggg agaaactctg 300
tgggattccc tccttaaaaa tatagcaatc ctttttcttc acaacgattg ctatatgacc 360
ccccccctaa gcattcattg cttttatata tatttaataa tgtatttctc ttgttcagga 420
taattatcac tatttgtgac gtttaatttt tacatttctt cttcttcttc ttcctatttc 480
aacattaaag aacatttaat atgtatttcc caatcattgt atgggtatat gtatctatca 540
cttttgtggg tgccaattat gggtttgatc aatggacaaa tgatgattta aaacaatttt 600
taaaagaacg taaagttgca ttcaatgatg ccttgagaaa tccaaaatta attagtttgg 660
ctaatagaag agctaagaaa ttagaaaaag gttacaagaa agttactgaa gaattaaata 720
acaatttgaa tcctccagat gattcattaa atgattattt gaattttgat tacttatttg 780
ggaaaagaaa agaaaattat tcaattaaag aatggatttt tgaaagttgg ccagtaacca 840
gtttgcaaac ttttttaact caaaaataata tccaatatag tgcaaaggat accaaagatg 900
atttaataca taaggttaaa gatcaatttg attctatttc taagaaaaat catgggtcta 960
gtttttatcc tggcaattgg ttatatgaat cttgggcaga aaatgatttg aaagatttgg 1020
tgaaatctta tggcattgaa tttaatccta gttcaacaaa ggatcaattg gttgaaaaat 1080
taaaagaatt tagttatcaa gccactcatt caattagaga ttccaaagaa tctttatttg 1140
attcattgga tttatttgat aaaaccattt ttgataaaaa aggtcaaatt gaagatgaat 1200
ttttccaaac ttggtcatat tctcaattac tggaatggct ttatttcat ggatttattg 1260
acactaaacc aggaatttac gttgaagatt tggataagga aaaattagtc aagattgccc 1320
aaagttataa gaaatgtttg ttgagtgaac ttcatacttg gttggcaaac actgaaaaga 1380
agtctcaacc ttggatcaca aaggagagaac aaaagtctca gaaaaagaag ggtagtaatt 1440
tgattaatga tacattcttt gttggtatta ataattggct caaggataaa ttgcgtgaat 1500
tgggcaatct tgactaa 1517

<210> 416
<211> 338
<212> PRT
<213> *Candida albicans*

<400> 416
Met Tyr Phe Pro Ile Ile Val Trp Leu Tyr Val Ser Ile Thr Phe Val
1 5 10 15
Val Ala Asn Tyr Gly Phe Asp Gln Trp Thr Asn Asp Asp Leu Lys Gln
20 25 30
Phe Leu Lys Glu Arg Lys Val Ala Phe Asn Asp Ala Leu Glu Asn Pro
35 40 45
Lys Leu Ile Ser Leu Ala Asn Glu Glu Ala Lys Lys Leu Glu Lys Gly
50 55 60

<210> 417
 <211> 2243
 <212> DNA
 <213> *Candida albicans*

<400> 417
 atgagttcat agatgatctg tttcactttc aaataacgtg tcaacaaaaa taaagttaga 60
 gcatagatatt tgccgccact tgtacagatg gatagaattg aatgcaaatt ctgcataaag 120
 attaaagtga aaaacaattt ccgaaaaaag aagaaaatcg aacacattag aaaaagaaac 180
 gaacaaaaga aaaaaaattt caaattgtag ttgcatgtat ataaaataat ataaaagata 240
 tatcaccagc acaactgatt actttttatt tatatcacct gtcaacaaca aatttccaaa 300
 taaatacaac tcagaaaaaa cacttactat cttttcttag tttggtttct ataattttat 360
 taaacattct tgcccttcat ccttgattat catattagat cttatcttta atttgtttga 420
 aaaaataata ccaataatct tcccattaga acttacaaca caacaacaaa aaaaccatt 480
 ctaaactact attctccatt atgaaaattt tcagattatt ttcactacta atcgtacaat 540
 ttatcataaa taccactggt gcagtatcac ctgtgtcagc agttttacca aaactgagtt 600
 tcagtccatt tgattcacca gaattttgtt cacagatcat aactcccact tgtaatacaa 660
 ctttcaccta cattgatgaa ttgaataaag atattcgtcc ctacttgctg gaatttagca 720
 agaccctgta tttccgttat tttaaagtca atttagataa acaatgtcgt ttttggaatg 780
 ctcaacattt ttgtgctagt gaaaactgtg ctggtgaaat attggaagat ttcaattgga 840
 gtcaagtcac caatgaaagt ttgaaacctt caggattagg taagatttca ttacctgaca 900
 aatcatcaat tgataattcc attgaaaccg aagaagttca aacttgtgaa gatttagatt 960
 atagtgaat agatgatgac catcattgtg tttatgtcaa cttggtaaat aaccagaaa 1020
 gatttactgg gtatggtggt aatcaaagtt ttgatgtttg gaaggctatt tacctggaaa 1080
 attgtttccc taataactaat ccaatgtcag tgacaaatga tgccgacaat ggtggtgaac 1140
 aatgtatcga aaagaacttg ttttatcgtg ttggttagtg tatgcatgct tcaattgcag 1200
 tacatttatc aagagaatat ttgaattctg aaactggtga attttatect aatttaaagg 1260
 tgtttatgga aagagtaggt atgcataatg acagattatc taatatttat ttcaattatg 1320
 ccttagtgtc ccaagctata gttaaattga gtgaaatttt accattgaga gagttcattc 1380
 aactggggta tgatgacatt actccagctc aaaagcaaca tttattggct aataatgatg 1440
 tcgaatcagt cgaagtttat gatcgtttgt tgtttagatga cattattcct agtttggaag 1500
 caaatgttgt gtttaatact tccaacttgt ttgataatag caatttgagg gatgaattta 1560
 gatcaagatt tagaaacatt tctgccatta tggatttgtt tggttgtgat agatgcagaa 1620
 tgtgggggaa aatccaaacc attggttatg gtaccgctct caagatttta tttgaagatg 1680
 acaactatga taatcacaat ttgaaattta gaagaattga aattggtgcc ttgattaata 1740
 cttttgatcg tttatctaaa tctattgaaa gtattaatat gtttaaagaa atgtatttgc 1800
 aacaccttaa agatattgct gaaggattaa cccaacctgg tgtttacgac aaaatacaaa 1860
 acaacaaacc aggtaacgga tttgccttcc catttgttag tccattacct cagaaaaaac 1920
 ctgaccaaac caacaccccc aaaaatcaac aacaaaaaca acctcaagaa actgacaaaa 1980
 aaagacttac attagaagaa attgcccaca caaaacctga agatcgaact tttattgaag 2040
 acttcagatt atcctttgat gaagtttggc aagcattaag atttgtttta actagttatc 2100
 aaagattccc agccgtattg agtagattca cattggttca attgaatgaa tgggtggaata 2160
 aattgcttgg taaaccaaca gtttatgatt accaaagttc ttttgatggt gatgccctac 2220
 aatacagtca agtccttgga taa 2243

<210> 418
 <211> 580
 <212> PRT
 <213> *Candida albicans*

<400> 418
 Met Lys Ile Phe Arg Leu Phe Ser Leu Leu Ile Val Gln Phe Ile Ile
 1 5 10 15
 Asn Thr Thr Val Ala Val Ser Pro Val Ser Ala Val Leu Pro Lys Ser
 20 25 30

[illegible]

```

<400> 422
Met Ile Ser Arg Ile Gly Leu Leu Lys Arg Pro Thr Val Ser Thr Leu
  1             5             10             15

Asn Asn Tyr Val Lys Leu Gln Ser Thr Leu Ala Leu Lys Arg Tyr Thr
      20             25             30

Ser Thr Val Pro Ala Thr Ser Asn Gln Glu Gln Glu Ile Leu Val Ala
      35             40             45

Gln Arg Lys Asn Arg Pro Thr Ser Pro His Leu Gln Ile Tyr Glu Pro
      50             55             60

Gln Leu Thr Trp Ile Met Ser Ser Phe His Arg Ile Thr Gly Val Ala
      65             70             75             80

Met Ala Gly Ala Phe Tyr Ala Leu Thr Cys Gly Phe Ala Ala Thr Ser
      85             90             95

Ile Leu Asn Ile Pro Phe Asp Thr Thr Thr Leu Val Ser Ala Phe Thr
      100             105             110

Thr Leu Pro Thr Phe Ala Gln Tyr Gly Ile Lys Ala Ile Cys Ala Tyr

```

<400> 424
Met Leu Ile Pro Lys Glu Asp Arg Lys Lys Ile His Gln Tyr Leu Phe
1 5 10 15
Gln Glu Gly Val Val Val Ala Lys Lys Asp Phe Asn Gln Pro Lys His
20 25 30
Asp Glu Ile Asp Thr Arg Asn Leu Phe Val Ile Lys Ala Leu Gln Ser

35					40					45						
Leu	Thr	Ser	Lys	Gly	Tyr	Val	Lys	Thr	Gln	Phe	Ser	Trp	Gln	Tyr	Tyr	
50					55					60						
Tyr	Tyr	Thr	Leu	Thr	Asp	Glu	Gly	Val	Glu	Phe	Leu	Arg	Thr	Glu	Leu	
65					70					75					80	
Asn	Ile	Pro	Glu	Gly	Ile	Leu	Pro	Leu	Thr	Arg	Leu	Lys	Asn	Ala	Pro	
85					90					95						
Ala	Glu	Arg	Pro	Arg	Pro	Ser	Arg	Gly	Gly	Pro	Arg	Arg	Gly	Gly	Tyr	
100					105					110						
Arg	Gly	Arg	Ala	Arg	Asp											
115																

```
<210> 425
<211> 2840
<212> DNA
<213> Candida albicans
```

<400>	425					
tgttggggagt	attctggcac	aacaaatact	tacttttagg	ttactaacat	tatttttctt	60
cagctaacta	attatctagt	ttatatctat	atccattatt	gttgaaatca	ctatcgtgag	120
gtaaataaca	actacagagt	tgtcacagta	tccaaaaaaa	actttgtacc	tatcaataca	180
ttttaagcaa	taggtcattt	attgctgtaa	tcaagtgtta	ccagtatctc	tagttaatgt	240
tgacatttata	cctaaaacat	gaactatata	aacttttaat	gcccctaata	acgtgatata	300
gcagatggga	atttgctgat	cttgcttctt	tgcacgtaca	cggcacatgt	acacgacttt	360
tttttctaaa	tatttttttt	tttgttgttg	ttgttattaa	acaatattat	tttcatatat	420
ataattgctt	agtttacttg	cttcttacac	cctttgcata	tttttttttt	ttcctttttc	480
tgccaacttg	atcaaattcg	atgctacatc	ctaataatte	agtagtcgat	atgtctagca	540
ctggaaacat	gaatgaaaaa	acagatgtct	caccgaaaca	gcagacgaaa	aagaaaaaat	600
caaaacagaa	ttcaaccaa	accgattttt	ttgtctgcag	attggctagt	gcggttgacg	660
atatagaaag	cagtgatagt	gatgaaacgt	ttatatatga	gaataatgat	actgaaactg	720
atgataatgc	tagtaatat	aacaataaca	acaataacag	caccaataac	attatcaatt	780
tagataatgc	tagtgttaac	ggaagtatga	ttgcttcata	caatgcaatg	gtgactgggt	840
ctcccggaac	atcgatagcg	ttaggatcgg	gccttcgatc	gccatccata	ctagaggggg	900
aacagcttca	atatttttcat	gaccacagtga	ggcaacaaca	gttcaaactt	ccttctacca	960
aggctccgtc	aattttccaac	tccatcagca	gttcaaataa	tatagattca	atactaaaac	1020
gacctgtaca	tctacgtgag	gcatacaacgt	attcagtgaa	tgataatgac	caccgaaatc	1080
ttgtgctacc	aaactcaact	gaaaggttta	ctgcttcacc	ttcgaacaat	attggtaatg	1140
aaaatatacc	tcaataccag	aaaactagta	gtggtgcccc	ctcaatcaat	gaaggatata	1200
atgatgatac	attttcatat	aatgaagttg	aggataattt	aattgatgaa	gattccacgg	1260
acgatgggga	tttgacaaaa	aataccatta	ctaataacaa	caatccacca	accacgtcga	1320
gccaacagca	accacaaccg	caaccacagc	cgcaaccaca	gcaaccacaa	ctacatactc	1380
tgtctcctct	aaatcagata	caagcagcga	catcagcaac	accttctgtg	tccactaaaa	1440
acgcgtctaa	agaaaatttac	aaaacctcat	ccacttcttc	aaaattaaga	tcaactacat	1500
caaaactttt	cgataaaaaa	gggtcacaa	caagaagata	cagtaccatt	cctgatgata	1560
ttgacattga	agatttcgat	gatgagctta	tatactatga	caacacagct	aggttcccag	1620
cgaacgaatc	aacttcatta	ctaaatcaaa	accaaagaat	ccccatttat	agatcactta	1680
atttgaattt	ccctcaggtg	aagcgccaaa	gcaagcgcta	tttgtcaact	ggccaacctt	1740
tagagagttc	tgatcgtggc	tctaacaaga	atggactatga	taattggaac	aacagtgatc	1800
acaatattaa	ttctctcttg	actgctaata	ataataataa	taacgtcaat	cacaacgatc	1860
atggtgataa	caaaaagagt	aataccaaca	acaacaacat	tgctaataat	agagcatttc	1920

<400>	426																
Met	Leu	His	Pro	Asn	Asn	Ser	Val	Val	Asp	Met	Ser	Ser	Thr	Gly	Asn		
1				5					10					15			
Met	Asn	Glu	Asn	Thr	Asp	Ala	Pro	Pro	Lys	Gln	Gln	Thr	Lys	Lys	Lys		
			20					25					30				
Ile	Ser	Lys	Gln	Asn	Ser	Thr	Lys	Thr	Asp	Phe	Phe	Ala	Ala	Arg	Leu		
		35		40			40					45					
Ala	Ser	Ala	Val	Asp	Asp	Ile	Glu	Ser	Ser	Asp	Ser	Asp	Glu	Thr	Phe		
50						55					60						
Ile	Tyr	Glu	Asn	Asn	Asp	Thr	Glu	Leu	Asp	Asp	Asn	Ala	Ser	Asn	Ile		
65					70					75					80		
Asn	Asn	Asn	Asn	Asn	Asn	Ser	Thr	Asn	Asn	Ile	Ile	Asn	Leu	Asp	Asn		
				85					90					95			
Ala	Ser	Val	Asn	Gly	Ser	Met	Ile	Ala	Ser	Ser	Asn	Ala	Met	Val	Thr		
			100					105					110				
Gly	Pro	Pro	Gly	Thr	Ser	Ile	Ala	Leu	Gly	Ser	Gly	Leu	Arg	Ser	Pro		
		115					120					125					
Ser	Ile	Leu	Glu	Gly	Glu	Gln	Leu	Gln	Tyr	Phe	His	Asp	Pro	Val	Arg		
	130					135					140						
Gln	Gln	Gln	Phe	Lys	Leu	Pro	Ser	Thr	Lys	Ala	Pro	Ser	Ile	Ser	Asn		
145					150					155					160		
Ser	Ile	Ser	Ser	Ser	Asn	Asn	Ile	Asp	Ser	Ile	Leu	Lys	Arg	Pro	Val		
				165					170					175			

His Leu Arg Glu Ala Ser Thr Tyr Ser Val Asn Asp Asn Asp His Arg
 180 185 190
 Asn Leu Val Leu Pro Asn Ser Thr Glu Arg Phe Thr Ala Ser Pro Ser
 195 200 205
 Asn Asn Ile Gly Asn Glu Asn Ile Pro Gln Tyr Gln Lys Thr Ser Ser
 210 215 220
 Val Ala His Ser Ile Asn Glu Gly Tyr Asn Asp Asp Thr Phe Ser Tyr
 225 230 235 240
 Asn Glu Val Glu Asp Asn Leu Ile Asp Glu Asp Ser Thr Asp Asp Gly
 245 250 255
 Asp Leu Thr Lys Asn Thr Ile Thr Asn Asn Asn Asn Pro Pro Thr Thr
 260 265 270
 Ser Ser Gln Gln Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro Gln Gln
 275 280 285
 Pro Gln Leu His Thr Ser Ser Pro Leu Asn Gln Ile Gln Ala Ala Thr
 290 295 300
 Ser Ala Thr Pro Ser Val Ser Thr Lys Asn Ala Ser Lys Arg Asn Tyr
 305 310 315 320
 Lys Thr Ser Ser Thr Ser Ser Lys Leu Arg Ser Thr Thr Ser Lys Leu
 325 330 335
 Phe Asp Lys Lys Gly Ser Gln Pro Arg Arg Tyr Ser Thr Ile Pro Asp
 340 345 350
 Asp Ile Asp Ile Glu Asp Phe Asp Asp Glu Leu Ile Tyr Tyr Asp Asn
 355 360 365
 Thr Ala Arg Phe Pro Ala Asn Glu Ser Thr Ser Leu Leu Asn Gln Asn
 370 375 380
 Gln Arg Ile Pro His Tyr Arg Ser Leu Asn Leu Asn Phe Pro Gln Val
 385 390 395 400
 Lys Arg Gln Ser Lys Arg Tyr Leu Ser Thr Gly Gln Pro Leu Glu Ser
 405 410 415
 Ser Asp Arg Gly Ser Asn Lys Asp Gly Thr Asp Asn Gly Asn Asn Ser
 420 425 430
 Asp His Asn Ile Asn Ser Pro Leu Thr Ala Asn Asn Asn Asn Asn Asn
 435 440 445
 Val Asn His Asn Asp His Gly Asp Asn Lys Lys Ser Asn Thr Asn Asn
 450 455 460
 Asn Asn Ile Ala Asn Asn Arg Ala Phe Pro Phe Pro Tyr Gln Asp Gln
 465 470 475 480

Ser Lys Glu Ile Lys Leu Met Phe Pro Asn Ser Leu Lys Leu Asn Arg
 100 105 110
 Gly Asn Tyr Ile Ile Ser Asp Leu Val Ser Thr Cys Asn Arg Val Gln
 115 120 125
 Val Ser Asp Met Ile Leu Leu His Glu His Arg Gly Val Pro Ser Ser
 130 135 140
 Leu Thr Val Ser His Phe Pro His Gly Pro Thr Ala Ile Phe Thr Leu
 145 150 155 160
 His Asn Val Lys Leu Arg His Asp Leu Pro Asn Leu Gly Asn Val Ser
 165 170 175
 Glu Ser Tyr Pro His Leu Ile Phe Glu Asn Phe Gln Ser Asp Leu Gly
 180 185 190
 Lys Arg Val Val Lys Ile Leu Gln His Leu Phe Pro Pro Gly Val Lys
 195 200 205
 Lys Asp Ser Ser Arg Val Ile Thr Phe Val Asn Asn Asp Asp Tyr Ile
 210 215 220
 Ser Val Arg His His Val Tyr Val Lys Thr Lys Asp Ser Val Glu Leu
 225 230 235 240
 Ser Glu Ile Gly Pro Arg Phe Glu Met Arg Leu Tyr Glu Ile Arg Leu
 245 250 255
 Gly Leu Pro Asp Asn Lys Asp Ala Asp Val Glu Trp Gln Met Arg Arg
 260 265 270
 Phe Ile Arg Thr Ala Asn Arg Lys Asn Tyr Leu
 275 280

<210> 429

<211> 1061

<212> DNA

<213> Candida albicans

<400> 429

tccttttggt tttatttttg ctgtgttact ccagaaatgt gcataataat gataatagta 60
 atttgtgact aatatgagat gatcgtatgt ggggtgggtgg ggaggaaggg acccggaatt 120
 ctaggaacag gaaaaataaa aacgaataaa caaaaacccc ccaatcggca tgcacggaa 180
 ttctttcagc ccaattactt tatttttgcc cacttctttt ggattagggc aatagcccta 240
 aagctcgtgt tttagccctt tatatgcagt ctattttatt ttctctttt ttttttggct 300
 gttggtaaac tttttttttt ttgcgagggtg ttgaaaaaaa aatcattttt acagtttaca 360
 ttctctaac ctgcaaaaag ctctcgtttt tttgtagtga gagttactcg ttcaacaatag 420
 tatactttac aggggagttc ttttcttttg gaatagtcaa ccaacagcaa atagccaagg 480
 atcaagcttc atcattaatc atgtcctcta agatcttatc agaaaaccca actgaattag 540
 aattaaaagt tgcetcaagct ttcgttgatt tggaatctca agctgattta aaagctgaat 600
 tgagaccatt acaattcaaa tctatcaaag aaattgatgt taatggaggt aaaaaagctt 660
 tagctgtttt cgttccacca ccaagtttac aagcttacag aaaagttcaa actagattaa 720
 ctagagaatt agaaaaaaa ttcccagata gacatgttgt ctttttagct gaaagaagaa 780

<400>	436															
Met	Lys	Phe	Thr	Thr	Val	Ala	Thr	Val	Phe	Ala	Ile	Ser	Ser	Leu	Ala	
1				5					10					15		
Ala	Ala	Lys	Gly	Gly	Glu	Lys	Asp	His	Gly	Lys	Ala	Ser	Thr	Val	Thr	
			20					25					30			
Lys	Tyr	Val	Thr	Glu	Thr	Thr	His	Arg	Tyr	Gly	Arg	Phe	Asp	Lys	Thr	
		35					40					45				
Ser	Arg	Ser	Lys	Lys	Pro	Lys	Glu	Thr	Gly	Thr	His	Arg	Tyr	Gly	Lys	
	50					55					60					
Phe	Asn	Lys	Thr	Pro	Arg	Pro	Val	Thr	Thr	Thr	Val	Leu	Val	Lys	Glu	
65					70						75				80	
Ser	Asp	Leu	Pro	Lys	Lys	Arg	Asp	Ala	Val	Val	Ala	Arg	Asp	Ser	Lys	
				85					90					95		
Asn	Ala	Ser	Ser	Asn	Ser	Thr	Thr	Ser	Ser	Gly	Asn	Asn	Gly	Val	Ala	
			100					105					110			
Thr	Gly	Val	Ser	Leu	Gly	Leu	Ala	Gly	Val	Leu	Ala	Val	Gly	Ala	Ala	
		115					120					125				

```

<400> 438
Met Ser Ala Asn Asp Phe Tyr Ser Ser Gly Asp Gln Ser Asn Tyr Asp
  1                      5                10          15

Pro Lys Arg Ser Ser Asn Gln Gly Ser Ser Ser Ser Asn Asp Glu Gln
      20                25          30

Gln Asp Arg Gly Leu Leu Ser Thr Val Ala Gly Gly Val Ala Gly Gly
      35                40          45

Tyr Gly Gly His Lys Leu Gly Glu Lys Ala Gln His Gly Thr Leu Gly
  50                55                60

Thr Val Leu Gly Ala Ile Gly Gly Ala Ile Gly Ala Asn Lys Leu Glu
  65                70                75          80

Asp Ala Tyr Glu Asp Arg Lys Glu His Lys Lys His Glu Gln Gln Tyr
      85                90          95

Gly Gly Ser Gly Lys His Glu Gly Gly Arg His Glu Gly Gly Phe Gly

```

100 105 110
 Gly Gly Arg Pro Asp Asp Arg Tyr Glu Gly Asp Arg Arg Asn Asp Asn
 115 120 125
 Tyr Gly Gly Gly Tyr Asn Asp Arg Arg Asp Asp Gly Tyr Gly Gly Gly
 130 135 140
 Tyr Gly Gly Gly Arg Pro Asp Asp Arg Arg His Glu Gly Gly Phe Gly
 145 150 155 160
 Gly Gly Arg Pro Asp Asp Arg Phe Gly Gly Gly Arg Pro Asp Asp Arg
 165 170 175
 Phe Gly Gly Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Trp
 180 185 190

<210> 439
 <211> 1745
 <212> DNA
 <213> Candida albicans

<400> 439
 ttggtattga agacaccgaa gacttggtga aagatattga acaagcttta caaaaggctg 60
 cttctgtttg aggggatggt cattagcaat gtatataatt attgtatatt atgacaaaga 120
 aagaaaaaag aaaaccagaa aagtgggtta tacaggaata ttttaataga aatatcgctt 180
 atattgtgat aaaaaatttg aaagacaatc cgaatgtagt gcttggttta ttctgcttgg 240
 gaatactgta gtattagcat caattgagga aattccagat agctaacggt ttgcgatta 300
 cgaatttcgc aaccaaataa atatgtgaca aggaatacac tactgatcaa gggtattctt 360
 agtacaatgg aaaaaaaaaa aaagaagcaa acaaaaaaac gagaaattaa tgaacacgac 420
 ttcacttcta caacctactg ggaaaaaaa ggcagagagt tattgaaaaa ggatcatatc 480
 aagttcttat tgtatattat atgaagtttt ctgttttagt attacttgcc agttacttag 540
 ttgggtgtgaa ttctctgatt gttgatactt cagaggaatt aatttgtcca gatccagaaa 600
 accctttaga ttgttatcca aaattgtttg ttccaacaaa cgagtggcaa accattaaac 660
 cagggtcaaga tataccacct ggggttacacg ttagattaaa tatagatacg ttggaaaaag 720
 aggccaaagct aatgagtgtc gacgaaaaag acgagccagt tcaagaagta gttgttgggtg 780
 gcgaattgca ggatcattcg agggaagcca tcaactgagaa tctacaaaag ttgcatgagc 840
 tgaaacatcc tgaagtaaaa caggagcacg ctcatcgtag aaagggttagc caggagatt 900
 tgagtaattt tgacgcagct tgtctggaaa ttgagagttt caagccacat gagagtgatg 960
 tggaaagggt gcatttggca ctagatactt tagaggaatt aagtcattgat atcgaatttg 1020
 ggggtgaaat gacctcagac aaagccatat ttcagagttt tgtcaacatt gccaatgggtg 1080
 cttctgatcc aaaaataacc gaaaagggtat atcgtgtaat ggggtctagt ttgagaaata 1140
 atcctgaagc gattagtaat atcttgacca acttcgacaa gagctatgtg gataatttgt 1200
 ttgagcaatt agcgaatgaa aatgatgttc taaaaaagag gattttgggt ataattcaag 1260
 ctttagtcca aaatagccat ttgcaagac aatatttttc atttgaccac agttccgggt 1320
 taaatgattt aatagcgatt ttcccaaac ttggtccaaa ctcaaagtcc agggcaagta 1380
 acattttaga ggatttacaa ttgttcccag taacaaacga tagaagatca cttgaagatc 1440
 aagatcctga atcacaggtt tcaaaattta ttcagaattc ctttggttga aataaacttg 1500
 acgagaagaa ttccaagtct tattttgatc aactagtaaa ttgcatcag ctgaataaga 1560
 gtttgcgacc aagtgggtgac tttctcaatt ggttagctga agaagtggag tcgcgtaaaag 1620
 agaataaaaa aagagacgat tattcacaag aagacaaaga ctttgatgag tacatgttgc 1680
 gagcacgtca tgaagtattt ggcaatccaa tgggattaag aaaggcaatt gccgacgagt 1740
 tgtag 1745

448

<210> 440

<211> 414

<212> PRT

<213> Candida albicans

<400> 440

Met Lys Phe Ser Val Leu Val Leu Leu Ala Ser Tyr Leu Val Gly Val
 1 5 10 15

Asn Ser Ser Ile Val Asp Thr Ser Glu Glu Leu Ile Cys Pro Asp Pro
 20 25 30

Glu Asn Pro Leu Asp Cys Tyr Pro Lys Leu Phe Val Pro Thr Asn Glu
 35 40 45

Trp Gln Thr Ile Lys Pro Gly Gln Asp Ile Pro Pro Gly Leu His Val
 50 55 60

Arg Leu Asn Ile Asp Thr Leu Glu Lys Glu Ala Lys Leu Met Ser Ala
 65 70 75 80

Asp Glu Lys Asp Glu Pro Val Gln Glu Val Val Val Gly Gly Glu Leu
 85 90 95

Gln Asp His Ser Arg Glu Ala Ile Thr Glu Asn Leu Gln Lys Leu His
 100 105 110

Glu Ser Lys His Pro Glu Val Lys Gln Glu His Ala His Arg Thr Lys
 115 120 125

Val Ser Gln Gly Asp Leu Ser Asn Phe Asp Ala Ala Cys Ser Glu Ile
 130 135 140

Glu Ser Phe Lys Pro His Glu Ser Asp Val Glu Arg Leu His Leu Ala
 145 150 155 160

Leu Asp Thr Leu Glu Glu Leu Ser His Asp Ile Glu Phe Gly Val Lys
 165 170 175

Leu Thr Ser Asp Lys Ala Ile Phe Gln Ser Phe Val Asn Ile Ala Asn
 180 185 190

Gly Ala Ser Asp Pro Lys Ile Thr Glu Lys Val Tyr Arg Val Met Gly
 195 200 205

Ser Ser Leu Arg Asn Asn Pro Glu Ala Ile Ser Asn Ile Leu Thr Asn
 210 215 220

Phe Asp Lys Ser Tyr Val Asp Asn Leu Phe Glu Gln Leu Ala Asn Glu
 225 230 235 240

Asn Asp Val Leu Gln Lys Arg Ile Leu Gly Ile Ile Gln Ala Leu Val
 245 250 255

Gln Asn Ser His Phe Ala Arg Gln Tyr Phe Ser Phe Asp His Ser Ser
 260 265 270

<400>	441						
atgatttttt	ccttgatttt	agagctgtta	attatacctt	ttttgttccc	aaataagcgc	60	
taaaaatgat	tgaaatataa	aataactaatt	attccaggtc	aaagtaaaca	ctataaaaaca	120	
atataatttca	ataacaggag	cagtaatttag	cttcaacatc	aaggtactct	tttattttttc	180	
tacaaaaaac	acatctgaag	tagctcttat	ccatagatcc	aaatatttta	acctttttttt	240	
tttctacttc	tcattctact	ttttttgcaa	cacttagtcg	tcacaacgcc	aatgaccata	300	
ccattaatttt	caataatcaa	atcaagagct	tatttgtatc	ctctcaaggt	atgttaatgt	360	
attaacaaca	ccgattctat	ttcaccaact	aacacgacag	aaaggggttg	tactatttttg	420	
taacacatcc	caccgtttgg	ccctttttca	taaccataatt	gataacctcaa	ttggctcctta	480	
cactagtcct	taccctgatt	atgtttttcat	tgttcttccc	acctcaagct	attgtatata	540	
cattgttaat	gggaccatta	ggggtgattg	gtgcgtggta	tagtttgatc	ctgcaagcga	600	
gcacattgtc	tatatttggt	gtcacaaatat	ccttaatgcc	tcacatacaa	cgagtggcat	660	
atgatgcaat	attgagtaga	gagtggtgcaa	atgatgtggg	actaatggga	aaacttagga	720	
gggtatagaaa	actaccatt	agagtaaggg	ccagagaata	ccttaaggcc	attccagatt	780	
tttctgactct	tccttctct	ttgctcaagc	tacttgtgtt	tttcgggtatt	tacttctaac	840	
cccttgtagg	tccaatcatt	gtattgtttt	tccaatcttc	caagcgtgga	ctaaaggcac	900	
atgcaagata	ctttaagttg	aaagggtttc	tgcgtagtga	cataagaaca	atccacaagc	960	
taaacagacc	agcatatatg	gggtacggag	tggttgcgct	ttggctcgag	ctgtttccat	1020	
ttatcaatat	gttttttatg	ttcaccaata	ctttgggagc	tgctttgtgg	gcagttgata	1080	
ttgaacaaca	agagaaggcc	gtcacgata	atgtggccgc	agctactacc	accgccacag	1140	
atacgaatat	cgtaactcaa	caaggctag	ttatacccg	acacaatgaa	ccagcaata	1200	
atacactga	ggctacccca	aaaactgcta	caaataccat	ctaa		1244	

450

<210> 442

<211> 247

<212> PRT

<213> Candida albicans

<400> 442

Met Phe Ser Leu Phe Phe Pro Pro Gln Ala Ile Val Tyr Thr Leu Leu
 1 5 10 15
 Met Gly Pro Leu Gly Val Ile Gly Ala Trp Tyr Ser Leu Ile Ser Gln
 20 25 30
 Ala Ser Thr Leu Ser Ile Phe Val Val Thr Ile Ser Leu Met Pro His
 35 40 45
 Ile Gln Arg Val Ala Tyr Asp Ala Ile Leu Ser Arg Glu Cys Ala Asn
 50 55 60
 Asp Val Val Leu Met Gly Lys Leu Arg Arg Tyr Arg Lys Leu Pro Ile
 65 70 75 80
 Arg Val Arg Ala Arg Glu Tyr Leu Lys Ala Ile Pro Asp Phe Ser Ile
 85 90 95
 Phe Pro Phe Ser Leu Leu Lys Leu Leu Val Phe Phe Gly Ile Tyr Phe
 100 105 110
 Ile Pro Phe Val Gly Pro Ile Ile Val Leu Phe Phe Gln Ser Ser Lys
 115 120 125
 Arg Gly Leu Lys Ala His Ala Arg Tyr Phe Lys Leu Lys Gly Phe Ser
 130 135 140
 Arg Ser Asp Ile Arg Thr Ile His Lys Leu Asn Arg Pro Ala Tyr Met
 145 150 155 160
 Gly Tyr Gly Val Val Ala Leu Trp Leu Glu Ser Phe Pro Phe Ile Asn
 165 170 175
 Met Phe Phe Met Phe Thr Asn Thr Leu Gly Ala Ala Leu Trp Ala Val
 180 185 190
 Asp Ile Glu Gln Gln Glu Lys Ala Val Thr Glu Asn Val Ala Ala Ala
 195 200 205
 Thr Thr Thr Ala Thr Asp Thr Asn Ser Val Asn Gln Gln Gly Leu Val
 210 215 220
 Ile Pro Val His Asn Glu Pro Ala Thr Asn Ile Pro Glu Ala Thr Pro
 225 230 235 240
 Lys Thr Ala Thr Asn Thr Ile
 245

<210> 443
 <211> 2270
 <212> DNA
 <213> *Candida albicans*

<400> 443
 gcattttact tatttagata ttacttcata ttgcttttat ttagattgat tttgtttaac 60
 agtgaaagtt tttatttttt ttttgtttaa agttttttatt ttttttttgt ttaaagtttt 120
 tgtattatac aatattttaa ttatagtaat catcctataa atttcaaagt caaaagacag 180
 atcttaaggt ctaattaata actctctatg gccttctgtg tcaaatttgt gtcgtttgat 240
 aacaagtttg gaacggtaat ggttgaaatt agaaaagaaa aaaattacac atggtagcag 300
 ctgatgtata gaactttcta gcaaaaaaaa aaagaaagaa tttttttttc ttccattttt 360
 caaatttgag agatcgaaat aattttcttg aattttattaa aaggggaaccc cttcccga 420
 aatccaaaac caaaacttcc acccaaatat caaataacta acttatcatt ccaacagata 480
 atattcccac ttcaataaca atgacaacag ctgacgaata caaagcagaa ggtaacaaat 540
 attttgctgc taaagatttt gaaaaggcga ttgaagcatt cactaaagca attgaagcat 600
 cacctgaacc aaaccatggt ctttattcaa atcgttctgg atcttatgcc tctttaaaag 660
 attttaacaa cgcattaaaa gatgctcaag aatgtgtcaa gatcaatcct agttgggcca 720
 aagggtataa tagaattgct ggggctgaat ttgggttagg taattttgat caagccaaat 780
 ccaattatga aaaatgtttg gagttggatc caaataatgc catggctaaa gaaggtttaa 840
 aatcagttga atctgcttta tcatctggtg gtgggtgatga caaggattta ggatttggt 900
 aaattttaaa tgatccta atcttatacta aattgaaaaa taatcctaaa acaagtgaat 960
 ttatgaatga tctcaattt gttgctaaac ttgaacgtct taaaactaat ccacaattgg 1020
 gtaatcctga tatgtttagt gatccaagat tattgacggc ttttgctgct ttaatgggt 1080
 ttgacatgga tttaacaaat atgggattca ctgctccaaa cgaatcacaa tccaatgcat 1140
 cagaacccaa actggaacca aaatcagtac cagaatctaa accagaacca aaagcagaac 1200
 aaaaggaaga agaatcaacc tcagccaaag atgaagacac tccaatgact gatgcccaag 1260
 acgacactaa tgataatgat gccaaaaccc aagctgacaa tgctaaagct gaaggtaatg 1320
 ccttatacaa gaaacgtcaa tttgatgaag caattgccgc ctataataag gcttggaat 1380
 tacataagga tatcacttat ttaaacaatc gtgctgctgc cgaatatgaa aaagggtgatt 1440
 atgatcctga tattgctaca tcttgctaca ccattgatga aggtagagac atgagagctg 1500
 attataaatt gattgctaaa tcatttgcta gattaggtaa tatttatttg aaaaaagatg 1560
 aattaccgga agcagtga aaatttgaaa aatctttaac tgaacatcgt acccctgatg 1620
 ttttaataaa attaagatca actcaacgtg aaattaaaac tagagaatta aatgcttata 1680
 tagatccaga aaaggctgaa gaagcaagat tacaaggtaa agaattttc accaaaggag 1740
 attggccaaa tgccgttaag gcttatactg aaatgattaa aagagcacca gaagatgcta 1800
 gaggatattc taatcgtgct gctgcattgg caaaatttgt atcatttcct gatgctatac 1860
 aagattgtaa taaagccatt gaaaaagatc caaatttcat tagagcttat attagaaaag 1920
 ctaatgctca attggcaatg aaagaatata gtcatgtcat ggatacttta accgaggcaa 1980
 gaactaaaga tgttgaaatt ggtggtaaat caattcatga aattgatgaa ttaatgaata 2040
 aagctactta tcaaagattt caagccattg aagggtgaaac tcctgaacaa actatggaaa 2100
 gagtttctaa agatccagaa attgttcaaaa ttttacaaga tccagtaatg caagggaattt 2160
 tagctcaagc tagagaaaat cctgctgctt tacaagatca tatgaaaaat cctgaagttt 2220
 ataaaaaaat taatatgttg attgctgctg gtgtttattcg taccagataa 2270

<210> 444
 <211> 589
 <212> PRT
 <213> *Candida albicans*

<400> 444
 Met Thr Thr Ala Asp Glu Tyr Lys Ala Glu Gly Asn Lys Tyr Phe Ala
 1 5 10 15
 Ala Lys Asp Phe Glu Lys Ala Ile Glu Ala Phe Thr Lys Ala Ile Glu
 20 25 30

452

Leu Ile Ala Lys Ser Phe Ala Arg Leu Gly Asn Ile Tyr Leu Lys Lys
 340 345 350
 Asp Glu Leu Pro Glu Ala Val Lys Asn Phe Glu Lys Ser Leu Thr Glu
 355 360 365
 His Arg Thr Pro Asp Val Leu Asn Lys Leu Arg Ser Thr Gln Arg Glu
 370 375 380
 Ile Lys Thr Arg Glu Leu Asn Ala Tyr Ile Asp Pro Glu Lys Ala Glu
 385 390 395 400
 Glu Ala Arg Leu Gln Gly Lys Glu Tyr Phe Thr Lys Gly Asp Trp Pro
 405 410 415
 Asn Ala Val Lys Ala Tyr Thr Glu Met Ile Lys Arg Ala Pro Glu Asp
 420 425 430
 Ala Arg Gly Tyr Ser Asn Arg Ala Ala Ala Leu Ala Lys Leu Leu Ser
 435 440 445
 Phe Pro Asp Ala Ile Gln Asp Cys Asn Lys Ala Ile Glu Lys Asp Pro
 450 455 460
 Asn Phe Ile Arg Ala Tyr Ile Arg Lys Ala Asn Ala Gln Leu Ala Met
 465 470 475 480
 Lys Glu Tyr Ser His Val Met Asp Thr Leu Thr Glu Ala Arg Thr Lys
 485 490 495
 Asp Val Glu Leu Gly Gly Lys Ser Ile His Glu Ile Asp Glu Leu Met
 500 505 510
 Asn Lys Ala Thr Tyr Gln Arg Phe Gln Ala Ile Glu Gly Glu Thr Pro
 515 520 525
 Glu Gln Thr Met Glu Arg Val Ser Lys Asp Pro Glu Ile Val Gln Ile
 530 535 540
 Leu Gln Asp Pro Val Met Gln Gly Ile Leu Ala Gln Ala Arg Glu Asn
 545 550 555 560
 Pro Ala Ala Leu Gln Asp His Met Lys Asn Pro Glu Val Tyr Lys Lys
 565 570 575
 Ile Asn Met Leu Ile Ala Ala Gly Val Ile Arg Thr Arg
 580 585

<210> 445

<211> 1019

<212> DNA

<213> Candida albicans

<400> 445

ccactaacaa actttttttt gactatacac cactgaaaaa aaaaaaaaaa tttttgtaaa 60
 aaatcttaag aatttcagtt tagaagggtat tcaacaacaa ccgaagagta tggtcaacat 120
 cgttataata gaatagaata agagcatgac aacaaaggga tacaagcttg aaaaaagaaa 180
 aaggggtggga tatcttaaaa ttattaaaga gtttttttta taacatgtca ttgagattga 240
 gattgggaat actgaattcg atttttaaagt cattggatgg gagagttaat tattcgtttt 300
 attattagga ttaccaatga atagtaatga agtgatggag agatagaatg aaagtattca 360
 gaagagcatc aagtccttta taagtttggtg agacataata tgtctacccc cttgtcaact 420
 tgtcataaat tttattgctc gtccctttaa agaaatgaat aaaaagattt actaacttaa 480
 tttcaattat ttatagaaag atgtctagat taaacgaata tcaagttatt ggtcgttaatt 540
 taccaactga atccgttcca gaaccaaagt tggtcagaat gagaattttt gtcctaaaca 600
 ccgttggtgc caaatcaaga tattggtatt tcttgcaaaa attgcataaa gttaaaaaag 660
 cttctgggtga aattgtatct gtcaacatta tttctgaagc taaaccaact aaagttaaaa 720
 cttttggtat ttggttaaga tatgaatcca gatctggtat tcataacatg tacaaagaat 780
 acagagatgt tactagagtt ggtgctggtg aaaccatgta ccaagattta gctgctagac 840
 acagagctag atttagaagt atccatattt tgaaagttgt tgaattagaa aaaactgatg 900
 atgttaaaag acaatacgtt aaacaatttt tgactaaaga tttgaaattc ccattaccac 960
 acagagtcga aaaatctaag aaattgttcc aagctactgc tccaaccact ttctactaa 1019

<210> 446

<211> 172

<212> PRT

<213> *Candida albicans*

<400> 446

Met Ser Arg Leu Asn Glu Tyr Gln Val Ile Gly Arg Asn Leu Pro Thr
 1 5 10 15

Glu Ser Val Pro Glu Pro Lys Leu Phe Arg Met Arg Ile Phe Ala Pro
 20 25 30

Asn Thr Val Val Ala Lys Ser Arg Tyr Trp Tyr Phe Leu Gln Lys Leu
 35 40 45

His Lys Val Lys Lys Ala Ser Gly Glu Ile Val Ser Val Asn Ile Ile
 50 55 60

Ser Glu Ala Lys Pro Thr Lys Val Lys Thr Phe Gly Ile Trp Leu Arg
 65 70 75 80

Tyr Glu Ser Arg Ser Gly Ile His Asn Met Tyr Lys Glu Tyr Arg Asp
 85 90 95

Val Thr Arg Val Gly Ala Val Glu Thr Met Tyr Gln Asp Leu Ala Ala
 100 105 110

Arg His Arg Ala Arg Phe Arg Ser Ile His Ile Leu Lys Val Val Glu
 115 120 125

Leu Glu Lys Thr Asp Asp Val Lys Arg Gln Tyr Val Lys Gln Phe Leu
 130 135 140

Thr Lys Asp Leu Lys Phe Pro Leu Pro His Arg Val Gln Lys Ser Lys
 145 150 155 160

Lys Leu Phe Gln Ala Thr Ala Pro Thr Thr Phe Tyr
 165 170

<210> 447
 <211> 932
 <212> DNA
 <213> *Candida albicans*

<400> 447
 tgtttacttt ttctgtagtt ttaaagtttc ctaatttaac ttccaaaagt ttcattaaca 60
 acaatattaa catacctttg tcacaagcaa ttatattgaa gttttttgat acaagtgtgt 120
 tgtttttttg tgtacatgtg agatatataa ttgtgtatat acagtcacgt gaatagagca 180
 gaaaaattac gaagtagaaa tattggtagc gcgttagggc tatagcccta tttagtttgt 240
 gcaccacacg acttacaatt tttttttttt tctttcttag aatccttgag gcactgacac 300
 tgtactctct ctctctctct ctctctctcg taggtagtga aaaatttcca ctagtcttcc 360
 cataaccacac ctaggttctt tcttttgga accactgagc agtaaatcaa tttacttgac 420
 gaagaagtct atacataaat ataaacttgt cccctccccc cctttttttt ttaactaact 480
 aagaagaaaa aattaaaaaa atgtctgacg ttgaacaaga acaaattggt gaagaagttg 540
 ttgttgaaaga acaatccggt gccatcacca ttgaagatgc tttaaaagtt gttttaagaa 600
 cttcttttagt ccatgatggt ttagctagag gtttaagaga agcttctaaa gctttatcta 660
 aaagagaagc tcaattatgt gttttgtgtg actctgttac tgaagaatca atcatcaa 720
 tgggtgaagc tttatgtaat gaaccagaag aaaaaatccc attgattaaa gtttccgatg 780
 ctaaattatt ggggtgaatgg gctggtttat gtcaattaga tagagatggg aatgctagaa 840
 aagttgttgg tgctcttgt gttgtgtgca aaaactgggg tgctgattct gatgaaagaa 900
 acatcttggt ggaacacttt tctcaacaat aa 932

<210> 448
 <211> 143
 <212> PRT
 <213> *Candida albicans*

<400> 448
 Met Ser Asp Val Glu Gln Glu Gln Ile Val Glu Glu Val Val Val Glu
 1 5 10 15
 Glu Gln Ser Gly Ala Ile Thr Ile Glu Asp Ala Leu Lys Val Val Leu
 20 25 30
 Arg Thr Ser Leu Val His Asp Gly Leu Ala Arg Gly Leu Arg Glu Ala
 35 40 45
 Ser Lys Ala Leu Ser Lys Arg Glu Ala Gln Leu Cys Val Leu Cys Asp
 50 55 60
 Ser Val Thr Glu Glu Ser Ile Ile Lys Leu Val Glu Ala Leu Cys Asn
 65 70 75 80
 Glu Pro Glu Glu Lys Ile Pro Leu Ile Lys Val Ser Asp Ala Lys Leu
 85 90 95
 Leu Gly Glu Trp Ala Gly Leu Cys Gln Leu Asp Arg Asp Gly Asn Ala
 100 105 110
 Arg Lys Val Val Gly Ala Ser Cys Val Val Val Lys Asn Trp Gly Ala
 115 120 125

456

Asp Ser Asp Glu Arg Asn Ile Leu Leu Glu His Phe Ser Gln Gln
 130 135 140

<210> 449
 <211> 881
 <212> DNA
 <213> Candida albicans

<400> 449
 aaaatttcca atcttgaatt tcatcttcaa cgtcataaac ttgttctggt tgaaatttat 60
 cgtcttcatt atcgttgtca ttttcattgt cattgtcaat attacgggta cgatttttgtt 120
 ttccctttga agtctttgac tctagctggt catctgtcat tacccttggc ttgggtttgtc 180
 ttactgttga gcgatgagac aaactttttg attgattgca actgaacaaa aaaaaatagc 240
 acagacacac acacacacac acacacacaa ttttcagctc cttccaagtc gtgtttttttt 300
 ggaagaaaaa aaaaacaact tggccctaaa aactctatgc tctaaccgac aacattagat 360
 tactttgata actcacaacc tttaattaac actatctaca aaatatgaca agtacaccaa 420
 taacgtacaa gacactagta tgaaaggcaa gcacaaactt gcaaacaaaa aacccttaac 480
 ttttattata gttttgtttg atgttatttt gttttatact aactaaaatc tgttttttttt 540
 ttttttcaaa ggccgattct atatttaatg atctaataca caatatcatt aaacaacata 600
 cattaaccag ttttaaccaat attaaagatc attcctcatt attaaattca tctaatagca 660
 atactaatag caataccaac ggtacaattg ccagtaattg tggaaatggg actacaagtg 720
 atgaaaataa tgaaattgaa aattcaacaa ttcaagataa atcaaaatta aaacaattag 780
 aaacttcaag gtatttcga tgtcttaatt gtggtagaaa tattgccggt ggaagatttg 840
 catctcatat aagtaagtgt ttagaacgga aacggaaatg a 881

<210> 450
 <211> 126
 <212> PRT
 <213> Candida albicans

<400> 450
 Met Leu Phe Cys Phe Ile Leu Thr Lys Ile Cys Phe Phe Phe Phe Ser
 1 5 10 15
 Lys Ala Asp Ser Ile Phe Asn Asp Leu Ile Asn Asn Ile Ile Lys Gln
 20 25 30
 His Thr Leu Thr Ser Leu Thr Asn Ile Lys Asp His Ser Ser Leu Leu
 35 40 45
 Asn Ser Ser Asn Ser Asn Thr Asn Ser Asn Thr Asn Gly Thr Ile Ala
 50 55 60
 Ser Asn Gly Gly Asn Gly Thr Thr Ser Asp Glu Asn Asn Glu Ile Glu
 65 70 75 80
 Asn Ser Thr Ile Gln Asp Lys Ser Lys Leu Lys Gln Leu Glu Thr Ser
 85 90 95
 Arg Tyr Phe Arg Cys Leu Asn Cys Gly Arg Asn Ile Ala Gly Gly Arg
 100 105 110
 Phe Ala Ser His Ile Ser Lys Cys Leu Glu Arg Lys Arg Lys
 115 120 125

<210> 451
 <211> 5344
 <212> DNA
 <213> *Candida albicans*

<400> 451
 ctctagaagt aggcacatcgt atagtgtata aacactcaat aagtaatgaa gaaacacggt 60
 ttgtttgtgca atggttagctg gcgagctcaa tattgggtct ctccgcgctc tgtctgcctt 120
 gcattctact ttttttctcc ttatggaaaa cattagtact agtagtggtg gtagtagttg 180
 ctgttgtttg cactttgcac gtagttgttt tccctcatt ctttcatctg attattctgt 240
 ctttgttaac tgcatacaaa gggaggggaa gaagaaacaa caaaagggga atttgaatat 300
 acgtcaatct tttaatccta ctaccacggg gggggggggg gtcatacttc ttggtgtaaa 360
 taatgtatgg agattgaggt tattagactt ttagaaagag gtcttggttg agtaaggcgg 420
 gatagcacia ataatgcgtg tctaattggg cagagaataa tatgctttgg ggaacaatag 480
 aaagatgtag cgagagaaat agaattncaa gggttaaggat gattaacttt tttttttttt 540
 aatgcttgga gtactttgtt gttggaaaaga gtattgcaga agtaatagtt taataaaaaga 600
 aaagtatata acttttagtaa tcggagaaca attgaaatca atattttgaa aatatagttt 660
 tatagagtaa cctgggtcga ggtgaacccg aattcaatat tgggtttcgg ttgttatatg 720
 ctacataacc atcctcatct tgaatgaaac aaggataata gaaatgagta tattaacaa 780
 acaacattat gttgttactg ttgtattctg ttttttgggc attgccatgg taatttcata 840
 tttagtaaca atttagtgtt catcgtaagt ctctccttct ctgggagatg ttctctctct 900
 ctttctctct cttgttggtg ttgttggttaa ttgtaattg ttgattattg attgttcccc 960
 aattaaaatt ccgataaact tgaacaataa attgtcatca taaatttttt tttagaaaat 1020
 cactccataa attaaattta tttatatatt aaatttttaa tcggaacttc cgtcaattgg 1080
 attcggtttt tttttttttt atttgttcat tttttcttg attttatatt ctttttgctt 1140
 cctacttctc ttttattttc ttagtttcat aatttttgac agataatact tgaaactggt 1200
 taatttttaa tcaacttcgt gatttttttc cggaaatcta ataatatcaa tgaccagtaa 1260
 tctgccacca cttggttcta caactaacga tcagagacta ccccaaagcg gagtttctc 1320
 cataccacca aataaattgc ctttacctaa tgccaatgaa gattttgcca cgggtgtgtc 1380
 gaatggagat gttgactggc tatttcgagg taaatcaaaag aaattgggga aaaagatggc 1440
 taacaacaat gccataaagg atgaacgaaa gaatagtcac ggtaacatca aaaactcggg 1500
 aaaaactacc gcaaaaccca atgaaactaa acatgagtc aatgggtgaga agttagaatt 1560
 caatgttcca aaatctgtaa tgccaacaaa gcatacatcg tctgggaacc caaaagcacc 1620
 taccaatgga caaatctcaa atgtaacacc aagtcaacca agtccgaaac agaccacttc 1680
 tgggtcaaca atgcaaatg atatacctcc atatttctct aaacaaccag aaaaggcatc 1740
 aaagtctaat aaactaaaaa ttgggcggtt aagatcgtct tctgcatcaa cagtcgtacc 1800
 ttcacttaca acagcttcaa ctactactaa tctggagat cctaaaagtc aaccaaaaag 1860
 acggagcagt agttttaact ttgttactcc ttccttgacg agtgatttgg catatgacga 1920
 tctgcattg gtatctcaat tatcaaacaa ttcaaattct ctgaactcat cctcgcctaa 1980
 tgtttctcgt tcaaatagca aaaaagggtg gttattcagt tcactttcat caaaatttag 2040
 atcaagctcg gttcatcta aacaaccaca actgcattca tctctacac catcaaccac 2100
 aacgacaaat ggtggcggtg actcgtccgc tgcctcaaaa tcatcccatc actcccccac 2160
 atttaactct tcacttggtg gtccagtatc aaagcacaat cgagaagctg aagatttggg 2220
 gtctcttacc aatactttgc ctgctgggag tggaaatcca attaaacgta aaccatcaat 2280
 atcgggaaat tcaattttca aagattcatt tctcgatgat gcaagttctt caccgtcatc 2340
 ttcattaaac tctgatgggg ggcttaagtt tttcaggaga cgttcctctg tggcatctac 2400
 accatcaaca cagcgtcaa cacctcgagt gattttgaac aaaaacccca ataggagaaa 2460
 agtaccattt gaagaaatat ctgaagttcg attgcgtcgg gttacctttt ctgttgataa 2520
 actcgagcac gatccgaac agcagattcc ttcaagaaga cctaaacgag gtaatgtttt 2580
 aattccacag gacatcaatg caccacctcc aagactatgt cttgggattt cagttaatga 2640
 accaaataat aaagatgacg gtaaatcaca caaccattcc aaatatagtg atcatgaaat 2700
 tgcattagct gaagatgctc aacgcgagc aattattgaa gcagaaaaac atgctcaaga 2760
 agctcatcga caagccaaaa agattgctca agaagtttct gggatatagat cacatagatt 2820
 catatccatt aaagaagggtg gtagtggttg taattctaac accaacggca acgacaatga 2880

cgaagatgat gatgagggtg aagaagcagt tgataagaaa ttggcaaagt atgtttctgt 2940
 ggatggaccg ttgcatgtcc acgaacaaca tttcgaagaa gaaattgaaa gcaaaacagg 3000
 tgaaaagacc atttcattgg aaacaatcta tacaagatgt tgcattttac gagaaatttt 3060
 accaatccca gcaacattga aacaattgaa aaataagaca gcaccgttgg aagtgtttaa 3120
 gatgctcaac ccaaaaccaa cttaattgaa tgtgttatct ttttcagatt ttattgccat 3180
 tacacctatt aacacggtca tttttgataa cgtgactatg acaacagaga tgttgaaaaa 3240
 ctttcttgga tcgttgacat ataataaaca attggaaaag ttatcggtga gaaatgtttc 3300
 cattgatgag ttgggatgga agtatttgtg tgaatttttg gcaacaaata aaacagttaa 3360
 gaaattggat atatcacaac aacgtatcaa gccagatacc ccagacacaa gcattcgtgg 3420
 taatatgaac tgggacttat ttattcgatc attaattttg cgtggtggaa tagaagaatt 3480
 ggttatcaat ggatgtaaac tatccgatgc aatatttgaa aagttcatca atcaagcgg 3540
 taagaagtca acctatcgat taggtattgc tggattatgat ttgaatgtta aaaaatcaga 3600
 aatggtcaca tcgtgggttaa ctgatggtaa ttctcaatgt gttggtgttg atattgcttt 3660
 taatgatttg agcaaggac aattacgtcc attcattaat gcgtttaaca ctggcaaagt 3720
 caacaattta gtgttttttt cattgaattc aaccaattta ctgaacattg aagaaaacttc 3780
 tgacttgatc aagtcattaa ttaattgttaa aacattacga ttttttagatt taagttccat 3840
 acctaatatc ttcccgaata taattaccca tttggacaaa tacttgccca gatatcctaa 3900
 tcttcgaaga atacattttg atcttaattga aataaccgca caagctattg ggtcattggc 3960
 ggggtgttta ctgaaaatgc cccaattagt tcatgtctcg ttattgggta atagaaattt 4020
 gtcaactacg tcagcagcta cattatacgg agcagttaaa caatccaaga ccttgtttgc 4080
 tcttgatttg gactacgatt taataacctga tcaattatca caacgtattg ctttttattt 4140
 gatgagaaac ttggaataca ctttgaagcc atctcatggc ggcaatattg aaagcaatcc 4200
 agaaaaacca gaggatttga tgtatgatgg atcgttatta atggaaacag ctgaaaaatt 4260
 attagttgaa atagaaaagg gtaagaaaga ggatatcaaa atgcaaagaa ttatatccga 4320
 ttcagtattg gaaagaacaa gatcgattcg taaggatatt cacaaaacca ttgatacatt 4380
 attcgaacaa agaaatttag gtaaattatc atttgaagggt aaagagaatt tagttcgatt 4440
 ttgtttatta gattcgtctt tagaaaaatt gggtgttatg gttgaggaac atgccaacgg 4500
 attattatta acaccaacga cctccacgga cgatctcaga agtagagcca tgtcgccatc 4560
 ggctactggt gatacaatcc atgaaagtgc aaatgagttg attactgctg gaccaatttt 4620
 atcaccacat gtcaatagga aagcagaaca aagctcgtat ttcccagtgt ttgccaataa 4680
 tgataatttg acccctcatc aagttgtcgt tgagtcaaat gatgaaggta gagatgttcc 4740
 aatagataaa atgacaggac gaccagtttt gattcgatca attagtcaaa cttctgtgca 4800
 tgcaaaagag caagaaattg aagaagggga gcttcataaa tttggattct ttattcaaca 4860
 aaaagagaga caaaaacaac aacaacaaca acaacaaca cagaactcac accaccagca 4920
 ccaaccggcc cagctgatcc aacaagaaaa ccagctgccg ctgccacaac aaggaaaata 4980
 tgaagattta ccgatattaa atacattacc gtcaggacca gagttgagag atgctataat 5040
 ggcagctaag ggagtagcaa atgttactga attaatgtat cgaattaata atcatcgtgt 5100
 taaaatcgat gcccatcgaa caaaacacca catgaattg aacaaacca attctgacaa 5160
 agtagttgag gatgaagttg aagtttctga taatgcctct attgattcta ctaatggtga 5220
 cgatttacat caacttggtg acggtaaaca taatggtaat ggtacggttg atcccatggt 5280
 tagtgaagtt tatgacaagt tgttaaatga tgctgaacga gtcagactga atagagatat 5340
 ataa 5344

<210> 452
 <211> 1364
 <212> PRT
 <213> Candida albicans

<400> 452
 Met Thr Ser Asn Ser Pro Pro Leu Gly Ser Thr Thr Asn Asp Gln Arg
 1 5 10 15
 Leu Pro Gln Ser Gly Val Ser Ser Ile Pro Thr Asn Lys Leu Pro Leu
 20 25 30
 Pro Asn Ala Asn Glu Asp Phe Ala Thr Gly Val Ser Asn Gly Asp Val

35					40					45					
Asp	Trp	Leu	Phe	Arg	Gly	Lys	Ser	Lys	Lys	Leu	Gly	Lys	Lys	Met	Ala
50						55					60				
Asn	Asn	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Lys	Asn	Ser	His	Gly	Asn	Ile
65					70					75					80
Lys	Asn	Ser	Glu	Lys	Thr	Thr	Ala	Lys	Pro	Asn	Glu	Thr	Lys	His	Glu
				85					90					95	
Ser	Asn	Gly	Glu	Lys	Leu	Glu	Phe	Asn	Val	Pro	Lys	Ser	Val	Met	Pro
			100					105					110		
Thr	Lys	His	Thr	Ser	Ser	Gly	Asn	Pro	Lys	Ala	Pro	Thr	Asn	Gly	Gln
		115					120					125			
Ile	Ser	Asn	Val	Thr	Pro	Ser	Gln	Pro	Ser	Pro	Lys	Gln	Thr	Thr	Ser
130						135					140				
Gly	Ser	Thr	Asn	Ala	Asn	Asp	Ile	Pro	Pro	Ile	Ser	Pro	Lys	Gln	Pro
145					150					155					160
Glu	Lys	Ala	Ser	Lys	Leu	Asn	Lys	Leu	Lys	Ile	Gly	Arg	Ser	Arg	Ser
				165					170					175	
Ser	Ser	Ala	Ser	Thr	Val	Val	Pro	Ser	Ser	Thr	Thr	Ala	Ser	Thr	Thr
			180					185					190		
Thr	Asn	Pro	Gly	Asp	Pro	Lys	Ser	Gln	Pro	Lys	Arg	Arg	Ser	Ser	Ser
		195					200					205			
Phe	Asn	Phe	Val	Thr	Pro	Ser	Leu	Thr	Ser	Asp	Leu	Ala	Tyr	Asp	Asp
		210				215					220				
Pro	Ala	Leu	Val	Ser	Gln	Leu	Ser	Asn	Asn	Ser	Asn	Ser	Ser	Asn	Ser
225					230					235					240
Ser	Ser	Pro	Asn	Val	Ser	Arg	Ser	Asn	Ser	Lys	Lys	Gly	Gly	Leu	Phe
				245					250					255	
Ser	Ser	Leu	Ser	Ser	Lys	Phe	Arg	Ser	Ser	Ser	Ala	Ser	Ser	Lys	Gln
			260					265					270		
Pro	Gln	Ser	His	Ser	Ser	Ser	Thr	Pro	Ser	Thr	Thr	Thr	Thr	Asn	Gly
		275					280						285		
Gly	Gly	Asn	Ser	Ser	Ala	Ala	Pro	Lys	Ser	Ser	His	His	Ser	Pro	Lys
		290				295					300				
Phe	Asn	Pro	Ser	Leu	Val	Gly	Pro	Val	Ser	Lys	His	Asn	Arg	Glu	Ala
305					310					315					320
Glu	Asp	Leu	Val	Ser	Leu	Thr	Asn	Thr	Leu	Pro	Ala	Gly	Ser	Gly	Ile
				325					330					335	
Pro	Ile	Lys	Arg	Lys	Pro	Ser	Ile	Ser	Gly	Asn	Ser	Ile	Phe	Lys	Asp

460

340	345	350
Ser Phe Leu Asp Asp Ala Ser Ser Ser Pro Ser Ser Ser Leu Asn Ser		
355	360	365
Asp Gly Gly Leu Lys Phe Phe Arg Arg Arg Ser Ser Val Ala Ser Thr		
370	375	380
Pro Ser Thr His Ala Ser Thr Pro Arg Val Ile Leu Asn Lys Asn Pro		
385	390	395
Asn Arg Arg Lys Val Pro Ile Glu Glu Ile Ser Glu Val Arg Leu Arg		
405	410	415
Arg Val Thr Phe Ser Val Asp Lys Leu Glu His Asp Pro Gln Gln Gln		
420	425	430
Ile Pro Ser Arg Arg Pro Lys Arg Gly Asn Val Leu Ile Pro Gln Asp		
435	440	445
Ile Asn Ala Pro Pro Pro Arg Leu Cys Leu Gly Ile Ser Val Asn Glu		
450	455	460
Pro Asn Asn Lys Asp Asp Gly Lys Ser His Asn His Ser Lys Tyr Ser		
465	470	475
Asp His Glu Ile Ala Leu Ala Glu Asp Ala Gln Arg Arg Ala Ile Ile		
485	490	495
Glu Ala Glu Lys His Ala Gln Glu Ala His Arg Gln Ala Lys Lys Ile		
500	505	510
Ala Gln Glu Val Ser Gly Tyr Arg Ser His Arg Phe Ile Ser Ile Lys		
515	520	525
Glu Gly Gly Ser Val Gly Asn Ser Asn Thr Asn Gly Asn Asp Asn Asp		
530	535	540
Glu Asp Asp Asp Glu Val Glu Glu Ala Val Asp Lys Lys Leu Ala Asn		
545	550	555
Asp Val Ser Val Asp Gly Pro Leu His Val His Glu Gln His Phe Glu		
565	570	575
Glu Glu Ile Glu Ser Lys Thr Gly Glu Lys Thr Ile Ser Leu Glu Thr		
580	585	590
Ile Tyr Thr Arg Cys Cys His Leu Arg Glu Ile Leu Pro Ile Pro Ala		
595	600	605
Thr Leu Lys Gln Leu Lys Asn Lys Thr Ala Pro Leu Glu Val Leu Lys		
610	615	620
Met Leu Asn Pro Lys Pro Thr Leu Ile Asp Val Leu Ser Phe Ser Asp		
625	630	635
Phe Ile Ala Ile Thr Pro Ile Asn Thr Val Ile Phe Asp Asn Val Thr		

645					650					655					
Met	Thr	Thr	Glu	Met	Leu	Lys	Asn	Phe	Leu	Gly	Ser	Leu	Thr	Tyr	Asn
			660					665					670		
Lys	Gln	Leu	Glu	Lys	Leu	Ser	Leu	Arg	Asn	Val	Ser	Ile	Asp	Glu	Leu
		675					680					685			
Gly	Trp	Lys	Tyr	Leu	Cys	Glu	Phe	Leu	Ala	Thr	Asn	Lys	Thr	Val	Lys
	690					695					700				
Lys	Leu	Asp	Ile	Ser	Gln	Gln	Arg	Ile	Lys	Pro	Asp	Thr	Pro	Asp	Thr
705					710					715					720
Ser	Ile	Arg	Gly	Asn	Met	Asn	Trp	Asp	Leu	Phe	Ile	Arg	Ser	Leu	Ile
				725					730					735	
Leu	Arg	Gly	Gly	Ile	Glu	Glu	Leu	Val	Ile	Asn	Gly	Cys	Lys	Leu	Ser
			740					745					750		
Asp	Ala	Ile	Phe	Glu	Lys	Phe	Ile	Asn	Gln	Ala	Val	Lys	Lys	Ser	Thr
	755						760					765			
Tyr	Arg	Leu	Gly	Ile	Ala	Gly	Ile	Asp	Leu	Asn	Val	Lys	Lys	Ser	Glu
	770					775					780				
Met	Val	Thr	Ser	Trp	Leu	Thr	Asp	Gly	Asn	Ser	Gln	Cys	Val	Gly	Val
785					790					795					800
Asp	Ile	Ala	Phe	Asn	Asp	Leu	Ser	Lys	Gly	Gln	Leu	Arg	Pro	Phe	Ile
				805					810					815	
Asn	Ala	Phe	Asn	Thr	Gly	Lys	Val	Asn	Asn	Leu	Val	Phe	Phe	Ser	Leu
			820					825					830		
Asn	Ser	Thr	Asn	Leu	Ser	Asn	Ile	Glu	Glu	Thr	Ser	Asp	Leu	Ile	Lys
		835					840					845			
Ser	Leu	Ile	Asn	Val	Lys	Thr	Leu	Arg	Phe	Leu	Asp	Leu	Ser	Ser	Ile
	850					855					860				
Pro	Asn	Ile	Phe	Pro	Lys	Ile	Ile	Thr	His	Leu	Asp	Lys	Tyr	Leu	Pro
865					870					875					880
Arg	Tyr	Pro	Asn	Leu	Arg	Arg	Ile	His	Phe	Asp	Leu	Asn	Glu	Leu	Thr
				885					890					895	
Ala	Gln	Ala	Ile	Gly	Ser	Leu	Ala	Gly	Cys	Leu	Ser	Lys	Met	Pro	Gln
			900					905					910		
Leu	Val	His	Val	Ser	Leu	Leu	Gly	Asn	Arg	Asn	Leu	Ser	Thr	Thr	Ser
		915					920					925			
Ala	Ala	Thr	Leu	Tyr	Gly	Ala	Val	Lys	Gln	Ser	Lys	Thr	Leu	Phe	Ala
	930					935					940				
Leu	Asp	Leu	Asp	Tyr	Asp	Leu	Ile	Pro	Asp	Gln	Leu	Ser	Gln	Arg	Ile

<400>	453						
acggaataat	gttatgcgaa	cagagtaact	gggattatca	acaagcatca	gtcaattttca	60	
aaaactcggc	tgcttctttg	cctagtgatg	catttgtaca	atagaattat	aattaaaaga	120	
aaggtagaat	agaattcaat	gtaggtgata	tcactttctg	agagttctta	ttacgatata	180	
taaaaatacat	agccaaaaat	ataatgaagt	aaaaacatgt	aactgtgtaa	ttttattcaa	240	
gtccaaagg	attgattaat	atttgagagt	ggttgacatg	taaaatatga	aggaagaccg	300	
ataacctaata	gttttctctca	gggtgtcgaa	ggctaggagg	aataaaatct	gagtagagaa	360	
ctttcgttta	tatcagtttt	ttgcaagaaa	aaaaggaaaa	caaaacaaaa	taacaccaca	420	
aacgaattac	acaagcacat	cctaaacacc	actctgttgg	agcaccaatc	aacctgagaa	480	
atgcaaactt	gtaataaaat	atgggataca	atatagcaat	ggtaacagat	tttttttacc	540	
ctcaacctgg	aggagtagag	tttcatgtgt	atcattttatc	acaaaaactc	attgaactag	600	
gacactcagt	ggttatcata	actcataaatt	attctcaag	aaatgggtga	cgagtattaa	660	
cgaattgggt	gaaagtgtat	tatgtaccac	tttgggtgat	ctatagaagc	tcagttttcc	720	
caactgtatt	tctgtgcttc	ccaatatattga	ggaatatctt	catacgagaa	aacattgaga	780	
ttattcacgg	acatggttcc	ttcagcacat	tatgccacga	agctatatta	catggccgaa	840	
caatgggatt	aaaaacagtc	ttcactgatc	attcactttt	tggatttgcc	gagattggat	900	
caattatggg	gaataaagca	ttaaaggttca	ctttcagtg	tggtggccat	gttatctgtg	960	
tcagtcacac	ctgtaaagaa	aacacgggtt	taaggaggat	aatagacccc	ataaaaggta	1020	
gtgtgatacc	gaatgcagtt	attctgaaag	atttcaagcc	caaatcgcat	tgtgttaaca	1080	
agaactatac	taagagatc	accttgtgg	tgatcacgag	attgtttcca	aataaaggag	1140	
ccgatctatt	aacggctggt	atcccccata	tttgccagtt	gaaacaaaaa	gtgaaatttc	1200	
taattgctgg	tgacggcccc	aagtttttag	atttgaaca	aatgagagaa	aagtactttc	1260	
ttcaggaaag	ggttacatta	gtaggcgcta	taaaacacga	agaagtaaga	gatgtaatgg	1320	
tccaagggtga	catatactta	catccttcat	taacagaggc	gtttggtaca	gttattgtgg	1380	
aagctgcac	atgtggggtta	tatgttgtca	ctacaaaaat	tggaggcata	cccgaagtct	1440	
taccaaacga	aatgacaagc	tttgcgtgaac	cgaagaaaaa	ctcacttatt	gatgctgcta	1500	
tagatgctat	aaataaaaatt	gaaagttaatg	aaatcgatac	ctcaaaattt	cacgatgcqg	1560	

ttgcaaagat gtacagttgg aatgatattg caagaagaac agaaaatggt tataattcac 1620
 ttgatttaga caaactaaac gagtcctttac ttcaccgatt acaaagatac tattgttggtg 1680
 gtataatagc aggcaaactt tatgctttat gtgtaatagt ggatattttt attttcgtga 1740
 tactagaatg gttgtatccc gctgatcata tcgataaagc aacaaaatgg ccactggcta 1800
 tcaaggaaga agacgagctg gaagaagaaa catttatttt tccgaacaaa gtaaattag 1859

<210> 454

<211> 452

<212> PRT

<213> *Candida albicans*

<400> 454

Met Gly Tyr Asn Ile Ala Met Val Thr Asp Phe Phe Tyr Pro Gln Pro
 1 5 10 15

Gly Gly Val Glu Phe His Val Tyr His Leu Ser Gln Lys Leu Ile Glu
 20 25 30

Leu Gly His Ser Val Val Ile Ile Thr His Asn Tyr Ser Ser Arg Asn
 35 40 45

Gly Val Arg Val Leu Thr Asn Gly Leu Lys Val Tyr Tyr Val Pro Leu
 50 55 60

Trp Val Ile Tyr Arg Ser Ser Val Phe Pro Thr Val Phe Ser Cys Phe
 65 70 75 80

Pro Ile Leu Arg Asn Ile Phe Ile Arg Glu Asn Ile Glu Ile Ile His
 85 90 95

Gly His Gly Ser Phe Ser Thr Leu Cys His Glu Ala Ile Leu His Gly
 100 105 110

Arg Thr Met Gly Leu Lys Thr Val Phe Thr Asp His Ser Leu Phe Gly
 115 120 125

Phe Ala Glu Ile Gly Ser Ile Met Gly Asn Lys Ala Leu Lys Phe Thr
 130 135 140

Phe Ser Asp Val Gly His Val Ile Cys Val Ser His Thr Cys Lys Glu
 145 150 155 160

Asn Thr Val Leu Arg Gly Ser Ile Asp Pro Ile Lys Val Ser Val Ile
 165 170 175

Pro Asn Ala Val Ile Ser Lys Asp Phe Lys Pro Lys Ser His Cys Val
 180 185 190

Asn Lys Asn Tyr Thr Lys Glu Ile Thr Ile Val Val Ile Thr Arg Leu
 195 200 205

Phe Pro Asn Lys Gly Ala Asp Leu Leu Thr Ala Val Ile Pro Lys Ile
 210 215 220

Cys Gln Leu Lys Pro Lys Val Lys Phe Leu Ile Ala Gly Asp Gly Pro
 225 230 235 240

Ser Gly Tyr Gly Glu Ala Phe Lys Trp Leu Ser Gln Tyr Ile

180

185

190

```
<210> 457
<211> 899
<212> DNA
<213> Candida albicans
```

<400>	457						
tatatgacgg	caagtgtctc	actgttgcac	tacgcgatgt	ttcttttctt	tggtcttcta	60	
agcgcgattt	taccagaact	agatggcgct	cgtgatcctg	aaaacgggga	gaaattttga	120	
gaacaccgct	ttattaggcg	aagcgggtggg	cacagctcac	gcgtaagggtg	ttcccattat	180	
ttctcaaagt	gatgcgaatt	tcagagaaca	cattaacctg	ggggccataa	acgcgacgtg	240	
ctaccatttt	cgttacgtat	acttagggcca	gagattacaa	catgactact	aatatcaaac	300	
ataaactctat	atataaggga	tgaagatgta	tgctttctta	gaatttcaaa	catgttccgt	360	
taaagttttta	cttttcgatt	tcaatttcga	ctgcatgatg	cttttcttag	gtagtttttt	420	
gttattaaat	agtatcataa	attcttgtct	ttttacataa	gaattaggaa	agtacagaac	480	
aagagcaaata	ttaatatata	atgtccgggtg	gtaaagggtgg	taaagctggg	tcagctgcta	540	
aagctttctca	atctagatct	gctaaagctg	gtttaacatt	cccagttggg	agagtgcaca	600	
gatttgctaag	aagaggtaac	tacgcccgaga	gaattgggtc	tggtgctcca	gtctatctaa	660	
ctgctgtctt	agaatatttg	gctgctgaaa	ttttagaatt	ggctggtaat	gctgctagag	720	
ataacaaaaa	aaccagaatt	attccaagac	atttacaatt	ggccatcaga	aatgatgatg	780	
aattgaacaa	gctattgggtg	aatgtttacca	tcgcccgaag	tggtgttttg	ccaaacattc	840	
accaaaactt	gttgccaaag	aagtctgccca	agactgccaa	agcttctcaa	gaactgttaa	899	

```
<210> 458
<211> 132
<212> PRT
<213> Candida albicans
```

<400>	458															
Met	Ser	Gly	Gly	Lys	Gly	Gly	Lys	Ala	Gly	Ser	Ala	Ala	Lys	Ala	Ser	
1				5					10					15		
Gln	Ser	Arg	Ser	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Pro	Val	Gly	Arg	Val	
			20					25					30			
His	Arg	Leu	Leu	Arg	Arg	Gly	Asn	Tyr	Ala	Gln	Arg	Ile	Gly	Ser	Gly	
		35					40					45				
Ala	Pro	Val	Tyr	Leu	Thr	Ala	Val	Leu	Glu	Tyr	Leu	Ala	Ala	Glu	Ile	
	50					55					60					
Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ala	Arg	Asp	Asn	Lys	Lys	Thr	Arg	Ile	
65					70					75					80	
Ile	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Asn	Asp	Asp	Glu	Leu	Asn	
				85					90					95		
Lys	Leu	Leu	Gly	Asn	Val	Thr	Ile	Ala	Gln	Gly	Gly	Val	Leu	Pro	Asn	
			100					105					110			
Ile	His	Gln	Asn	Leu	Leu	Pro	Lys	Lys	Ser	Ala	Lys	Thr	Ala	Lys	Ala	
		115					120					125				

<400> 460																
Met	Ser	Arg	Lys	Thr	Leu	Pro	Glu	Lys	Val	Tyr	Leu	Ser	Glu	Arg	Ile	
1				5					10					15		
Ile	Asp	Glu	Glu	Val	Ala	Val	Cys	Thr	Val	Ala	Ala	Glu	Val	Leu	Ala	
			20					25					30			
Ile	Phe	Thr	Leu	Val	Cys	Thr	Arg	Val	Phe	Ile	Ile	Phe	Phe	Thr	Ala	
		35					40					45				
Arg	Ile	Cys	His	Gly	Ile	Trp	Pro	Ser	Ser	Pro	Ser	Glu	Arg	Pro	Tyr	
	50					55					60					
His	Thr	Phe	Arg	Ala	Ala	Arg	Leu	Arg	Asn	Ser	Ser	Lys	Met	Val	Ser	
65					70					75					80	
Ser	Asn	Cys	Val	Leu	Ser	Glu	Cys	Gly	Gln	Phe	Lys	Arg	Leu	Thr	Ala	
				85					90					95		
Asn	Leu	Ser	Gln	Thr	Val	Ser	Pro	Ser	His	Phe	Leu	Asn	Leu	Ile	Lys	
			100					105					110			
Ala	Pro	Leu	Leu	Ile	Ala	Gln	Arg	Cys	Cys	Glu	Cys	Ala	Ser	Gly	Asn	
		115					120					125				

Phe Ile Ser Phe Asp Lys Glu Ser Asn Trp Asp Thr Ile Ser Thr Ile

475

<210> 472
 <211> 167
 <212> PRT
 <213> Candida albicans

<400> 472
 Met Thr Ser Phe Gln Ala Val Ser Phe Ala Leu Gly Cys Asn Thr Leu
 1 5 10 15
 Val Ala Cys Tyr Ala Phe Thr Val Leu Glu Lys Arg Ser Leu Met Thr
 20 25 30
 Ser Cys Thr Asn Ala Leu Ser Phe Leu Phe Phe Leu Leu Thr Leu Arg
 35 40 45
 Arg Ile His Arg His Trp Tyr Lys Pro Tyr Gly Ala Phe Leu Leu Ile
 50 55 60
 Phe Val Leu Thr Leu Arg Trp Phe Arg Gly Pro Ile Ala Trp Val Val
 65 70 75 80
 Val Asp Val Val Phe Ala Ser Cys Asn Val Val Phe Phe Ser Pro Ala
 85 90 95
 Leu Ser Asp Glu Asn Trp Pro Tyr Val Ser Phe Phe Gly Val Val Val
 100 105 110
 Val Ile Ala Val His Ile Ile Val Val Thr His Ile Gly Ala Phe Thr
 115 120 125
 Ala Cys Cys Leu Leu Lys Arg Val Ser Leu Lys Ser Ser Glu Glu Lys
 130 135 140
 Lys Lys Lys Lys Lys Lys Lys Glu Lys Ser Leu His Thr Glu Arg
 145 150 155 160
 Glu Lys Lys Lys Lys Lys Phe
 165

<210> 473
 <211> 1343
 <212> DNA
 <213> Candida albicans

<400> 473
 tcttatcttg tatgcccgat atagcaacct tgttggtacc aatctaacgg ttccgtact 60
 ttgcaatgaa gagatgagga ggcattgggtc acttatttaa tatgtacggg tggttacatg 120
 gagttgcttt ctttttttgt ctcagcagtc attgtgcgcc aaaaaaagag aaaaccgtga 180
 gccgaagtcc acgctctgga gttaggctct cccattacgg agagaagcat ttcctcagcc 240
 tgggagcccc gttggaacag tcaggctaaa ctgggccttc ctaccactg cttgctgttt 300
 ctactggac gcacaagggg attttctttc taccttcggc ttgcctcact gcgttggggc 360
 ttccaatgc aacttcgttc gtatgcatac aatcttttag atattatctt ttaaaattat 420
 tttaaaacaa ttttaaatgt atctcatatg cttttcttct gctgttgaaa aggctaaaca 480

aagaagatca ataagataaa atggctccat ctggtatgtg aactgcaata ttaatagcac 540
gagaaaattg agaggaagat agatgggaac tagtagagtt gatattgatg agatacgaaa 600
accacacgta aataaactat ccgacgacaa gaatagtga ttaaggactt gattaagata 660
tggtagagcaa cgtaattatc gggctcaaca gtttattagc aatcgttttg atagaagcgt 720
tgatgctgtg gaagttgttc tttttactac caacagccat taacaaatcc attagagtgt 780
tcgttcgttt ttctgctcag attcaagaaa attattccat cctcattata cttttttctt 840
ctatttcgtg ctccacgtcg aggtatcaag gaacatagtt tactaacatt aacgaattca 900
tctcctatga atttactttt tgtatagcta aggtactgct cgctaagaaa gctgtcgtta 960
agggactactaa tggtaagaag gctttgaagg tcagaacttc tgctaccttc agactaccaa 1020
agaccttgaa gttggctaga gctccaaaat atgcttccaa ggctgttcca cattacaaca 1080
gattggactc atacaagggtc attgagcaac caatcacttc tgaaaccgct atgaagaagg 1140
ttgaagatgg taacattttg gttttccaag tttccatgaa agctaacaaa taccaaataca 1200
agaaggccgt caaggaatta tacgaagttg acgtattgaa ggtaaacact ttggtttagac 1260
caaacggtac caagaaggct tacgtagat tgactgctga ctacgatgct ttggacattg 1320
ctaacagaat cggttacatt taa 1343

<210> 474

<211> 142

<212> PRT

<213> Candida albicans

<400> 474

Met Ala Pro Ser Ala Lys Ala Thr Ala Ala Lys Lys Ala Val Val Lys
1 5 10 15
Gly Thr Asn Gly Lys Lys Ala Leu Lys Val Arg Thr Ser Ala Thr Phe
20 25 30
Arg Leu Pro Lys Thr Leu Lys Leu Ala Arg Ala Pro Lys Tyr Ala Ser
35 40 45
Lys Ala Val Pro His Tyr Asn Arg Leu Asp Ser Tyr Lys Val Ile Glu
50 55 60
Gln Pro Ile Thr Ser Glu Thr Ala Met Lys Lys Val Glu Asp Gly Asn
65 70 75 80
Ile Leu Val Phe Gln Val Ser Met Lys Ala Asn Lys Tyr Gln Ile Lys
85 90 95
Lys Ala Val Lys Glu Leu Tyr Glu Val Asp Val Leu Lys Val Asn Thr
100 105 110
Leu Val Arg Pro Asn Gly Thr Lys Lys Ala Tyr Val Arg Leu Thr Ala
115 120 125
Asp Tyr Asp Ala Leu Asp Ile Ala Asn Arg Ile Gly Tyr Ile
130 135 140

<210> 475

<211> 429

<212> DNA

<213> Candida albicans

477

<400> 475

```

cttatagcaa ctactaaagc ttcagctgct aaaaaagctg ctttgaaagg tggttaacggg 60
aaaaaggctt taaaagttag aactagtact actttcagat taccaaaaaac cttaaaatta 120
accagatctc caaaatacca aagaaaatca gtcccacact acaacagatt ggatgcccac 180
aaaatcattg ttgctccaat tgccactgaa actgctatga aaaaagtcga agatggtaac 240
actttgggtt tccaagttga catcaaatcc aacaaacacc aaatcaaatac tgctgttaaa 300
gaattatacg atgttgatgc cttatacggtt aacactttga tcagacctaa cggtagcaag 360
aaagcttaca tcagattaac ctctgactac gatgctttgg atattgctaa cagaatcggg 420
tacatctaa

```

<210> 476

<211> 142

<212> PRT

<213> *Candida albicans*

<400> 476

```

Leu Ile Ala Thr Thr Lys Ala Ser Ala Ala Lys Lys Ala Ala Leu Lys
  1             5             10             15

Gly Val Asn Gly Lys Lys Ala Leu Lys Val Arg Thr Ser Thr Thr Phe
          20             25             30

Arg Leu Pro Lys Thr Leu Lys Leu Thr Arg Ser Pro Lys Tyr Gln Arg
      35             40             45

Lys Ser Val Pro His Tyr Asn Arg Leu Asp Ala His Lys Ile Ile Val
      50             55             60

Ala Pro Ile Ala Thr Glu Thr Ala Met Lys Lys Val Glu Asp Gly Asn
      65             70             75             80

Thr Leu Val Phe Gln Val Asp Ile Lys Ser Asn Lys His Gln Ile Lys
          85             90             95

Ser Ala Val Lys Glu Leu Tyr Asp Val Asp Ala Leu Tyr Val Asn Thr
      100             105             110

Leu Ile Arg Pro Asn Gly Thr Lys Lys Ala Tyr Ile Arg Leu Thr Ser
      115             120             125

Asp Tyr Asp Ala Leu Asp Ile Ala Asn Arg Ile Gly Tyr Ile
      130             135             140

```

<210> 477

<211> 117

<212> DNA

<213> *Candida albicans*

<400> 477

```

ttagataccc aacttagttc ttctccagtg tcttctttta gcattgtatc tgattttggt 60
gtcagttctc aatctgatcc attgtggcaa tggctctgtt tgcttttgag ccttagc 117

```

<210> 478

```

<400> 478
Leu Asp Thr Gln Leu Ser Ser Ser Pro Val Ser Ser Phe Ser Ile Val
 1              5              10              15

Ser Asp Phe Val Val Ser Ser Gln Ser Asp Pro Leu Trp Gln Trp Ser
      20              25              30

Val Leu Leu Leu Ser Leu Ser
      35

```

```
<210> 479
<211> 198
<212> DNA
<213> Candida albicans
```

```
<400> 479
atggttgacag tccttgggtcg tttacttgaa agaaactcaa tctacgttgc cactatcttt 60
ggcgggtgctt ttgctttcca aggttttttc gatgttgacg tgaacaaatg gtgggaggaa 120
cacaacaaag ctaaattatg gaaaaacgtc aaaggaaaat tccttgaagg tgaagggtgaa 180
gaagaagatg acgaataa                                     198
```

```
<210> 480
<211> 65
<212> PRT
<213> Candida albicans
```

```

<400> 480
Met Leu Thr Val Leu Gly Arg Leu Leu Glu Arg Asn Ser Ile Tyr Val
  1                      5                      10                      15

Ala Thr Ile Phe Gly Gly Ala Phe Ala Phe Gln Gly Phe Phe Asp Val
      20                      25                      30

Ala Val Asn Lys Trp Trp Glu Glu His Asn Lys Ala Lys Leu Trp Lys
      35                      40                      45

Asn Val Lys Gly Lys Phe Leu Glu Gly Glu Gly Glu Glu Glu Asp Asp
      50                      55                      60

Glu
  65

```

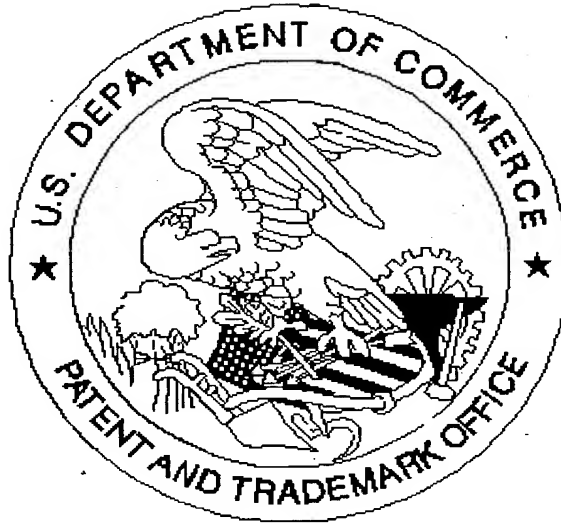
```
<210> 481
<211> 457
<212> DNA
<213> Candida albicans
```

<400> 481

```
<400> 483
ctacaattct tgagaagcct taacaccacc tttacctgat ttctttggca acaagttttg 60
atggatgttt ggtaacacac caccttgggc gatggtgaca tcaccaaca atttgtttaa 120
ttcttcatca tttctgatgg ccaattgtaa gtgtcttggg attattctgg atttcttgtt 180
```

```
<400> 484
Met Ser Gly Gly Lys Gly Lys Ala Gly Thr Ser Glu Lys Ala Ser Thr
   1           5             10              15
Ser Arg Ser Ala Lys Ala Gly Leu Thr Phe Pro Val Gly Arg Val His
          20            25            30
Arg Leu Leu Arg Lys Gly Asn Tyr Ala Gln Arg Ile Gly Ser Gly Ala
      35            40            45
Pro Val Tyr Leu Thr Ser Val Leu Glu Tyr Leu Ala Ala Glu Ile Leu
    50            55            60
Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Ser Arg Ile Ile
   65            70            75            80
Pro Arg His Leu Gln Leu Ala Ile Arg Asn Asp Glu Glu Leu Asn Lys
          85            90            95
Leu Leu Gly Asp Val Thr Ile Ala Gln Gly Gly Val Leu Pro Asn Ile
         100          105          110
His Gln Asn Leu Leu Pro Lys Lys Ser Gly Lys Gly Gly Val Lys Ala
       115          120          125
Ser Gln Glu Leu
     130
```

United States Patent & Trademark Office
Office of Initial Patent Examination -- Scanning Division



Application deficiencies found during scanning:

☐ Page(s) _____ of _____ were not present
for scanning. (Document title)

☐ Page(s) _____ of _____ were not
present
for scanning. (Document title)

☐ *Scanned copy is best available. Some figures are dark.*